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#### 14. ABSTRACT

Early identification of the specific proteins, which indicate delayed healing are critical to long-term success of the patient and the development of new treatments. It is the objective of this research to correlate changes in the proteome of wounds with clinical outcome and develop technology to sense these changes. A technique to classify a sampling timepoint based on a sliding 3 timepoint scale was developed. Proteomic analysis of the wound fluid utilized antibody dependent and independent techniques. The quantitative microarray demonstrated significantly different levels of S100A8 and TGFBR3 between healing and worsening wounds. The utilization of SRM-MS for wound fluid analysis is a significant development in the path to wound outcome diagnosis. Ultimately this work may allow the development of personalized wound care based on the proteomic characteristics of the wound.

#### 15. SUBJECT TERMS

Wound healing, proteomics, biomarkers, microarray, xerogel, SRM-MS, wound fluid, S100A8, S100A9, CXCL9, L-selectin, wound trajectory, MMP-9, TGFB3, RBP4

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### **INTRODUCTION:**

Early identification of the specific proteins, which indicate delayed healing are critical to long-term success of the patient and the development of new treatments. It is our hypothesis that real time sensing of the wound proteome can be used to predict wound outcome, resulting in tailored treatment that improve acute and chronic wound healing. The focus of this proposal is to correlate protein targets and wound outcome and develop a technology that can sense the microenvironment in acute and chronic wounds.

### **KEYWORDS:**

Wound healing, proteomics, biomarkers, microarray, xerogel, SRM-MS, wound fluid, S100A8, S100A9, CXCL9, L-selectin, wound trajectory, MMP-9, TGFB3, RBP4

## **OVERALL PROJECT SUMMARY:**

### **Statement of Work**

### Technical Objective 1:

Develop technologies for sensing multiple proteins in the wound microenvironment, in real time.

- Subtask 1.1 Develop xerogel-based elements.
- Subtask 1.2 Develop PBG-based sensor platforms.
- Subtask 1.3 Sensor design and evaluation using wound fluids.

### Technical Objective 2:

Test the suitability of our technology for the detection of multiple proteins from acute and chronic wounds in vitro and in vivo, and correlate results with clinical outcomes.

- Subtask 2.1 Collect fluid form subjects with pressure ulcers
- Subtask 2.2 Collect samples from wounds in porcine model
- Subtask 2.3 Proteomic analysis of wound fluid

## **Technical Objective 1:**

Subtask 1.1 Develop xerogel-based elements.

Luminescence based detection is frequently used in chemical, medical, and biomedical diagnostic applications. These sensors have several advantages including fast response and high efficiency. They are less prone to contamination, and display high sensitivity and specificity compared to competing approaches. Sol-gel derived xerogels have been widely used as the platforms for immobilization of active agents. They are meso-porous materials that encapsulate the optically active recognition elements while providing maximum surface interaction area. New integrated sensors that included the xerogel as the selective sensing element were fabricated and the polymer porous photonic bandgap (P³BG) structure as a tunable, high efficiency and noise-free bandpass filter and wavelength selector. This integration provided a template for luminescence based sensing with enhanced analytical signals (AS).

## Subtask 1.2 Develop PBG-based sensor platforms.

Monitoring of the biochemical environment on the curved surface of animal and human skin requires the development of a new class of sensing platform. A flexible optical sensing element that conforms to the curved surfaces could potentially be integrated into a bandage. Porous polymeric photonic bandgap (P³BG) structures have been demonstrated to be excellent platforms for gas and liquid analyte sensing. Two main mechanisms are generally used for sensing with these structures: 1) detecting the wavelength shift of the photonic bandgap caused by the refractive index change induced by filling the pores with gaseous or liquid analytes; and 2) embedding analyte specific luminophores within the pores and detecting the quenching of their luminescence due to binding with the analyte. Porous polymeric PBG structures were fabricated on large area flexible substrates (Figure 1).

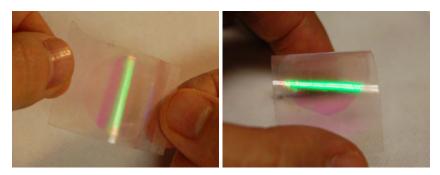
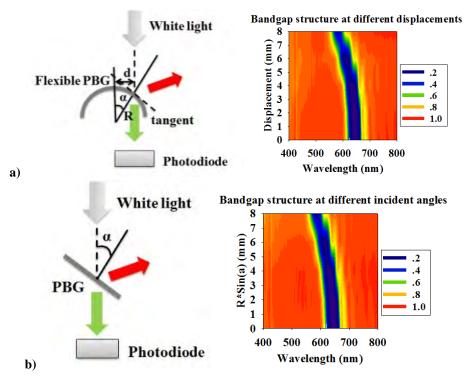


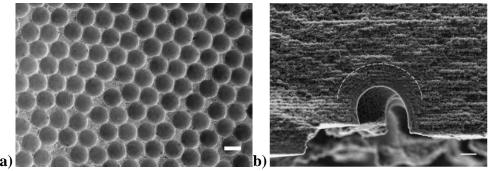
Figure 1. Images of flexible PBG structures.

The optical properties were characterized and compared as a function of angle of incidence for curved and flat porous polymer PBG structures. Specifically, samples were illuminated with the white light beam at positions with a displacement of d (d=0mm, 2mm, 4mm,...) from the center of the curved flexible PBG structure attached to the column of radius 12mm. The resulting transmission spectra, as a function of displacement, are plotted (Figure 2a). This result can be directly compared to the measurement of the transmission spectra of a flat PBG structure at angles  $\alpha$ = $sin^{-1}(d/R)$  (Figure 2b). The colors in the graph stand for the transmission efficiency. The dispersion curves from these two sets of data are in a good agreement with each other.

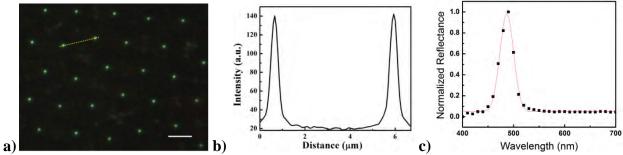


**Figure 2.** Measurement geometry and dispersion curves of a) flexible PBG structure for different displacements, d, and b) flat PBG structure at the corresponding incident angle  $\alpha = \sin^{-1}(d/R)$ .

Optical concentrators in the micron scale are important components for photonics devices. These micro-concentrators can be used to enhance the detection of fluorescence signals in biosensors. Micro-concave shaped Bragg reflector were fabricated using holographic photo-patterning by recording the interference of plane wave and divergent wave from the reflection of a spherical surface. The fabrication of these structures with dimensions down to several microns was successfully completed (Figure 3). The resulting structures demonstrate good light focusing (Figure 4). This method is more efficient and lower-cost when compared to other fabrication methods such as atomic layer deposition and electrochemical anodisation.



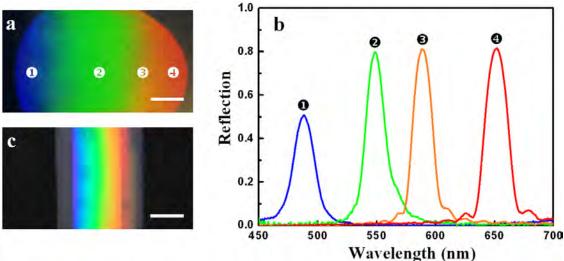
**Figure 3.** The SEM images of a) the top-view of the formed concave shaped Bragg reflector array (Scale bar:  $5 \mu m$ ); b) the cross-section of one concave shaped Bragg reflector (Scale bar:  $1 \mu m$ ), the white dash line indicates the profile of the concave layers.



**Figure 4.** The microscope images of a)the microscopic image of the micro-spherical array illuminated using white light (scale bar:  $5 \mu m$ ); b) The variation of the gray value across the centers of two concave shaped Bragg reflectors and c) The normalized reflectance spectrum of the focusing points.

A one-step fabrication method was used to create a graded holographic photopolymer reflection grating by using cylindrical lens. The period of the Bragg reflector at different lateral positions along the structure is varied gradually, leading to a unique rainbow-colored reflection image in the same viewing angle (Figure 5). Compared to previously reported graded photonic or plasmonic structures prepared by expensive focus ion beam (FIB) milling or electron beam lithography techniques, this holographic photopatterning method is low-cost and amenable to large area fabrication. The dimension of these grating is scalable by using cylindrical lenses with different focal lengths and diameters.

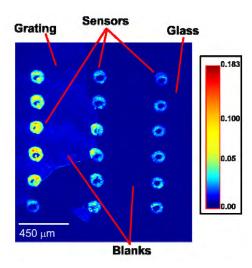
These graded holographic photopolymer reflection gratings provide a low-cost and light-weight solution for multispectral imaging technology. By integrating these grating filters with other imaging devices, they can be applied in bio-imaging and sensing. Sensing for wound healing involves analyzing multiple proteins and growth factors in the wound microenvironment. The graded grating has the potential to serve as multiplexed-channel analyte sensors. Series of fluorescent labels with distinctive emission wavelengths can be employed to detect multiple analytes on one sensor.



**Figure 5.** a) The reflection image of the graded holographic photopolymer grating under white light illumination; b) The reflection spectra measured at different positions indicated by circles in (a); c) A second example of a graded holographic photopolymer grating fabricated using a shorter focal length cylindrical lens. Scale bar: 5 mm.

## Subtask 1.3 Sensor design and evaluation using wound fluids.

Oxygen responsive sensor platforms were fabricated by pin printing tris (4,7-diphenyl-1,10-phenanthroline) ruthenium(II) ( $[Ru(dpp)_3]^{2+}$ ) doped sols onto reflective Bragg gratings. The polymeric reflective Bragg gratings were fabricated using holographic lithography method. In an epi-luminescence configuration, these Bragg gratings were designed to reflect selectively the  $O_2$  responsive  $[Ru(dpp)_3]^{2+}$  emission toward the detector to enhance the emission signal intensity. The results show that this hybrid sensor platform exhibits linear, statistically equivalent  $O_2$  sensitivities and yields up to an eight fold increase in analytical signal in comparison to the original sensor platform consists only with pin printing tris(4,7-diphenyl-1,10 phenanthroline) ruthenium(II) ( $[Ru(dpp)_3]^{2+}$ ) doped sols (Figure 6).



**Figure 6.** False-color image at 610 nm in the presence of 50%  $N_2$ ; an  $O_2$  responsive hybrid pin printed sol-gel sensor array comparing with an original pin printed sol-gel sensor array.

The PIXIES (protein imprinted xerogels with integrated emission site) platform was used to detect cytokines of both in vitro and in vivo wound fluids. Porcine wound fluids were analyzed for KGF, IL-1, IL-6, IL-12, TNF $\alpha$  TGF-beta, VEGF and EGF. Detection limits were  $\leq 2$  pg/ml and results were compared with ELISA.

Preliminary studies were undertaken to evaluate novel amino acid-modified hydrogel materials for wound healing. HaCaT keratinocyte cells were tested for ability to attach and proliferate on these materials and culture fluid was collected for growth factor/cytokine analysis using PIXIES.

Ultimately issues remain with implementation of PIXIES for wound sensing. The primary issue is the long timeline ahead of the technology. The PIXIES sensor technology must be integrated into another platform for use. Ultimately, it is not a common technology and has a long road to bedside use due to the early stages of the technology. Additionally, the wound bed presents an extremely challenging environment for any type of proteomic technology. Wound fluid is a complex mixture of proteins and protein fragments due to the aggressive proteolysis in the environment. PIXIES is a molecular imprinting technology and although it has been shown to work well with intact proteins, but protein fragments are likely abundant in wound fluid and it may prove difficult to keep the fragments necessary for fluorescence change to occur in a timely fashion. During the analysis of samples using iTRAQ technology as part of the planned workflow for the proteomic analysis, a new potential tool for analysis of the wound fluid in a cost effective, low sample usage technology came to light. Selected reaction monitoring mass

spectrometry (SRM-MS) is a targeted proteomics technology used to identify and quantify proteins with high sensitivity, specificity and high reproducibility. SRM-MS is ideally matched to analysis of intact proteins and peptides. SRM-MS is a much more sensitive and reproducible method for quantifying lower abundance proteins in complicated biological samples. It is a targeted technique that differs from the mass spectrometry approaches widely used in discovery proteomics. Furthermore, SRM-MS is being developed for use in a wide variety of applications including the diagnosis of disease processes including different types of cancer (1-3). The technique identifies and quantifies the proteins present and it allows much greater flexibility for samples analyzed. Rather than requiring sample collection directly from the wound bed, wound exudate collected as part of treatment using negative pressure wound therapy (NPWT) could be analyzed. This common treatment is widely used in chronic, acute, and burn wounds. SRM-MS is a repeatable technique across laboratories and does not require development of new technology for the platform, thus allowing a faster track to development and bedside application.

SRM-MS findings are in section *Subtask 2.3* of this report.

## Technical Objective 2:

Subtask 2.1 Collect fluid from subjects with pressure ulcers

Enrollment was below the target set even though no cost extensions allowed additional time for recruitment. Final enrollment was 15 men and 2 women with an average age of 63.2 years.

Wound surface area (WSA) measurements were completed for each subject and weekly time point using VeVMD software. The percent change in WSA from the original timepoint was calculated and plotted as the wound trajectory. A combined plot of all wounds is shown below (Figure 7).

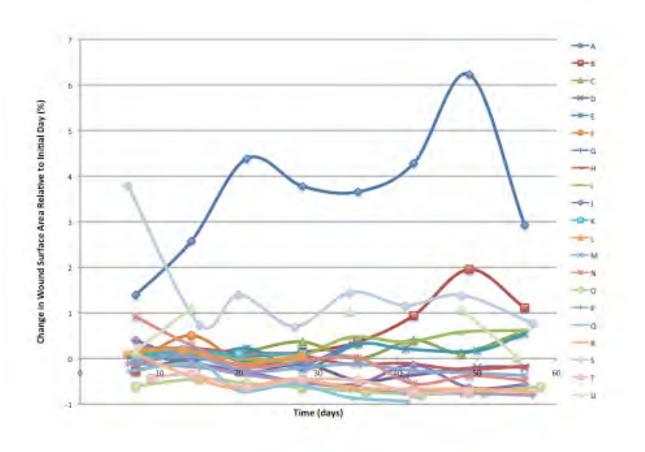


Figure 7. Wound trajectories, the change in wound surface area relative to the initial area, for chronic wounds observed for up to 8 continuous weeks.

This second plot of WSA (Figure 8) differs by the exclusion of 3 wounds (A,S, and U) that increased dramatically in area or were intermittently sampled and is shown to illustrate the trend in area changes for the remaining chronic wounds enrolled.

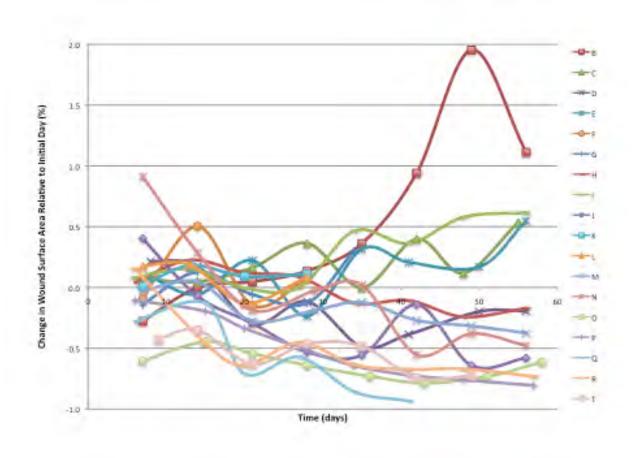


Figure 8. Wound trajectories with wounds with large-scale area changes (n=3) removed to illustrate fine scale differences for the remaining and majority of enrolled wounds.

Evaluation of wound fluids for markers of clinical outcomes is a rapidly expanding field, but the determination of outcome for subjects and sample timepoints is not generally agreed upon. Many studies rely on subjective clinical appearance when classifying wounds and samples (4). Previously, we determined that tissue type does not predict wound outcome for chronic wounds (5). Additionally, although wound healing trajectories can be indicative of healing (6), the overall trend of a wound does not accurately reflect the status of the wound at any single timepoint. Use of measurements comparing initial size to subsequent timepoints, healing trajectories, are generally accepted for tracking progress (tracking). There is no known rate of healing in chronic wounds.

Commonly, chronic wounds experience fluctuations in wound dimensions, both decreasing and increasing in size during the overall path to wound closure. Figure 9 shows 2 wounds sampled in this study. One wound is clearly healing throughout and the other is fluctuating, which makes

the determination of status for the timepoints difficult to classify. If overall a wound heals, but during a period the wound worsens should that point be a healing or worsening sample?

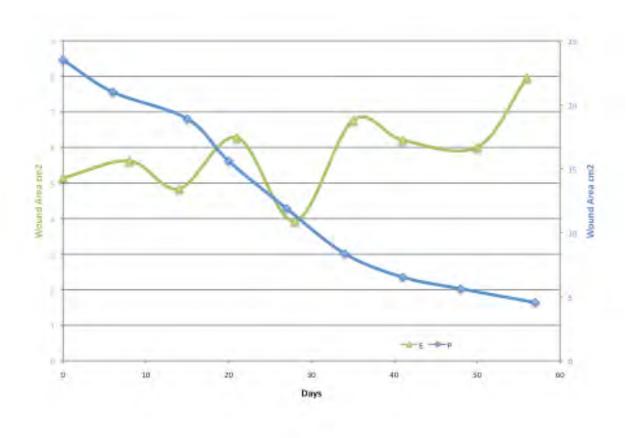


Figure 9. Trends in wound surface area changes for two wounds. Wound E has oscillating area changes, but after 8 weeks is larger than when initially measured. Wound P remains on a healing course throughout the 8 weeks of observation.

Clearly the wounds have varying surface area trends and amplitudes. Commonly, wound outcomes are determined by final percentage of healing, ignoring healing and declining phases throughout the study. When using wound fluid samples to evaluate potential biomarkers it is critical that the samples be sorted into healing and non-healing cohorts correctly. Without any standard in the literature, we sought to define a technique to classify a sampling timepoint based on a sliding 3 timepoint scale that uses the prior and following timepoint data to describe the trend for the wound during the middle timepoint. We divided the timepoints into categories for analysis and comparison using the area changes calculated on a weekly basis with the week prior as the standard to measure changes in WSA rather than the initial measurement. A sliding scale

was used to identify wound timepoints that serve as representative samples for wounds that are decreasing in area or increasing in area. A 2 point sliding scale considers only area changes from the last timepoint, The 3 point sliding scale uses 3 consecutive area measurements and evaluates if the wound was following a constant trajectory of increased or decreased area. Three consecutive wound area data measurements must be consistently increasing or decreasing for the middle timepoint to be assigned to a cohort. The scale slides down the temporal scale considering each set of 3 data measurements in turn. The first and last samples are never considered for cohort inclusion since their immediate history and future are unknown. If the middle point decrease in size and the next point increases in size it is not possible to determine the status of the middle point. The 3<sup>rd</sup> point is being used to confirm the direction of the middle point and allow sorting of the samples. The middle timepoint is selected as a potential representative of closing or expanding wound healing processes.

Further refinement of the data requires a minimum change in WSA. A threshold is used to filter the wound timepoints based on a minimum change in wound area. Filtering in one direction, single threshold, requires the threshold to be true for only one direction from the middle timepoint. Filtering on the percent change in area before and after, dual threshold, further refines the potential representatives. As the degree of change filter increases (more stringent), fewer wound timepoints are included as representative samples. A one-way or single threshold of 15% yields 10 or more samples in each category (Figures 10 and 11). 15% was chosen based on the pressure ulcer and chronic wound healing literature, which indicates 20-40% healing over a course of 2-4 weeks is indicative of healing (6).

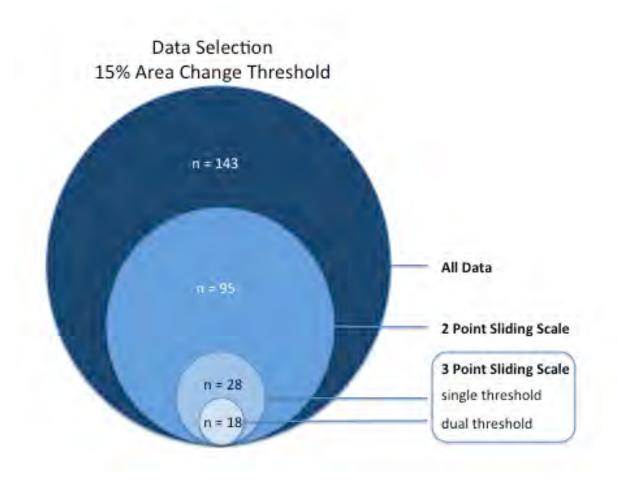


Figure 10. The sampling space for enrolled wounds begins with 143 timepoints. The application of a 2 point sliding scale and imposing a minimum 15% change in wound area relative to the previous measurement reduces the number of timepoints to 95. Further refining the data by applying a 3 point sliding scale where the trajectory must be unidirectional increases the confidence that the wound fluid proteins are representative of a healing or worsening wound. Applying a one-way threshold of 15% reduces the number of data points to 28. The highest confidence is achieved with a dual threshold, applied to both the previous and following area measurement but the data is reduced to 18 timepoints.

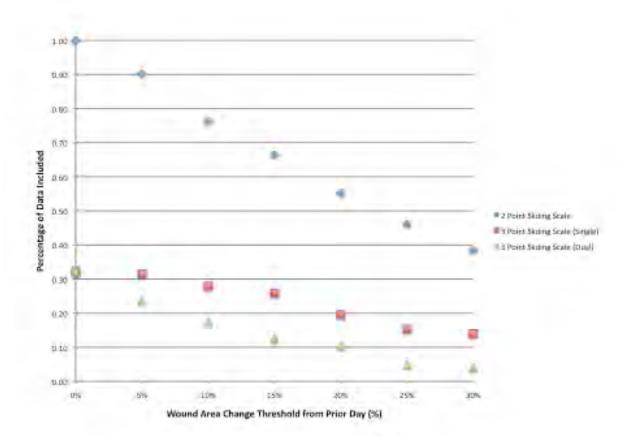


Figure 11. Effect of scale and threshold on data inclusion. As the inclusion criterion increases in stringency from a 2 point to a 3 point scale the amount of data used in each analysis is reduced. This relationship is true also for the threshold set for increasing levels of area change between measurements. With increased stringency comes greater confidence, but fewer data points.

A technology to evaluate the proteome for biomarkers of healing would not be particularly useful in wounds that are obviously healing, but for chronic wounds that are slow to respond to treatment, a biomarker would allow for identification of improving or worsening wounds. In order to identify and validate these biomarkers samples from wounds must include points throughout the wounds progress. The classification technique described is applicable to all wounds. All wound samples were evaluated using the above analysis and divided into bigger (worsening) or smaller (healing). Samples were then group accordingly for proteomic analysis (Figure 12).

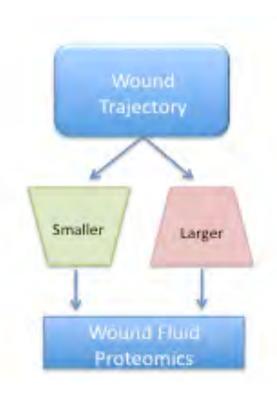


Figure 12. Using wound area measurements, the samples were divided into healing or smaller and increasing or larger sample groups. The groups were built using a 2 point scale and 15% threshold, a 3 point scale with single 15% threshold and a 3 point scale with dual 15% threshold before proteomic analyses.

### Subtask 2.2 Collect samples from wounds in porcine model

A partial-thickness dermatome-induced wounds were generated in a porcine model and wound healing parameters included wound fluid cytokine analysis.

## Subtask 2.3 Proteomic analysis of wound fluid

Porcine wound fluid samples were analyzed using PIXES see section Subtask 1.3

Human wound fluid samples were analyzed in using both antibody dependent and antibody independent techniques. The workflow for the analysis is shown in Figure 13.

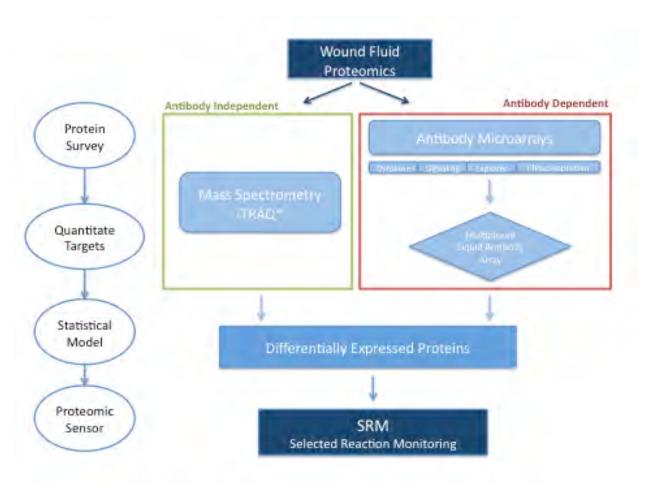


Figure 13. Pooled wound fluid samples were subjected to antibody independent and antibody dependent surveys to identify new potential biomarkers.

Antibody Independent

iTRAQ Analysis

Two sets of pooled samples, one representing wounds increasing in area and the other representing wounds decreasing in area were submitted for mass spectrometry using iTRAQ methodology. The iTRAQ experiments included a biological replicate as well as a technical replicate and data was normalized for direct comparison. Through iTRAQ labeling quantitative proteomics analysis, the expression levels of 2561 proteins were analyzed.

For the plots below, the technical replicates are defined as Experiment 1 and Experiment 2 and in each experiment, there were two ratios, a Larger/Smaller ratio (corresponding to 115/114 ratios in both datasets) and a biological repeat of Larger/Smaller ratio (corresponding to 117/116 ratios

in both datasets). See Appendices A and B for data. The experimental matrix is represented in Figure 14.

	Exp	periment 1	Experiment 2						
Protein Accession	Larger /Smaller	Larger /Smaller (biological repeat)	Larger /Smaller	Larger /Smaller (biological repeat)					
126032350	0.949	1.093	0.967	1.169					
•••	•••	•••	•••	•••					

Figure 14. Technical repeat data are shown with 4 relative ratios from 2 datasets corresponding to a unique protein ID.

Outliers were observed from comparisons of biological repeats in both technical replicate experiments and the data were manually inspected. Outliers were identified as not reproducible in biological replicates, which indicates the possibility of random bias for certain proteins with iTRAQ channel specificity. Raw spectrum data of the outliers were checked and their data qualities were confirmed. Median normalization was chosen to apply to raw data and normalize the reported ratios of the proteins comparing Larger Wound group to Smaller Wound group. Histograms were made to compare the data before and after normalization (Figures 15a and 15b).

# **Box Plot for Un-Normalized Dataset**

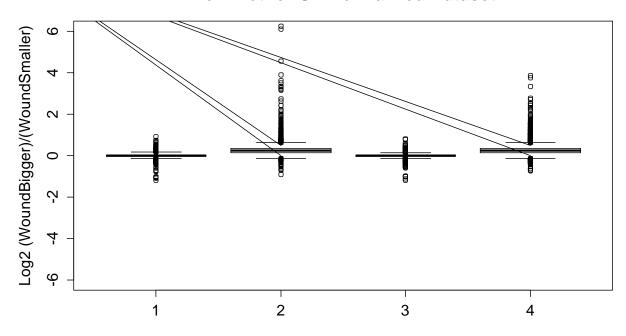


Figure 15a. Histogram of data prior to normalization.

# **Box Plot for Normalized Dataset**

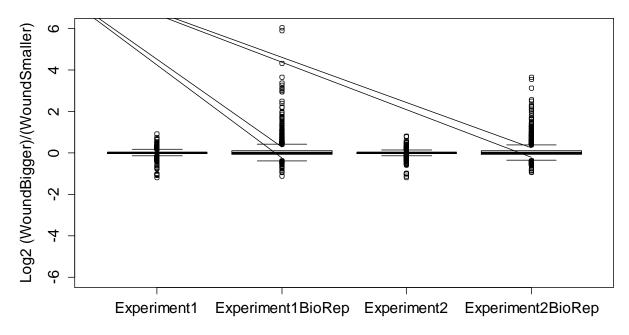


Figure 15b. Histogram of data after normalization.

From the different expression levels of 2561 proteins analyzed by iTRAQ, the top 20 proteins overexpressed in wound fluid from the wounds that are worsening are shown in Figure 16.

			EXP 1		EXP 2
GI	Protein Names	EXP 1	BioRep	EXP 2	BioRep
	msx2-interacting protein [Homo				
14790190	sapiens]	NA	NA	1.2659	2.5466
	PREDICTED: 26S proteasome				
	non-ATPase regulatory subunit 6				
530373465	isoform X1 [Homo sapiens]	1.3928	2.5876	NA	NA
	pterin-4-alpha-carbinolamine				
4557021	dehydratase isoform 1 [Homo	1 120 6	2 20 61	27.4	37.4
4557831	sapiens]	1.1306	2.3861	NA	NA
570006201	PREDICTED: kinesin-like protein	1.5600	2 1505	1.70.40	2 4224
578806381	KIF15 isoform X2 [Homo sapiens]	1.5623	2.1505	1.7042	2.4234
£7000£0 <i>€</i> £	PREDICTED: protein TANC1	1 2014	1.5000	NT A	NT A
578805065	isoform X8 [Homo sapiens]	1.2014	1.5009	NA	NA
	vacuolar protein sorting-associated protein VTA1 homolog isoform c				
556503347	[Homo sapiens]	1.1944	1.4609	0.9064	1.0607
330303347	2'-deoxynucleoside 5'-phosphate	1.1744	1.4009	0.9004	1.0007
	N-hydrolase 1 isoform 2 [Homo				
40354201	sapiens]	1.2841	1.4524	NA	NA
.000.201	pre-mRNA-processing factor 19	1.2011	11.02	1,111	1,11
7657381	[Homo sapiens]	1.1834	1.4294	1.0737	1.7417
	PREDICTED: CUGBP Elav-like				
	family member 2 isoform X22				
578818239	[Homo sapiens]	1.5374	1.4107	NA	NA
	PREDICTED: retinoblastoma-like				
	protein 1 isoform X1 [Homo				
578836106	sapiens]	1.2901	1.3265	NA	NA
	PREDICTED: large proline-rich				
	protein BAG6 isoform X12 [Homo				
578811945	sapiens]	1.1216	1.2781	NA	NA
	phospholipid transfer protein				
5452014	isoform a precursor [Homo	1 1505	1 2201	NI A	NA
5453914	sapiens] PREDICTED: dynamin-1-like	1.1595	1.2381	NA	NA
	protein isoform X2 [Homo				
530398960	sapiens]	1.0499	1.2372	1.0030	1.1129
330370700	PREDICTED: AP-3 complex	1.0477	1.2372	1.0030	1.112)
	subunit beta-2 isoform X2 [Homo				
578827454	sapiens]	1.4237	1.2185	NA	NA
	sialic acid synthase [Homo				
12056473	sapiens]	1.0249	1.1539	NA	NA
	probable G-protein coupled				
	receptor 158 precursor [Homo				
93204867	sapiens]	1.4516	1.1182	1.5050	1.3661
	angiogenin precursor [Homo				
4557313	sapiens]	1.2682	1.1156	NA	NA

Figure 16. Top 20 proteins overexpressed in wound fluid from the wounds that are getting larger over the 8 week period.

## Antibody Dependent

#### Antibody Microarrays

Antibody arrays are a high-throughput ELISA based platform for efficient protein expression profiling in chronic wound fluid. A large number of targets can be profiled using a small volume of sample leading to the identification of differentially expressed proteins. The wound fluid proteins are biotin labeled, incubated with the antibody array, and detected using dye or fluorescent-tagged streptavidin. Because the proteins remain non-denatured, false positives may result from protein-protein interactions and non-specific binding and follow-up validations are necessary. Pooled samples using a dual threshold of 15% and a 3 point sliding scale were used on the arrays.

Four antibody arrays were utilized to test for differentially expressed proteins from chronic wound fluid. The cytokine profiling array (Appendix C) features 310 unique antibodies for profiling cytokines and related biomarkers in human cells, tissues, serum or culture media. The explorer antibody array (Appendix D) is a broad-scope antibody array with 656 highly specific and well-characterized antibodies from more than ten signaling pathways. The signaling explorer array (Appendix E) features 1358 unique antibodies covering twenty biological signaling pathways and is ideal for high-throughput biomarker screening and discovery. Targets with a greater than 2 fold difference in expression are differentially given in Figure 17.

Protein Target	Expression Ratio	Array
Vacular Endothelial Growth Factor(VEGF)	4.59	Е
Tubulin alpha	4.41	SE
Actin beta	3.40	Е
Survivin	2.78	Е
Beta actin	2.62	С
CD57	2.47	Е
CD2	2.33	Е
ADP-ribosylation Factor (ARF-6)	2.28	Е
TGF beta Receptor III	2.27	C
HPV 16-E7	2.23	Е
FSH	2.20	Е
Golgi Complex	2.20	Е
Total PSA	2.18	С
BAD	2.15	SE
CD1	2.12	Е

Laminin-s	2.11	Е
Catenin-alpha1	2.02	С
CEA	2.01	С
MHC I (HLA25 and HLA-Aw32)	2.01	Е
Thymidylate Synthase	2.00	Е
p18INK4c	0.50	Е
DFF40 (DNA Fragmentation Factor 40) / CAD	0.50	Е
c-Src	0.50	Е
PARP	0.50	Е
Endostatin	0.49	Е
Cullin-1 (CUL-1)	0.49	Е
PARP (Poly ADP-Ribose Polymerase)	0.49	Е
XRCC2	0.48	Е
MyD88	0.48	Е
Cdk3	0.44	Е
MMP-23	0.44	Е
Cullin-2 (CUL-2)	0.42	Е
Stat-1	0.42	Е
CDC34	0.41	Е
BRCA2 (aa 1323-1346)	0.35	Е
PTHrP	0.10	C

<sup>\*</sup> Cytokine (C), Explorer (E), Signaling Explorer (SE)

Figure 17. Targets with a greater than 2 fold difference in expression.

Finally, a phophoprotein array was used to look for differences in protein abundance, phosphorylation and protein-protein interactions. The array utilizes ~510 pan-specific antibodies for protein expression and ~340 phosphosite-specific antibodies for phosphorylation. The antibodies profile 287 different phosphosites, 189 protein kinases, 31 protein phosphatases and 142 regulatory subunits of these enzymes and other cell signaling proteins that regulate cell proliferation, stress and apoptosis. Two strategies were used to explore differences between healing and worsening wound fluid, evaluation of the 15% dual threshold pooled sample groups (Appendix F) and individual testing of 10 wounds in each category (Appendix G). Differentially expressed targets from the microarrays are pre-validated using western blots to confirm antibody specificity by including molecular weight of the target. In all, 11 pre-validation blots tested 238 antibodies for their sensitivity and specificity. The blot images and potential targets are given in (Appendix H). Forty-four known and 41 cross-reactive unknown targets were identified as potential biomarkers from the pre-validation western blots. Eighteen antibodies were probed

using pooled samples to identify proteins with significant changes between sample groups (Figure 18).

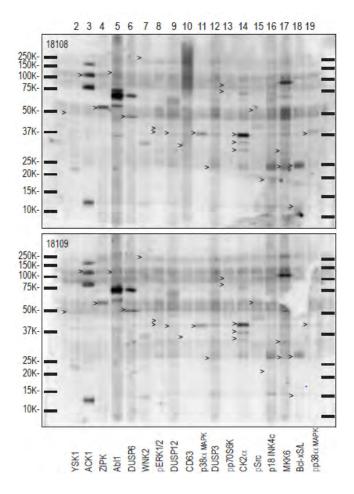


Figure 18. Eighteen antibodies probed using pooled samples to identify proteins with significant changes between sample groups.

Overlays of the gel images were used to highlight similarities and differences in the samples (Figure 19).

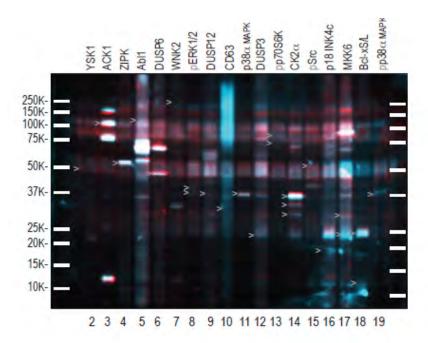


Figure 19. Overlay of the gel images, the blue color represents the pooled "worsening" samples and the red color the pooled "healing" samples. When the protein bands are of the same magnitute in both samples, then the protein bands show up as white.

Differences in expression for targets of the 18 antibodies are shown Figure 20. Eleven targets were measurable with 9 differentially expressed with a 25% minimum threshold.

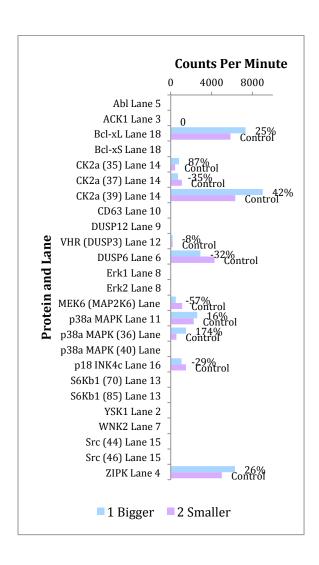


Figure 20. Differences in expression for targets of the 18 antibodies. Eleven targets were measurable with 9 differentially expressed with a 25% minimum threshold.

A microsphere-based suspension microarray was used to simultaneously measure the concentration of 7 analytes, C-X-C motif chemokine 9 (CXCL9), L-selectin (SELL), matrix metalloproteinase-9 (MMP9), protein S100-A8 (S100A8), protein S100-A9 (S100A9), Transforming growth factor beta receptor type 3 (TGFBR3), and retinol binding protein 4 (RBP4) in 96 wound fluid samples. The assay methodology is based upon the Luminex ® bead-based immunoassay platform. Samples were measured in duplicate and standardized using the wound fluid total protein concentration (Appendix I). The three cohorts of healing and worsening wounds were tests for differential expression and p values are given in Figure 21. Of the 6 targets, S100A8 and TGFBR3 were significantly different between healing and worsening wounds.

				p va	alue		
Scale	Threshold	CXCL9	MMP9	RBP4	S100A8	S100A9	TGFBR3
2 point	15%	1.000	0.347	0.097	0.029	0.149	0.035
3 point	15% Single	0.785	0.379	0.205	0.644	0.750	0.575
3 point	15% Dual	0.525	0.351	0.226	0.022	0.062	0.093

Figure 21. Quantitative Microarray for 7 analytes, C-X-C motif chemokine 9 (CXCL9), L-selectin (SELL), matrix metalloproteinase-9 (MMP9), protein S100-A8 (S100A8), protein S100-A9 (S100A9), Transforming growth factor beta receptor type 3 (TGFBR3), and retinol binding protein 4 (RBP4).

#### SRM-MS Analysis

Through iTRAQ labeling quantitative proteomics analysis, the different expression levels of 2561 proteins were evaluated and 6 proteins out of these were selected as SRM-MS protein targets. 14 proteins were further added into the SRM-MS quantification panel using data from previous research and the microarray results of this study. Four individual samples and 2 pooled samples were prepared and subject to SRM-MS analysis using algorithm based and/or iTRAQ data dependent SRM-MS methods. The pooled samples were taken from the highest confidence cohort, 15% dual threshold and 3 point sliding scale. The potential clinical diagnostic utility of the panel was further evaluated.

The abundance of each of the 20 SRM-MS target proteins was represented by a single peptide mapped uniquely to the target protein (Appendix J). Each protein was independently quantified in 6 wound fluid samples, containing 2 samples from the larger or worsening group and 2 samples from the healing group in addition to the pooled samples derived from the 3 point sliding scale and dual 15% threshold. Relative expression levels and a p value for each protein target is shown in Figure 22. The abundance of a target protein is represented by the relative ratios normalized to abundance in the pooled sample.

	Lar Wou				aller unds		
	A-14	B-35	15% Dual Threshold Pooled	N-14	O-28	15% Dual Threshold Pooled	p-value
Previous Research							
Protein S100-A7	2.1374	1.9030	1.9051	0.6081	1.1605	1.0000	0.0115
Protein S100-A9	2.6713	2.2497	2.1554	1.0347	1.5528	1.0000	0.0085
Retinol binding protein 4 (RBP4)	0.2684	0.3491	0.2202	0.9024	1.4188	1.0000	0.0292
Matrix Metalloproteinase-9 (MMP9)	7.8121	3.3984	5.9998	0.6842	1.6546	1.0000	0.0626
Profilin-1 (PFN1)	0.3224	0.4516	0.3517	0.6439	1.1512	1.0000	0.0578
TGFBR3	3.8634	4.0737	3.0818	0.9321	1.8031	1.0000	0.0042
L-selectin	0.3167	0.2136	0.2701	0.5844	0.8289	1.0000	0.0401
Microarrays							
VEGF-A	0.0652	0.1433	0.1512	0.4367	1.1530	1.0000	0.0740
Beta actin (ACTB)	0.1352	0.1965	0.0658	0.6448	0.7958	1.0000	0.0136
ADP-ribosylation Factor (ARF-6)	0.1927	0.1765	0.2414	1.1945	1.0360	1.0000	0.0023
Cdk3	0.3652	0.2209	0.3525	0.9531	0.9833	1.0000	0.0026
Cullin-2 (CUL-2)	5.6360	6.6595	4.4842	0.8459	2.3464	1.0000	0.0073
STAT1	6.0845	7.3875	6.2529	0.6372	1.0247	1.0000	0.0028
CDC34	6.8297	7.5555	5.6390	0.7289	1.3683	1.0000	0.0054
iTRAQ							
kinesin-like protein KIF15 isoform X2	9.2240	11.966 0	7.8970	1.0777	2.7340	1.0000	0.0102
DCC-interacting protein 13-alpha	2.2750	0.6348	2.7902	0.8614	1.9063	1.0000	0.4422
26S proteasome non- ATPase regulatory subunit 6 isoform X1	7.8246	6.2612	5.1769	0.6427	1.2660	1.0000	0.0153
CUGBP Elav-like family member 2 isoform X22	3.5516	4.9279	3.2949	0.5281	1.3657	1.0000	0.0149
pre-mRNA-processing factor 19	4.1619	5.6161	3.2654	0.5665	2.2474	1.0000	0.0259
pterin-4-alpha- carbinolamine dehydratase isoform 1	4.2906	4.8014	3.9016	0.4900	2.1487	1.0000	0.0107

Figure 22. Selected reaction monitoring (SRM-MS) analysis of 20 proteins in chronic wound fluid from pressure ulcers.

#### **KEY RESEARCH ACCOMPLISHMENTS:**

- Fabricated a new integrated sensor that included a xerogel as a selective sensing element
- Fabricated a porous polymetric PBG on large flexible substrates
- Methodology developed and refined during this project was employed in a project evaluating pressure ulcer fluid in people with and without SCI
  - Edsberg LE, Wyffels JT, Ogrin R, Craven C, Houghton P. A pilot study evaluating protein abundance in pressure ulcer fluid from people with and without spinal cord injury. J Spinal Cord Med. 2014 Jun 26. [Epub ahead of print] PMID: 24968005 [PubMed as supplied by publisher]
- 3 Point sliding scale threshold sample classification system

#### **CONCLUSION:**

The goal of this research was to evaluate the wound proteome and outcome and develop a technology to measure protein targets. The analysis of the proteome started with the development of a classification system for wound fluid samples. A technique to classify a sampling timepoint based on a sliding 3 timepoint scale that uses the prior and following timepoint data to describe the trend for the wound during the middle timepoint was developed. This technique offers the potential to standardize and objectively classify samples from a variety of wound types, rather than utilizing subjective clinical judgement. Classification of the samples is integral to the identification of targets.

The proteomic analysis utilized antibody dependent and independent techniques. Of the 6 targets analyzed using a quantitative microarray, S100A8 and TGFBR3 were significantly different between healing and worsening wounds. This finding further supports work by this team investigating the levels of S100 calcium binding proteins in chronic wounds.

PIXIES technology was fabricated, but ultimately it was decided that this novel technology has a longer timeline to clinical use due to the early stages of the technology. Additionally, the wound bed presents an extremely challenging environment for any type of proteomic technology due to the complex mixture of proteins and protein fragments. SRM-MS, cost effective, low sample usage technology, is well suited to analysis of intact proteins and peptides. Additionally, the technology has been shown to be suitable for a diagnostic tool in disease processes. The SRM-

MS data indicated several intriguing findings, but can be utilized in follow-up studies for panel marker confirmation. Validation of this technology is integral to the final development of a bedside collection sample being evaluated for markers of healing. The utilization of SRM-MS for wound fluid analysis is a significant development in the path to bedside wound outcome diagnosis. Ultimately this work may allow the development of personalized wound care based on the proteomic characteristics of the wound.

## PUBLICATIONS, ABSTRACTS, AND PRESENTATIONS

- "Bring Revised NPUAP Guidelines and Research to the Bedside", 20<sup>th</sup> Annual Symposium to Promote Clinical Excellence, Saratoga Springs, NY, May 22, 2015
- "Proteomic Characterization of Pressure Ulcers", Invited Lecture, World Union of Wound Healing Societies (WUWHS), 4th Congress, Yokohama, Japan, September 2012.
- Ka Yi Yung, Huina Xu, Ke Liu, Greggory J Martinez, Frank V. Bright, Michael R Detty, and Alexander N. Cartwright, "Hybrid Oxygen-responsive Reflective Bragg Grating Platforms", Analytical Chemistry 2012; 84 (3):1402–1407.
- Liu, K., Xu, H., Hu, H., Gan, Q. and Cartwright, A. N. (2012), One-Step Fabrication of Graded Rainbow-Colored Holographic Photopolymer Reflection Gratings. Adv. Mater., 24:1604–1609. doi:10.1002/adma.201104628
- Huina Xu, Ke Liu, Qiaoqiang Gan, and Alexander N. Cartwright, "Flexible Porous Polymer Photonic Bandgap Structures for Chemical and Biomedical Sensing", IEEE Photonics 2011 Conference, Oct. 2011, Arlington, Virginia.
- Ke Liu, Huina Xu, Qiaoqiang Gan, and Alexander N. Cartwright, "Polymeric Concave Bragg Reflectors Fabricated using Optical Lithography", Materials Research Society, Nov. 2011, Boston, Massachusetts.
- "What Are the Effects of Load on Tissue?", Scientific Basis of Wound Healing, Wound Principles & Assessment, Wound Management Track, Master's Clinical Science (MCISc) Program, School of Physical Therapy, University of Western Ontario, London, Ontario, September 2011.
- Ke Liu, Huina Xu, Qiaoqiang Gan, and Alexander N. Cartwright, "One-step Holographic Lithography Fabrication of a Rainbow-colored Photonic Bandgap Structure", IEEE Photonics 2011 Conference, Oct. 2011, Arlington, Virginia

• "Proteins and Pressure Ulcer Outcomes", Chronic Wounds – Mechanisms and Diagnostics, 2nd Meeting of the Australian Wound and Tissue Repair Society, Perth, Western Australia, March 2010.

### **INVENTIONS, PATENTS AND LICENSES:** Nothing to report

#### **REPORTABLE OUTCOMES:**

• Utilization of selected reaction monitoring mass spectrometry (SRM-MS) for wound fluid samples

#### **OTHER ACHIEVEMENTS:**

- Graduate Certificate in Bioinformatics & Computational Biology (May 2014) University of Delaware (not funded by award, but admission to program supported by need from funded grant for data analysis).
- Pilot studies (not funded by this award, but based on the work in this award) are being conducted to evaluate genomic methodology to identify genes involved with proteins present in healing and non-healing wounds. Sample type (fluid vs. tissue) is also being assessed.
- Novel Compounds From Shark and Stingray Epidermal Mucus With Antimicrobial Activity
  Against Wound Infection Pathogens. Department of Defense, U.S. Army Medical Research &
  Materiel Command (USAMRMC), Congressionally Directed Medical Research Programs.
  Basic Research Award W81XWH-11-2-0110. Non-traditional model antibody independent
  evaluation of mucus based on the methodology developed in this award.
- Integrated Proteomic Analysis and siRNA Therapy for Treatment of Heterotopic Ossification. Department of Defense, U.S. Army Medical Research & Materiel Command (USAMRMC), Congressionally Directed Medical Research Programs. Idea Development Award, W81XWH-10-2-0139. Wound fluid and tissue analysis based on the methodology developed in this award.
- A Randomized Controlled Pilot Study of Hyperbaric Oxygen Therapy versus Sham Controls in the Early Treatment of Deep Partial Thickness Burns. U.S. Army Medical Research and Materiel Command Broad Agency Announcement, 2014. Proteomics work flow and updated technology will be utilized for this project.

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quantification of clinically validated biomarkers in formalin-fixed, paraffin-embedded tumor tissue. J Mol Diagn. 2013 Jul;15(4):454-65. doi: 10.1016/j.jmoldx.2013.03.002. Epub 2013 May 11.

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#### **APPENDICES:**

Appendix A. iTRAQ Set 1

Appendix B. iTRAQ Set 2

Appendix C. Cytokine

Appendix D. Explorer

Appendix E. Signaling

Appendix F. Pooled Microarray

Appendix G. Individual Microarray

Appendix H. Pre-screen Results

Appendix I. Quantitative Microarray

Appendix J. SRM-MS Transition Parameters

# Appendix A<br/>iTRAQ Set 1

Accession	Description	\$Coverage	Σ# Proteins Σ# Unique Peptides	Σ# Pontidos	Σ# DSMc	AR: 115/114	AR: 115/114 Count	AR: 115/114 Variability (%)	AR: 117/11	6 AR: 117/116 Count	AR: 117/116 Variability [%]	Score 4/3 6 7)	Coverage A(3.6.7)	# Pantidas A(3 6 7)	# DSM A(3 6 7)	# AAs	MW [kDa]	calc. pl
109715837	protein NDNF precursor (Homo sapiens)	2.82	1	1 2	3	1.874	AU. 110/114 COUR	1		016 1	76. 1177 TO VALIDARY (70)	22.30	2.82	2	3	568	64.6	8.94
578807153	PREDICTED: basic helix-loop-helix domain-containing protein KIAA2018 isoform X1 [Homo sapi	3.17	3	1 7	18	1.681		1		180 1		28.33		10	18	2211	237.6	7.52
62632769 578806381	DNA-3-methyladenine glycosylase isoform a [Homo sapiens]	9.06 7.24	3	1 3 1 10	7	1.601 1.567		1	1.3	275 1		61.21 <b>69.08</b>		7	7	298	32.8	9.57
578806381 578818239	PREDICTED: kinesin-like protein KIF15 isoform X2 [Homo sapiens] PREDICTED: CUGBP Elav-like family member 2 isoform X22 [Homo sapiens]	7.24 13.65	36	1 10	21 11	1.567		1		i29 1 i59 1		69.08 145.25	7.24 13.65	17	21	1285 403	147.9 42.4	6.89 8.85
93204867	probable G-protein coupled receptor 158 precursor [Homo sapiens]	4.69	1 1	1 6	35	1.456		4 1.8			3.3	66.33		8	35	1215	135.4	8.28
578827454	PREDICTED: AP-3 complex subunit beta-2 isoform X2 [Homo sapiens]	3.37	5 1	1 4	6	1.428		1		133 1		33.18	3.37	4	6	1038	114.4	5.72
530373465	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X1 [Homo s	9.02	6 1	1 3	7	1.397		I .		143 1		160.84		7	7	410	48.0	5.54
578824847 578828247	PREDICTED: neurobeachin isoform X10 [Homo sapiens]	1.67	10	1 7	21	1.396		3 49.° 2 51.6		995 3	5.6	41.54 158.46		10	21	2938 158	326.8 18.0	6.16 8.66
555943926	PREDICTED: SUMO-conjugating enzyme UBC9 isoform X4 [Homo sapiens] heme oxygenase 2 isoform c [Homo sapiens]	6.62	3	2 3	2	1.370		2 51.6		124 1	1	43.84		7	2	287	32.8	8.00 5.91
578817959	PREDICTED: collagen alpha-1(XXVII) chain isoform X3 [Homo sapiens]	2.85	4	1 3	12	1.301		3 2.7	1.2	107 3	35.8	95.72	2.85	5	12	1087	107.8	7.85
578836106	PREDICTED: retinoblastoma-like protein 1 isoform X1 [Homo sapiens]	4.35	12	2 5	8	1.294		2 5.2		i60 2	21.0			5	8	896	101.1	7.56
40354201	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 isoform 2 [Homo sapiens]	22.30	2	1 1	3	1.288		1		108 1		196.54		3	3	148	16.2	6.79
149363656 4557313	exocyst complex component 6B (Homo sapiens) angiogenin precursor [Homo sapiens]	4.44 19.73	2	1 4	9	1.274 1.272		1		040 1 112 1		30.99 <b>50.70</b>		4	9	811 147	94.1 16.5	6.46 <b>9.64</b>
48675813	transportin-2 isoform 2 [Homo sapiens]	2.48	2	1 3	44	1.254		1		059 1	i	33.30		3	44	887	100.3	4.98
554595586	replication protein A 32 kDa subunit isoform 2 [Homo sapiens]	17.82	3	1 2	4	1.250		1	1.1	188 1	1	145.96	17.82	4	4	174	19.1	5.73
50053795	eukaryotic translation initiation factor 4B [Homo saplens]	9.49	2	2 4	13	1.249		3 8.3		047 1		395.67		10	13	611	69.1	5.73
625180307 14277685	hemicentin-2 precursor [Homo sapiens] protocadherin gamma-C5 isoform 2 precursor [Homo sapiens]	2.58	2	1 11	16	1.232		1		043 1 141 1	1	26.28 35.31	2.58	11	16	5079 878	543.7 95.1	5.87
11559929	coatomer subunit gamma-1 [Homo sapiens]	3.78	1	1 2	4	1.229		1		135 1		285.60		4	4	874	97.7	5.47
578805065	PREDICTED: protein TANC1 isoform X8 [Homo sapiens]	6.20	8	1 9	320	1.205		1	1.7	765 1		4107.27	6.20	13	320	1677	183.3	8.85
4502491	complement component 1 Q subcomponent-binding protein, mitochondrial precursor [Homo sa	14.18	1	1 2	7	1.200		2 6.4		052 2	57.1	473.33		4	7	282	31.3	4.84
556503347 6912280	vacuolar protein sorting-associated protein VTA1 homolog isoform c (Homo sapiens)	10.81	3	1 1	3	1.198		1		718 1 394 1		109.96	10.81	3	3	222 338	24.5 38.3	5.29 5.53
4557663	activator of 90 kDa heat shock protein ATPase homolog 1 [Homo sapiens] immunoglobulin-binding protein 1 [Homo sapiens]	6.49	1	1 2	25	1.193 1.193		1 12.6		187 2	2 24.4	122.63 379.65	8.88 6.49	4	25	338	38.3	5.38
40353729	ras and Rab interactor 3 [Homo saplens]	8.43	1	1 7	10	1.189		12.0	1.3	313 1	24.4	286.23		9	10	985	107.8	6.61
7657381	pre-mRNA-processing factor 19 [Homo sapiens]	6.94	1	1 4	17	1.187		1	1.6	581 1		79.05	6.94	9	17	504	55.1	6.61
190341024	SPARC-like protein 1 isoform 1 precursor [Homo sapiens]	13.10	2	2 4	11	1.186		2 1.		929 2	23.0			8	11	664	75.2	4.81
21361176 4506715	retinal dehydrogenase 1 [Homo sapiens] 40S ribosomal protein S28 [Homo sapiens]	3.39 40.58	10	2 2	5	1.186		2 28.1		025 2	7.5			5	5	501	54.8 7.8	6.73 10.70
4506/15 612407822	dus ribosomai protein 528 [Homo sapiens]  carcinoembryonic antigen-related cell adhesion molecule 6 preproprotein [Homo sapiens]	6.69	1	2 2	6	1.184		2 17		017 2	2 69.1		6.69	6	6	344	7.8 37.2	5.82
47458820	signal transducer and activator of transcription 3 isoform 3 [Homo sapiens]	16.90	6	2 11	27	1.180		3 1.5	1.	330 3	14.3			16	27	722	83.1	7.12
47933379	alpha-soluble NSF attachment protein [Homo sapiens]	5.08	1	1 2	4	1.179		1		251 1	1	146.99		4	4	295	33.2	5.36
206597509	arf-GAP domain and FG repeat-containing protein 1 isoform 4 [Homo sapiens]	1.92	8	1 1	3	1.174		1		714 1		84.54		3	3	522	54.1	8.92
209180448 385731627	target of Myb protein 1 isoform 3 [Homo sapiens]  UPF0687 protein C20orf27 isoform 2 [Homo sapiens]	18.70 19.54	3	2 2	15	1.173		2 6.		113 1 217 2	17.7	155.75 263.66		12	15	460 174	50.2 19.3	4.78 6.84
5453914	phospholipid transfer protein isoform a precursor [Homo sapiens]	4.06	4	2 2	22	1.163		3 1.3		456 2	20.6			5	22	493	54.7	7.01
16933567	ras-related protein Rab-8A [Homo sapiens]	27.54	21	1 6	72	1.163		1		028 1	1	1235.51	27.54	17	72	207	23.7	9.07
71773329	annexin A6 isoform 1 (Homo sapiens)	74.74	2	1 46	438	1.163		3 10.4		286 3	15.2			133	438	673	75.8	5.60
116734849 530362188	glycogen debranching enzyme isoform 2 [Homo sapiens]  PREDICTED: microtubule-associated serine/threonine-protein kinase 2 isoform X3 [Homo sapier	3.83	3	2 6	17	1.163		3 6.5		134 3	3 2.7			11	17	1515	172.5	6.71
578811543	PREDICTED: microtubule-associated serine/triteonine-protein kinase 2 isoform X3 [homo saples]  PREDICTED: disheveled-associated activator of morphogenesis 2 isoform X2 [Homo sapless]	4.51 3.17	8	1 4	42	1.162		2 1.6		365 1		85.93 30.38		7	42	1797	196.2 134.2	8.16 6.73
388240770	reticulon-3 isoform f [Homo sapiens]	1.74	5	1 2	8	1.154		2 12.8	3 1.0	059 2	37.2	221.29		4	. 8	920	100.8	4.93
46389554	alpha-endosulfine isoform 4 [Homo sapiens]	31.62	8	2 2	9	1.153		3 0.1	1 1.0	053 3	7.4	503.07	31.62	6	9	117	13.0	8.27
578823793	PREDICTED: nucleosome assembly protein 1-like 1 isoform X18 [Homo sapiens]	11.89	6	2 3	8	1.153		2 21.6		293 2	2 28.1	194.77	11.89	8	8	328	38.2	4.56
17986001 4507797	major histocompatibility complex, class I, B precursor [Homo sapiens] ubiquitin-conjugating enzyme E2 variant 2 [Homo sapiens]	13.54 42.07	12	2 3	10	1.151 1.150		3 13.9		131 3 144 1	5.9	307.53 674.87	13.54 42.07	7	10	362 145	40.4 16.4	5.85 8.09
530411696	PREDICTED: probable ATP-dependent RNA helicase DDX5 isoform X1 [Homo sapiens]	14.66	4	1 10	24	1.149		1		027 1		505.74	14.66	24	24	614	69.1	8.92
156564401	vesicle-fusing ATPase [Homo sapiens]	3.49	2	1 2	4	1.147		1		059 1		113.19	3.49	4	4	744	82.5	6.95
5729850	guanine nucleotide-binding protein G(k) subunit alpha [Homo sapiens]	21.19	14	1 7	21	1.146		1		383 1	1	688.56	21.19	17	21	354	40.5	5.69
91208426 530382450	pre-mRNA-processing-splicing factor 8 [Homo sapiens] PREDICTED: dystonin isoform X17 [Homo sapiens]	5.05 8.07	1	2 11	26	1.142		2 0.3		306 2 023 1	38.2	298.99 69.02	5.05 8.07	18	26	2335 3186	273.4 368.9	8.84 6.76
578838069	PREDICTED: dystorin isolorm X17 (nomo sapiens)  PREDICTED: protein-cysteine N-palmitoyltransferase porcupine isoform X10 (Homo sapiens)	4.33	14	1 30	17	1.140		1		116 1	1	86.12		45	17	323	36.3	7.99
578833709	PREDICTED: AP-3 complex subunit delta-1 isoform X1 [Homo sapiens]	3.82	3	2 4	7	1.136		2 10.4	9 1.3	276	9.1	160.70		7	7	1203	135.3	7.64
4885153	crk-like protein [Homo sapiens]	12.87	1	2 3	23	1.135		2 17.8		362 2	3.6			8	23	303	33.8	6.74
578833911 4557831	PREDICTED: tubulin-folding cofactor B isoform X1 [Homo sapiens]	12.95	2	1 2	6	1.134		1	1.1	210 1	1	249.49		4	6	193 104	21.8 12.0	4.94
4557831 223633991	pterin-4-alpha-carbinolamine dehydratase isoform 1 [Homo sapiens] pantetheinase precursor [Homo sapiens]	20.19	2	1 2	6	1.134		1		106 1		89.69 223.37		4	6	104 513	12.0 57.0	6.80 5.55
69122931	TAF5-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 5L is	11.38	3	1 3	48	1.134		1		329 1		85.76		5	48	325	37.0	6.18
239735600	tctex1 domain-containing protein 1 [Homo sapiens]	4.47	1	1 1	3	1.132		1	1.4	116 1		26.10	4.47	1	3	179	20.7	8.95
115495445	ankyrin repeat domain-containing protein 30A [Homo sapiens]	7.61	2	1 10	41	1.129		7 3.2		288 7	24.8			13	41	1341	152.6	6.33
539848098 578804706	biogenesis of lysosome-related organelles complex 1 subunit 2 isoform 3 [Homo sapiens]  PREDICTED: putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform X2 [Homo sapiens]	28.42 5.61	4	1 1	2	1.128		1		006 1 189 1	1	103.60 173.23		2	2	95 285	11.1 32.1	9.23 8.68
530384981	PREDICTED: putative GTP cyclonydrolase 1 type 2 NTP SCT Isolorm X2 [norno sapiens]  PREDICTED: aminoacyl tRNA synthase complex-interacting multifunctional protein 2 isoform X1	9.58	5	1 3	8	1.127		1		269 1	1	173.23		5	8	313	34.6	8.02
414144872	coatomer subunit zeta-1 isoform 3 [Homo sapiens]	6.25	3	1 1	2	1.126		1		987 1		42.33		2	2	160	18.4	4.91
578811945	PREDICTED: large proline-rich protein BAG6 isoform X12 [Homo sapiens]	6.55	22	1 4	10	1.125		1		503 1	l .	300.47		6	10	1114	117.5	6.00
4506121 578808297	vitamin K-dependent protein Z isoform 2 precursor [Homo sapiens]	10.00	2	1 2	7	1.125		1		187 1 269 1		62.22 49.07	10.00	4	7	400 1424	44.7 158.3	5.97 6.35
578808297 4501893	PREDICTED: protein FAM193A isoform X1 [Homo sapiens] alpha-actinin-2 isoform 1 [Homo sapiens]	3.30 24.27	39	2 24	16 268	1.124		1 5.0		269 1 392 1		49.07 8350.41	3.30 24.27	10	16	1424 894	158.3 103.8	6.35 5.45
52627151	olfactory receptor 2AE1 [Homo sapiens]	4.95	1	1 2	6	1.121		1				37.57	4.95	4	6	323	36.6	9.06
45545435	COMM domain-containing protein 2 [Homo sapiens]	23.62	1 :	2 4	15	1.121		2 26.1		407 2	363.5		23.62	9	15	199	22.7	6.73
578817221 17158044	PREDICTED: FK506-binding protein 15 isoform X2 (Homo sapiens)	5.65 16.47	3	1 7	48	1.121		1		907 1 048 1		214.51	5.65	14	48	1151 249	126.7	5.20
17158044 530361586	40S ribosomal protein S6 [Homo sapiens] PREDICTED: peptidyl-protyl cis-trans isomerase H isoform X5 [Homo sapiens]	16.47	1 14	1 5	Z1	1.120		1		048 1 374 1		121.83 110.02	16.47 10.27	9	21	249 146	28.7 16.0	10.84 8.07
530366678	PREDICTED: unhealthy ribosome biogenesis protein 2 homolog isoform X1 [Homo sapiens]	2.82	2	1 5	13	1.119		1		914 1		37.28	2.82	7	13	1487	166.5	7.20
5031767	heat shock factor protein 1 [Homo sapiens]	4.73	1	1 2	4	1.116		2 7.4	1.0	003 2	0.7	33.22	4.73	2	4	529	57.2	5.19
25777612	26S proteasome non-ATPase regulatory subunit 3 (Homo sapiens)	16.67	1 :	3 8	15	1.115		3 11.9		236 3	0.1	395.86	16.67	14	15	534	60.9	8.44
389565487 150417973	programmed cell death protein 6 isoform 4 [Homo saplens]	9.09 5.06	4	1 1	3 88	1.114		2 23.		005 1 087 3	1 15.3	77.96		3	3	121	14.4 247.6	5.29 6.98
150417973 65787364	supervillin isoform 2 [Homo sapiens] coronin-1B [Homo sapiens]	5.06 8.18	14	1 6	88 27	1.113		23.		087 2 069 1	15.3	215.40 229.84		21	88	2214 489	247.6 54.2	6.98 5.88
190341099	V-set and transmembrane domain-containing protein 4 isoform 1 precursor (Homo sapiens)	15.00	3	1 4	5	1.113		1				34.66		4	5	320	36.1	9.86
73622130	BolA-like protein 2 [Homo sapiens]	16.45	1	1 2	9	1.112		1		547 1	l .	159.88		6	9	152	16.9	8.19
530376803	PREDICTED: exocyst complex component 1 isoform X4 [Homo saplens]	8.65	4	1 8	39	1.112		1		136 1		219.73		17	39	879	100.2	6.60
6715607 530367946	hemoglobin subunit gamma-2 [Homo sapiens]  PREDICTED: serine/arginine-rich splicing factor 7 isoform X2 [Homo sapiens]	84.35 13.00	1 5	1 11	276	1.112 1.112		2 9.6		056 1 230 2	1 14.5	5785.98 88.24		32	276	147 223	16.1 25.6	7.20 11.80
116292750	apolipoprotein(a) precursor [Homo sapiens]	13.24	1	2 4	7	1.112		2 3.3		218 2	14.5			7	7	2040	226.4	6.07
38027914	COP9 signalosome complex subunit 8 isoform 2 (Homo sapiens)	8.75	2	1 1	- 1	1.111		1	1.3	376 1		24.14		1	1	160	17.9	7.25
392494084	eukaryotic translation initiation factor 6 isoform a [Homo saplens]	13.88	1	1 1	6	1.111		2 16.3		741 2	17.2			3	6	245	26.6	4.68
378404908 32129199	glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]  SAP domain-containing ribonucleoprotein [Homo sapiens]	92.83 4.76	3	1 24	2605	1.111		1		120 1 118 1		90307.10	92.83 4.76	72	2605	293 210	31.5 23.7	7.61 6.42
32129199 4758384	peptidyl-prolyl cis-trans isomerase FKBP5 isoform 1 [Homo sapiens]	12.25	2	2 5	15	1.110		2 6.1		945 2	2 0.8			11	15	210 457	51.2	5.90
532164720	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform isoform c [I	7.67	3	1 2	5	1.109		1	1.4	139 1	ı	77.12	7.67	4	5	391	46.2	5.92
5174731	translin-associated protein X [Homo sapiens]	19.31	1 :	2 4	18	1.109		4 21.5	1.1	150 4	35.0	555.33	19.31	8	18	290	33.1	6.55
5453832 261862352	hypoxia up-regulated protein 1 precursor (Homo sapiens)	11.11	2	3 8	21	1.108 1.107		3 8.0		104 2 360 1	3.0		11.11 7.66	14	21	999 483	111.3 53.4	5.22 8.15
261862352 312433975	serine hydroxymethyltransferase, mitochondrial isoform 3 [Homo sapiens] eukaryotic translation initiation factor 3 subunit C isoform a [Homo sapiens]	7.66 9.09	3	3 7	14	1.107		1 3 4. <sup>4</sup>		360 1 951 2	35.2	29.58 244.37	7.66	3	14	483 913	53.4 105.3	8.15 5.68
	,			,		1.101		**	0.	· · · · · · · · ·	30.2	244.37		14	21	7.0	.00.0	5.00

Accession 116063568	Description torsin-4A [Homo sapiens]	ΣCoverage 2.60	Σ# Proteins Σ# Uniqu	e Peptides Σ#	# Peptides	Σ# PSMs AB: 11!	5/114 A8: 115/114 Count 1.106	A8: 115/114 Variability [%]	A8: 117/116 1.25		A8: 117/116 Variability [%]	Score A(3,6,7) 31.26	Coverage A(3,6,7) 2.60	# Peptides A(3,6,7)	# PSM A(3,6,7)		MW (kDa)	calc. pl
116063568	torsin-4A [Homo sapiens] sacsin isoform 1 [Homo sapiens]	6.16	1	1	70	102	1.106	1	0.94		1	31.26 75.94		35	1 2 R 102	423 4579	46.9 520.8	7.94
4506687	40S ribosomal protein S15 [Homo sapiens]	24.14	1	2	2	5	1.104	2 6.2			2 22.7	133.14			5 5	145	17.0	10.39
8923417	poly(ADP-ribose) glycohydrolase ARH3 [Homo sapiens]	8.54	1	1	3	5	1.103	1	1.21	3	1	178.66	8.54		5 5	363	38.9	5.07
4507065	antileukoproteinase precursor [Homo sapiens]	9.09	1	1	1	2	1.103	1	0.81	3	1	97.39		2	2 2	132	14.3	8.75
42718017 352962174	DNA endonuclease RBBP8 isoform b [Homo sapiens] osteopontin isoform 4 precursor [Homo sapiens]	2.65 6.96	4	1	3	9	1.102	1	1.23	0 .	,	36.00 151.08		3	3 9	867 273	98.4 30.8	6.64 4.59
530376357	PREDICTED: ADP-ribosyl cyclase 2 isoform X3 [Homo sapiens]	25.26	4	4	5	20	1.100	6 4.7			5 3.4			13	3 20		32.7	7.08
122937185	protein LCHN (Homo sapiens)	4.40	1	1	2	2	1.100	1	3.37		1	39.95		2	2 2	455	51.4	5.31
578815866	PREDICTED: elongation factor 1-delta isoform X9 [Homo sapiens]	15.21	8	1	8	33	1.100	1	1.26		1	880.50		19	9 33		73.0	6.34
530373508	PREDICTED: serine/threonine-protein kinase OSR1 isoform X1 [Homo sapiens]	9.78	2	2	5	14	1.099	2 2.4			2 6.7			9	9 14		50.6	7.02
578837470 530426177	PREDICTED: DNA topoisomerase 3-beta-1 isoform X8 [Homo sapiens]  PREDICTED: transport and Golgi organization protein 2 homolog isoform X5 [Homo sapiens]	4.99 25.23	3	1	5	10	1.098	1	0.92		1	17.01 247.04	4.99 25.23		5 10	862	96.6 24.2	8.12 5.30
530420177	PREDICTED: transport and doign organization protein 2 formous solution x3 [Homo sapiens]	2.85	5	1	4	7	1.097	1	1.33		1	38.83			6 7	1019	112.0	5.45
5730027	KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 1 [Homo	9.93	5	3	5	17	1.096	2 2.1			2 29.9			11	1 17		48.2	8.66
194473714	latexin [Homo sapiens]	12.16	1	2	2	5	1.095	2 4.4	0.84	8 2	2 29.9	249.87	12.16	5	5 5	222	25.7	5.78
530419646	PREDICTED: MORC family CW-type zinc finger protein 2 isoform X2 [Homo sapiens]	7.29	3	1	10	21	1.095	1	0.84		1	30.52		11	1 21		117.4	8.44
530364823 211059425	PREDICTED: nitrilase homolog 1 isoform X3 [Homo sapiens]	24.40	7	3	4	9	1.095	3 7.3			1	135.70		9	9 9	291	31.8 15.0	6.87 5.29
211059425 578809385	small integral membrane protein 24 precursor (Homo sapiens) PREDICTED: extracellular matrix protein FRAS1 isoform X4 [Homo sapiens]	15.38	1 5	1	7	13	1.094	1	1.20		1	102.74 28.41	15.38	2	3 3 7 13	130 3897	430.3	5.29
378548190	40S ribosomal protein S3 isoform 1 [Homo sapiens]	11.93	3	2	3	26	1.093	2 1.4			2 17.5		11.93	9	9 26	243	26.7	9.66
48255933	non-histone chromosomal protein HMG-14 [Homo sapiens]	64.00	1	7	7	43	1.093	4 8.8			4 9.2	1324.63	64.00	21	1 43	100	10.7	9.60
4504011	glutamatecysteine ligase regulatory subunit (Homo sapiens)	15.69	2	2	4	17	1.092	2 5.8			2 1.2	339.37	15.69	10	17	274	30.7	6.02
41281564 300388183	WD repeat-containing protein 37 [Homo sapiens]  26S proteasome non-ATPase regulatory subunit 1 isoform 2 [Homo sapiens]	4.05 1.95	1	1	2	4	1.092	1	1.21		1	142.70 220.18	4.05 1.95	4	4 4	494 922	54.6 102.2	7.23 5.27
648216291	N-myc proto-oncogene protein isoform 2 [Homo sapiens]	5.93	2	1	2	4	1.091	1	1.18		1	45.30	5.93		3 3	253	28.3	8.95
530400242	PREDICTED: ADP-ribosylation factor-like protein 1 isoform X1 (Homo sapiens)	11.85	2	1	1	3	1.090	1	1.13		1	136.57		3	3 3	135	15.4	5.34
8922911	radical S-adenosyl methionine domain-containing protein 1, mitochondrial precursor [Homo saf	5.43	1	1	3	7	1.090	1				29.32	5.43	6	6 7	442	48.7	7.78
24111244	MAM domain-containing glycosylphosphatidylinositol anchor protein 1 precursor (Homo sapiens	2.62	2	1	3	26	1.090	2 4.5			2 18.0			3	3 26	955	105.7	8.34
635172849 5031839	beta-hexosaminidase subunit beta isoform 2 [Homo sapiens] keratin, type II cytoskeletal 6A [Homo sapiens]	22.05 27.30	2	3	6 18	14 84	1.089 1.088	3 5.7	1.33		7.0	296.13 2038.21	22.05 27.30	11	1 14		38.2 60.0	6.44 8.00
530386260	PREDICTED: colled-coll domain-containing protein 146 isoform X3 [Homo sapiens]	5.10	5	2	18	13	1.088	1	1.48		1	2038.21 35.37		50	7 13		97.2	9.20
495528154	collagen alpha-1(V) chain isoform 2 preproprotein [Homo sapiens]	2.50	2	2	4	8	1.087	2 8.6			1	137.01			7 8	1838	183.5	5.07
170763500	protein SET isoform 1 [Homo sapiens]	35.17	5	6	6	27	1.086	8 7.2	1.11		B 8.5	1084.55	35.17	18	В 27	290	33.5	4.32
145312241	differentially expressed in FDCP 6 homolog [Homo sapiens]	15.53	18	3	11	39	1.085	6 3.7			68.8			21	1 39		73.9	6.05
5174661 4507123	protein S100-A2 (Homo sapiens) U2 small nuclear ribonucleoprotein B" (Homo sapiens)	9.28 23.11	1	1	1	3	1.084	1	0.96		1	181.27 153.73	9.28 23.11	3	3 3 1 15	97	11.0 25.5	4.78 9.72
262118216	colled-coll domain-containing protein 88B precursor [Homo sapiens]	5.08	2	2	7	14	1.084	3 2.9			3 48.8			11	2 14		164.7	5.11
7661734	m7GpppX diphosphatase [Homo sapiens]	12.46	1	3	4	16	1.083	4 12.6			4 0.7	372.40		12	2 16		38.6	6.38
4503097	casein kinase II subunit alpha' (Homo sapiens)	7.43	8	1	3	9	1.083	1	1.01	5 '	1	95.26	7.43	9	9 9	350	41.2	8.56
530395150	PREDICTED: switch-associated protein 70 isoform X2 [Homo sapiens]	11.70	2	1	5	9	1.083	1	2.27		1	84.12		9	9 9	436	51.6	6.00
530407994	PREDICTED: hemoglobin subunit zeta isoform X2 [Homo sapiens]	30.99	2	1	3	96	1.082	1 2 11.3	1.51		1	2709.18			7 96	142	15.6	8.21
226056130 149773456	prostaglandin reductase 1 isoform 2 (Homo sapiens) uncharacterized protein KIAA0754 (Homo sapiens)	10.63	2	2	2	4	1.082	2 11.3	1.30		2 25.4	169.82		4	4 4	301 1427	32.9 150.4	7.20 4.32
116875826	HD domain-containing protein 2 [Homo sapiens]	9.80	1	1	2	6	1.080	1	1.03		1	123.27	9.80		6 6	204	23.4	5.49
578833510	PREDICTED: syntaxin-binding protein 2 isoform X1 [Homo sapiens]	31.63	7	11	13	45	1.079	1 10.2			1 25.1	1740.54		37	7 45		63.3	6.51
38202214	protein transport protein Sec23A [Homo sapiens]	9.93	4	3	6	18	1.079	3 9.4	1.07		2 0.3	340.86	9.93	15	5 18	765	86.1	7.08
68303549	argininosuccinate lyase isoform 3 (Homo sapiens)	10.96	4	2	5	25	1.079	2 0.7			2 0.7	314.77	10.96	13	3 25		48.7	6.13
13129078 530375442	tether containing UBX domain for GLUT4 isoform 1 [Homo sapiens]  PREDICTED: E3 ubiquitin-protein ligase CBL-B isoform X2 [Homo sapiens]	4.16 5.19	2	1	1	1	1.079	1	2.40 1.28		1	29.87 79.20	4.16 5.19	1	1 1 9 12	553 982	60.1 109.4	6.64 7.88
28372531	serine/threonine-protein phosphatase 4 regulatory subunit 2 [Homo sapiens]	6.47	1	1	2	4	1.078	1	1.11		1	153.11	6.47	1	9 12	417	46.9	4.54
132566536	voltage-dependent calcium channel subunit alpha-2/delta-4 [Homo sapiens]	1.76	1	1	3	11	1.078	1	1.09		1	45.69	1.76	-	6 11	1137	127.9	5.35
530421763	PREDICTED: protein PBDC1 isoform X1 [Homo sapiens]	4.31	2	1	1	2	1.077	1	1.10		1	57.38		- 2	2 2	232	26.6	9.36
7657015	tRNA-splicing ligase RtcB homolog [Homo sapiens]	12.08	1	1	4	14	1.077	2 5.4			2 28.1	302.22	12.08	8	B 14	505	55.2	7.23
530415691 55749779	PREDICTED: NACHT, LRR and PYD domains-containing protein 13 isoform X1 (Homo sapiens) DENN domain-containing protein 1A isoform 1 [Homo sapiens]	5.12 2.97	2	1	5	10	1.077	1 2 13.1	1.00		2 37.3	35.88 39.34	5.12 2.97		5 10	1036	118.1 110.5	5.54 6.96
24431935	reticulon-4 isoform A (Homo sapiens)	4.19	5	2	5	14	1.076	4 1.4			4 11.4	448.23		4	4 o B 14		129.9	4.50
5803092	methionine aminopeptidase 2 [Homo sapiens]	10.25	1	1	4	19	1.076	1	1.11		1	221.44	10.25	9	9 19		52.9	5.82
530396980	PREDICTED: lysosomal Pro-X carboxypeptidase isoform X1 [Homo sapiens]	19.69	3	5	5	33	1.076	1 11.5			1 7.4			15	5 33		43.9	6.30
186972143	tripeptidyl-peptidase 2 [Homo sapiens]	5.76	5	3	6	24	1.076	7 4.9			7 21.0		5.76	12	2 24		138.3	6.32
127139033	NADPHcytochrome P450 reductase [Homo sapiens] kininogen-1 isoform 2 precursor [Homo sapiens]	15.74	1	5	8	21 500	1.075	5 14.7 7 4.9			5 16.2 7 13.7			19	9 21		77.0 47.9	5.58 6.65
4504893	cAMP-dependent protein kinase catalytic subunit alpha isoform 2 [Homo sapiens]	63.70 27.70	2	2	12	500	1.074	7 7.5			7 13.7			82	2 500		47.9 39.8	8.66
27501446	density-regulated protein (Homo sapiens)	9.60	1	2	2	12	1.074	4 2.7			4 13.9			24	6 12		22.1	5.30
530380424	PREDICTED: protein diaphanous homolog 1 isoform X1 [Homo sapiens]	11.92	3	5	15	53	1.073	6 9.2	1.13	4 (	6.1	626.73	11.92	28	B 53	1250	139.3	5.31
4758440	glia maturation factor gamma (Homo sapiens)	44.37	2	4	6	78	1.073	3 6.6			3 10.3			18	B 78		16.8	5.26
207029439	histone-binding protein RBBP4 isoform c (Homo sapiens)	22.05	3	2	7	20	1.073	2 1.8			2 45.2			18	B 20		43.5	4.96
530371599	PREDICTED: THAP domain-containing protein 4 isoform X1 [Homo sapiens]  PREDICTED: tenascin isoform X4 [Homo sapiens]	2.95	21	1	4	27	1.073	1	1.29		1	130.96 78.24		10	D 27	711	76.0 171.2	9.58 5.10
39753957	PREDICTED: tenascin isoform X4 [Homo sapiens] torsin-1A-interacting protein 1 isoform 2 [Homo sapiens]	2.40	1	1	1	3	1.073	1	0.94		1	198.17			3 3	1564	1/1.2	5.10 8.18
540344580	probable guanine nucleotide exchange factor MCF2L2 (Homo sapiens)	5.03	1	1	6	102	1.072	2 6.5			2 13.4			12	2 102		126.9	6.42
25777713	S-phase kinase-associated protein 1 isoform b [Homo sapiens]	27.61	2	3	4	10	1.072	3 10.8			3 10.8			10	0 10		18.6	4.54
4502899	clathrin light chain A isoform a [Homo sapiens]	11.47	6	3	3	8	1.071	3 4.2			3 11.8			8	B 8	218	23.6	4.53
530392685 4504383	PREDICTED: chondroltin sulfate N-acetylgalactosaminyltransferase 2 isoform X1 [Homo sapiens		4	1	6	11	1.071	1	1.67		1	38.43		6	6 11	342	39.5	5.44 7.24
4504383 48762934	hepatocyte growth factor activator isoform 2 preproprotein [Homo sapiens] collagen alpha-2(I) chain precursor [Homo sapiens]	2.44 0.51	2	1	2	0	1.070	1	1.20			88.05 21.18		4	1 1	655 1366	70.6 129.2	7.24 8.95
530383030	PREDICTED: Lebercilin isoform X2 [Homo sapiens]	9.76	1	1	. 8	25	1.070	1	1.16		1	99.22		11	1 25		80.5	7.68
601984520	polyubiquitin-C (Homo sapiens)	95.33	7	14	14	158	1.070	3 9.4			3 9.3	5503.44	95.33	40	158		77.0	7.66
578842437	PREDICTED: leukocyte immunoglobulin-like receptor subfamily B member 1 isoform X6 [Homo	7.80	28	1	5	16	1.070	1	1.29		1	483.66		13	3 16		66.6	6.67
118918435 11225260	von Willebrand factor A domain-containing protein 3B [Homo sapiens]	1.16 9.93	3	1	2	9	1.069	3 4.8	1.03		3 10.3	120.05	1.16	3	3 9	1294	145.7 90.7	7.33 9.31
11225260 24308163	DNA topoisomerase 1 [Homo sapiens] protein fem-1 homolog A [Homo sapiens]	9.93 8.22	1	1	9	22	1.069	1	1.15		1	124.49 86.41	9.93 8.22	13	3 22	765 669	90.7 73.6	9.31 6.07
24308163	guanine nucleotide-binding protein G(t) subunit alpha-2 [Homo sapiens]	6.50	13	1	3	34	1.069	4 11.8			4 2.9	333.71	6.50	10	B 34	354	73.6 40.2	5.24
116256489	septin-9 isoform c [Homo sapiens]	14.79	8	7	8	30	1.068	8 5.4			B 19.0	747.81	14.79	24	4 30	568	63.6	8.40
571026657	BRISC and BRCA1-A complex member 1 isoform 2 [Homo sapiens]	9.06	2	1	1	2	1.068	1	1.40	6	1	34.79	9.06	3	2 2	254	28.1	4.54
221316573	barrier-to-autointegration factor [Homo sapiens]	34.83	1	2	2	8	1.068	3 5.4			3 24.6	89.76	34.83		6 8	89	10.1	6.09
38679892 311771535	peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 isoform 1 [Homo sapiens]	7.05	1	1	10	1 29	1.068	1	1.35		1	22.77 780.08			1 1	156 488	16.6 52.7	9.96
311771535	T-complex protein 1 subunit beta isoform 2 [Homo sapiens] inactive phospholipase D5 isoform 3 [Homo sapiens]	21.31	2	1	10	7	1.067	8 3.6	1.10		5.0 1	780.08 37.68		24	3 7	488	52.7 37.7	6.44 9.28
557128998	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase MESH1 isoform 1 [Homo sapiens]	17.88	2	1	2	4	1.067	1	1.18		1	108.35			4 4	179	20.3	6.74
578811315	PREDICTED: flotillin-1 isoform X3 [Homo saplens]	9.09	3	1	3	23	1.067	1	1.13		1	112.90	9.09	1	7 23	374	41.6	5.83
119703753	keratin, type II cytoskeletal 6B [Homo sapiens]	29.08	11	1	19	89	1.067	3 7.1			3.2			51	1 89		60.0	8.00
425905337	serine/threonine-protein phosphatase 2A activator isoform f [Homo sapiens]	34.01	5	5	8	28	1.066	6 14.9			6 42.2			20	0 28		33.4	6.29
530360793 285002251	PREDICTED: serine/arginine repetitive matrix protein 1 isoform X6 [Homo sapiens] N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase isoform 1 preproprotein [Homo sapiens]	0.68	7	1	1	5 22	1.066	2 2.1 7 10.2			2 31.6 7 6.5		0.68		3 5	888 346	100.2	11.77
28872800	CCAAT/enhancer-binding protein epsilon [Homo sapiens]	7.83	1	1	3	4	1.065	1 10.2	1.00		0.5	26.14		12	3 4	281	30.6	8.98
4506669	60S acidic ribosomal protein P1 isoform 1 [Homo sapiens]	19.30	1	1	2	13	1.064	2 2.5	1.05	0 :	2 61.7	216.75	19.30		6 13	114	11.5	4.32
4759270	translin isoform 1 [Homo sapiens]	44.74	21	7	8	44	1.064	2 8.3	1.17	2 1	1 21.2	1526.32	44.74	24	4 44	228	26.2	6.44

Accession	Description	FC	Ed Pastalas	Ed Halana Bantidas	F# Donkley	F# DCM-	40. 335/33	40. 115/114 0	AO. 235 (234 Verlebille: [0/]	40. 117/1	40. 117/11/ 0	AD. 227/22/ Martin III. (0/)	F 1/2 / 7	) Coverage A(3,6,7) # Peptides A(3,6,7)	7) # PCM 4/3 ( 7)	# AAs	MW [kDa]	anta at
194363758	Signal recognition particle 9 kDa protein isoform 1 [Homo sapiens]	ΣCoverage 23.17	2# Proteins	2# Unique Peptides	2# Peptides	2# PSMs	AB: 115/114 4 1.0		A8: 115/114 Variability [%]		248 AB: 11//116 Count	A8: 11//116 Variability [%]			6 # PSM A(3,6,7)	# AAS	MW (KDa)	calc. pl
	protein mago nashi homolog (Homo sapiens)	17.12	2		1 2	10	0 1.0		3 5.0		210 3	3 3.9			4 10	146	17.2	6.11
578836451	PREDICTED: lipase member I isoform X7 [Homo sapiens]	4.02	7	1	1 2	2	2 1.0	63	1	0.	982 1	1	0.00	0 4.02	2 2	2 398	45.8	9.35
287326622	tyrosine-protein kinase HCK isoform d [Homo sapiens]	11.90	100	3	3 6	23			3 1.5		010 3	3 11.4			16 23		57.2	6.86
4506743	40S ribosomal protein S8 [Homo sapiens]	5.77	3		2 2	6	6 1.0		2 4.9		990 2	2 15.6			6 6	5 208	24.2	
46094058 21314600	bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Homo sapiens]	4.01	1	1	1 2	7	7 1.0 7 1.0		1		341 1	1	147.40 716.87		4 7	7 624	70.8 38.1	
	carcinoembryonic antigen-related cell adhesion molecule 8 precursor [Homo sapiens]	24.64	11		5 6	27	7 1.0		9 10.5		107 S	9 12.1	716.87		15 27	7 349	38.1 69.6	
6912356	HAUS augmin-like complex subunit 3 [Homo sapiens] echinoderm microtubule-associated protein-like 2 isoform 2 [Homo sapiens]	8.63	1	1	1 1	12	2 1.0 7 1.0		4 10.6		126 4	4 7.9			2 2		70.6	
	histone-lysine N-methyltransferase 2C [Homo sapiens]	2.40	0		1 13	26			1 10.0		751 1	1 7.7	470.77		13 26		541.0	
4507129	small nuclear ribonucleoprotein E (Homo sapiens)	27.17	1		1 1	20			6 10.3		500 6	6 23.1			3 20		10.8	
	glutaminyl-peptide cyclotransferase precursor [Homo sapiens]	22.44	39	4	4 5	29			8 5.8		086 8	8 20.5			15 29		40.9	
5579478	dual specificity mitogen-activated protein kinase kinase 1 [Homo sapiens]	26.46	3	4	4 11	37	7 1.0	61	5 2.3	.3 1	302 5	5 5.3	810.44	4 26.46 2	27 37	7 393	43.4	6.62
419635906	tRNA-dihydrouridine(20) synthase [NAD(P)+]-like isoform 2 [Homo sapiens]	4.15	2	1	1 3	5	5 1.0	61	1	1.	695 1	1	20.93	3 4.15	3 5	5 458	51.4	7.33
	homeobox protein GBX-2 [Homo sapiens]	2.59	1	1	1 2	3	3 1.0	61	1		707 1	1	28.26	6 2.59	2 3	3 348	37.3	
	PREDICTED: myosin regulatory light chain 12A isoform X1 [Homo sapiens]	72.51	7	1	1 12				2 10.8		647 2	2 64.5			36 155		19.8	
94721241	isoleucinetRNA ligase, cytoplasmic (Homo sapiens)	4.68	1	1	1 5	13			1		168 1	1	107.96		11 13		144.4	
	PREDICTED: tyrosine-protein kinase CSK isoform X1 [Homo sapiens]	30.22	2		8 10	35			9 6.4	4 1.	149 9	9 15.0			26 35		50.7	
578801274 14249158	PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X6 [Homo sapiens]	2.31	2		1 9	62	2 1.0 0 1.0		2 5.3		211 2	2 17.4	192.22		18 62 7 10		325.3 74.2	
4826972	hepatoma-derived growth factor-related protein 2 isoform 2 [Homo sapiens]  RNA-binding protein 8A [Homo sapiens]	5.22 20.69	9		1 3	13			3 16.0		277 3	3 22.1			9 13		19.9	
	trifunctional purine biosynthetic protein adenosine-3 isoform 2 [Homo sapiens]	12.47	3		2 5	13			2 3.5		133 2	2 0.7			9 13		46.0	
4506005	serine/threonine-protein phosphatase PP1-beta catalytic subunit isoform 1 [Homo sapiens]	28.75	4		3 7	38			5 5.3		223 5	5 1.8			21 38		37.2	
34098946	nuclease-sensitive element-binding protein 1 [Homo sapiens]	23.46	5		2 6	23			4 4.8		219 4	4 13.5			12 23		35.9	9.88
	CD44 antigen isoform 8 precursor [Homo sapiens]	13.27	19	3	3 4	20			7 14.3		104 6	6 16.2			10 20		32.1	
530384106	PREDICTED: fibronectin type III domain-containing protein 1 isoform X1 [Homo sapiens]	3.46	2	1	1 5	90	0 1.0	59	1	2.4	144 1	1	94.69	9 3.46	9 90	1819	197.6	9.29
530403927	PREDICTED: protein Z-dependent protease inhibitor isoform X1 [Homo sapiens]	22.97	2	4	4 8	21			5 4.5		168 5	5 7.5			18 21		50.7	
4507669	translationally-controlled tumor protein isoform 2 [Homo sapiens]	62.21	6	8	8 8	57			5 7.6		162 12	10.9			24 57		19.6	4.93
14249348	thioredoxin domain-containing protein 17 [Homo sapiens]	30.08	1	3	3 3	10			4 11.2		089 4	4 17.1			8 10		13.9	
	26S proteasome non-ATPase regulatory subunit 10 isoform 1 [Homo sapiens]	26.11	1	1	1 3	8	B 1.0		2 0.0		208 2 987 3	2 0.0			5 8	B 226	24.4	
	PREDICTED: serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isofor ADP-ribosylation factor 1 (Homo sapiens)	12.11	20	3	3 5 4 10	17			3 6.6		987 3 331 10	3 12.1 0 16.7			13 17		51.6 20.7	
	ADP-ribosylation factor 1 [Homo sapiens] proteasome subunit alpha type-2 [Homo sapiens]	62.98 48.29	3		4 10	56 52					331 10 187 13	16.7 13 16.1			26 56 21 52		20.7	
	stromal membrane-associated protein 2 isoform 4 [Homo sapiens]	2.29			, ,	52	2 1.0		3 7.5	.5 1.		3 10.1	40.81		2 2	2 349	37.7	
118150678	epithelial cell-transforming sequence 2 oncogene-like [Homo sapiens]	8.85	2	1	1 6	14			1		B52 1	1	40.81		10 14		104.8	
	PREDICTED: ras-related protein Ral-B isoform X4 [Homo sapiens]	13.59	2		1 4	8	B 1.0		1		437 1	i	208.69		7 9	206	23.4	
126362971	serine/threonine-protein kinase 10 [Homo sapiens]	17.77	1	ç	9 14	58	B 1.0	57 1	1 6.4	4 1.	221 11	12.0	1642.06	6 17.77 3	37 58	968	112.1	6.95
4758516	hepatoma-derived growth factor isoform a [Homo sapiens]	70.00	12	15	5 17	149	9 1.0	57 4	8.0	.0 1.	086 48	18 13.9	5596.40	0 70.00 5	51 149	9 240	26.8	4.73
20336761	heme-binding protein 1 [Homo sapiens]	8.47	1	1	1 2	8	B 1.0	57	2 4.0	.0 1.	113 2	2 42.3	166.24	4 8.47	5 8	189	21.1	
	ADP-ribosylation factor 4 [Homo sapiens]	34.44	1	1	1 4	76			5 1.1		396	5 10.1			11 76		20.5	
	AT-rich interactive domain-containing protein 1A isoform b [Homo sapiens]	2.03	2	1	1 4	10	0 1.0		1	1.0		1	237.31		7 10		218.2	
4758356	flap endonuclease 1 (Homo sapiens)	22.89	1	4	4 8	26	6 1.0		6 5.1		130 6	6 5.2			17 26		42.6	
530385605 307746865	PREDICTED: leucine-rich repeat and WD repeat-containing protein 1 isoform X1 [Homo sapiens	5.21	3		1 3	5	5 1.0 5 1.0		1		2 <b>61</b> 1		33.50 47.24		3 5	5 595 5 565	65.3 61.2	
530367188	excitatory amino acid transporter 2 isoform 2 [Homo sapiens] PREDICTED: coiled-coil domain-containing protein 104 isoform X2 [Homo sapiens]	1.42	5		1 1		7 1.0		1		768 1		32.16		3 5	7 218	25.0	6.67 4.51
	PREDICTED: collect-coll domain-containing protein 164 isoform X2 [Homo sapiens]  PREDICTED: gamma-interferon-inducible protein 16 isoform X2 [Homo sapiens]	13.44	3		5 10	48			6 11.5		766 E	6 7.8			21 48		76.3	
	PREDICTED: H/ACA ribonucleoprotein complex subunit 1 isoform X1 [Homo sapiens]	4.15	1		1 1	3	3 1.0		1	1.3		1	71.75		3 2	3 217	22.3	
90669511	quinone oxidoreductase-like protein 1 [Homo sapiens]	7.16	1		1 3	12			2 2.3		081 2	2 3.6			6 12		38.7	
530416417	PREDICTED: apolipoprotein C-I isoform X1 [Homo sapiens]	38.55	7	4	4 5	27	7 1.0	56	8 6.0	.0 1	164 8	8 15.5	809.66		14 27	7 83	9.3	
	PREDICTED: isoamyl acetate-hydrolyzing esterase 1 homolog isoform X1 [Homo sapiens]	18.39	2	1	1 4	12	2 1.0	56	1		094 1	1	144.45	5 18.39	9 12	2 223	25.0	5.43
	class E basic helix-loop-helix protein 22 [Homo sapiens]	1.84	1	1	1 1	1	1 1.0		1		296 1	1	0.00		1 1	1 381	37.0	
530369184	PREDICTED: interleukin-1 receptor antagonist protein isoform X1 [Homo sapiens]	13.29	4	1	1 1	3	3 1.0		1		693 1	1	122.73		3 3	143	16.1	
7705431	translation machinery-associated protein 7 [Homo sapiens]	15.63	1	1	1 1	6	6 1.0		2 0.7		167 2	2 11.0			3 6	64	7.1	
	RNA-binding protein 25 (Homo sapiens)	5.58	23		2 6	25			2 0.5		098 2	2 50.8			15 25		100.1	
	PREDICTED: synaptotagmin-like protein 2 isoform X12 [Homo sapiens]	5.42	4	-	1 14				3 9.7			3 17.8			19 37		244.1	
	pyridoxine-5'-phosphate oxidase [Homo sapiens]  PREDICTED: acid ceramidase isoform X1 [Homo sapiens]	14.56 11.26	2		1 3	19	9 1.0 7 1.0		2 3.0		132 1 348 2	2 3.7	100.96		5 19	9 261 7 373	30.0 42.6	
	citrate synthase, mitochondrial precursor [Homo sapiens]	13.09	- 1		2 3	23			3 2.2		127 3	3 27.3			8 23		51.7	
	26S proteasome non-ATPase regulatory subunit 11 [Homo sapiens]	9.00			2 3	23	7 1.0		2 2.6		817 2	2 10.0			7 7	7 422	47.4	
	PREDICTED: roquin-1 isoform X5 [Homo sapiens]	2.36	4	-	1 4	8	В 1.0		1		198 1	1	36.44		4 8	1101	122.6	
	hexokinase-2 [Homo sapiens]	9.16	2	1	1 9	24			1		675 1	1	438.00		16 24		102.3	
45006986	aminoacyl tRNA synthase complex-interacting multifunctional protein 1 isoform a precursor [Ho	8.33	2	1	1 2	7	7 1.0	54	2 5.8	.8 1.	036 2	2 16.5	412.57	7 8.33	4 7	7 312	34.3	8.43
	PREDICTED: ras-GEF domain-containing family member 1B isoform X3 [Homo sapiens]	4.86	2	1	1 2	14			6 13.2			3 4.9			4 14	4 432	50.4	8.06
40254823	phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform b [Homo sapiens]	10.27	2		5 10	25			5 7.5			5 11.9			23 25		133.1	7.59
530391261	PREDICTED: TBC1 domain family member 13 isoform X1 [Homo sapiens]	4.63	1	1	1 2	4	4 1.0		1		023 1	1	30.14		2 4	4 324	37.7	4.97
38201680	meiotic recombination protein SPO11 isoform b [Homo sapiens]	9.22	4	1	1 4	7	7 1.0		1	4.2			32.13		6 7	7 358	40.3	
237681091	double-stranded RNA-specific editase 1 isoform 7 [Homo sapiens]	1.34	9	1	1 1	6	6 1.0		2 7.4		043 2	2 6.5			3 6	674	73.6	
	PREDICTED: dynamin-1-like protein isoform X2 [Homo sapiens] zinc finger protein 512 isoform a [Homo sapiens]	2.90 11.29	8		1	25	3 1.0 5 1.0		1		455 1 228 1	1	288.04 175.69		3 3	5 567	65.3 64.6	7.49 9.76
40217790 82880645	ubiquitin carboxyl-terminal hydrolase 14 isoform b [Homo sapiens]	23.31	4	1	8 10	25	7 1.0		2 10.6		228 T	1 13.5			12 25 25 37		52.4	
	PREDICTED: MAP kinase-activating death domain protein isoform X25 [Homo sapiens]	3.35	12		1 6	22			1	1	043 1	1	46.32		11 22		172.8	6.18
4507677	endoplasmin precursor [Homo sapiens]	24.28	13	13	3 18				8 5.2		145 18	18 14.1			48 73		92.4	
	PREDICTED: tubulin alpha-4A chain isoform X1 (Homo sapiens)	50.35	7		4 16				7 10.4		142 7	7 39.9			47 139		48.3	
4505981	platelet basic protein preproprotein [Homo sapiens]	7.81	1	1	1 1	2	2 1.0	51	1	0	984 1	1	128.69	9 7.81	2 7	2 128	13.9	8.79
324120908	doublecortin domain-containing protein 5 [Homo sapiens]	3.48	1		2 4	46	6 1.0	51	5 2.7	.7 1.	168 5	5 23.1	212.55	5 3.48 1	10 46	5 890	100.3	8.95
	helicase with zinc finger domain 2 isoform 1 [Homo sapiens]	4.11	24	1	1 10	25			1		978 1	1	89.60		17 25		294.5	
4506761	protein S100-A10 (Homo sapiens)	49.48	1	1	1 4	4	4 1.0		1		329 1	1	42.38		4 4	4 97	11.2	
	DNA damage-binding protein 1 [Homo sapiens]	4.82	1	1	1 4	17	1.0		1		949 1	1	248.40		8 17		126.9	
	PREDICTED: V-type proton ATPase subunit H isoform X1 [Homo sapiens]	8.82	2	1	1 4	10			2 0.7		261 2	2 9.0			7 10		54.1	
	acetyl-CoA acetyltransferase, cytosolic [Homo sapiens]	19.40	2	3	3 6	13			3 5.5	3 0.	937 3	3 25.0			13 13		41.3	
	39S ribosomal protein L17, mitochondrial [Homo sapiens] GTPase KRas isoform b [Homo sapiens]	8.57 9.04	1		2	4	4 1.0 4 1.0		1	+	068 1	1	23.41 91.55		4	4 175 4 188	20.0 21.4	
			1		2	4			6 15.2			6 15.2			15 21			
	septin-7 isoform 3 [Homo sapiens]  LYR motif-containing protein 5 [Homo sapiens]	13.22 17.78	18	3	3 5	31	1 1.0 B 1.0		3 15.2		156 é	1 15.2	960.12		15 31	1 401 3 90	46.5 10.9	
	enolase-phosphatase E1 isoform 2 [Homo sapiens]	24.28	2		2 2		7 1.0		2 3.5		169 2	2 8.2			7	7 173	19.2	
	nuclear autoantigen Sp-100 isoform 2 [Homo sapiens]	6.83	6	1	1 8	43			1		116 1	1	433.97		18 43		100.4	
16418381	vacuolar protein sorting-associated protein 26B [Homo sapiens]	10.42	1	1	1 3	8	B 1.0		1	0.		1	169.09		8 8	336	39.1	7.36
4507143	sorting nexin-3 isoform a (Homo sapiens)	19.14	3	3	3 4	19	9 1.0	50	4 5.5		174 4	4 3.8			12 19	9 162	18.8	8.66
	PREDICTED: myosin-6 isoform X4 [Homo sapiens]	6.10	76	1	1 16	61	1 1.0		1		194 1	1	417.33		30 61		226.6	
4758304	protein disulfide-isomerase A4 precursor [Homo sapiens]	19.53	2	1	7 11	41	1 1.0		8 4.8		135 8	8 5.9	1304.94	4 19.53	29 41		72.9	5.07
	PREDICTED: glutamine synthetase isoform X1 [Homo sapiens]	2.14	1	1	1 1	2	2 1.0		1		148 1	1	78.89		2 2	2 373	42.0	
	PREDICTED: 14-3-3 protein zeta/delta isoform X2 [Homo sapiens]	81.63	17	15	5 26	327			7 9.0		134 66	6 13.1			77 327		27.7	4.79
	PREDICTED: annexin A7 isoform X2 [Homo sapiens]	11.97	4	2	2 4	10	1.0		2 6.1		259 2	2 9.6			9 10		46.0	
5729804	diphosphoinositol polyphosphate phosphohydrolase 1 [Homo sapiens]	25.58	2	3	3 3	14			5 8.9	9 1.	121 5	5 16.8			8 14		19.5	
	PREDICTED: zinc finger CCCH domain-containing protein 7A isoform X3 [Homo sapiens]	5.11	2	1	1 5	7	7 1.0		1		193 1	1	26.92		5 7	7 958	109.2	
					2 4	20	0 1.0	49	5 6.9	.4 1	079 5	5 3.6	366.98	B 7.00 1	10 20	600	62.5	9.39
253970504	RNA-binding protein EWS isoform 4 (Homo sapiens)	7.00	0						1	_		1						
253970504 18860831	RNA-binding protein EWS soform 4 [Homo saplens] dynamin-like 120 kDa protein, mitochondrial isoform 2 [Homo saplens] zinc finger protein 280A [Homo saplens]	7.00 8.23 1.29	13	1	1 9	30	0 1.0	49	1 6.6		459 1 317 3	1 3 3.9	180.76	6 8.23 1	14 30		107.5	

		F.o.	Tere Term	F	F	T	T											
Accession 149589008	Description xaa-Pro dipeptidase isoform 1 [Homo sapiens]	ΣCoverage 16.02	Σ# Proteins Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/114 15 1.049	A8: 115/114 Count	A8: 115/114 Variability [%]		16 A8: 117/116 Count .505 4	A8: 117/116 Variability [%]	758.90	Coverage A(3,6,7) 16.02	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW (kDa) 54.5	calc. pl
530422764	PREDICTED: high mobility group protein B3 isoform X1 [Homo sapiens]	30.18	3	1 7	5	1.049		2 5.		.165 2	16.7	784.73	30.18	19	51	222	25.6	8.12
530398338	PREDICTED: alpha-tectorin isoform X1 [Homo sapiens]	1.16	2	1 3	1-			1.		.199 2	4.4	106.06	1.16	7	14		238.8	5.39
4885049	actin, alpha cardiac muscle 1 proprotein [Homo sapiens]	56.23	27	2 27	226			2 9.		.240 62	21.8	56764.70	56.23	77	2269		42.0	5.39
530390698	PREDICTED: adenylate kinase isoenzyme 1 isoform X3 [Homo sapiens]	18.72	3	1 3	2					.094 1		424.80	18.72	7	22		20.7	7.93
31652249	lipopolysaccharide-binding protein precursor (Homo sapiens)	12.27	1	4 5	3	7 1.048		16.	1.	.260 9	18.5	1348.47	12.27	14	31	481	53.3	6.70
578833192 296011001	PREDICTED: zinc finger protein 844 isoform X2 [Homo sapiens]	4.61 6.96	2	1 3		7 1.048		1 3 0.		.803 1 .146 3		25.23	4.61	3	7	499	57.5 42.6	8.59
578816553	abl interactor 1 isoform k [Homo sapiens] PREDICTED: centlein isoform X2 [Homo sapiens]	7.00	17	1 13	2	, 1.040		0.		.146 3	8.0	483.13 40.06	6.96	10	24		42.6 155.6	6.04 8.40
10800140	histone H2B type 1-B [Homo sapiens]	68.25	14	2 12	_			5.		.129 6	20.8	6662.32	68.25	36	217		13.9	10.32
354721179	ras-related protein Rab-5B isoform 2 [Homo sapiens]	28.16	5	2 5	2			15.0		310 3	103.5	607.81	28.16	12	23		19.1	7.30
10835067	lupus La protein [Homo sapiens]	21.32	1	6 9	4	1.048		6.	1.	.279 8	9.0	943.95	21.32	24	41	408	46.8	7.12
530406418	PREDICTED: tropomyosin alpha-1 chain isoform X18 [Homo sapiens]	47.76	29	3 17				3 2.		.073 3	6.5	3394.57	47.76	48	118		28.5	4.78
71274132	phosphoglycerate mutase 4 (Homo sapiens)	40.16	22	1 8	11					.178 1		3840.54	40.16	24	111		28.8	6.65
54607080 530374901	carboxypeptidase B preproprotein (Homo sapiens)  PREDICTED: protein CDV3 homolog isoform X4 (Homo sapiens)	3.12 46.67	1	1 1	1	4 1.047 6 1.047		I 5 1.		.255 1	24.7	33.63 615.52	3.12 46.67	2	16	417	47.3 21.7	6.61 5.54
578799563	PREDICTED: protein CDV3 nomolog isoform X4 [nomo sapiens]  PREDICTED: serinetRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	10.45	8	2 6	1			5 5.		.261 3	46.0	419.39	10.45	13	17		61.3	7.06
390635651	ras-related protein Rab-44 [Homo sapiens]	9.11	1	4 6	2			5 4.		.130 6	27.7	1074.55	9.11	14	20		110.8	5.08
4759300	vesicle-associated membrane protein 3 [Homo sapiens]	23.00	1	1 2	-	5 1.047				.124 1		263.30	23.00	4	. 5	100	11.3	8.79
42518068	trans-Golgi network integral membrane protein 2 isoform 1 precursor [Homo sapiens]	9.38	3	1 3		6 1.047		1		.206 1		80.69	9.38	5	6	437	45.9	5.63
4506193	proteasome subunit beta type-1 [Homo sapiens]	45.23	1	8 8	6	0 1.047	1	6.		.132 19	21.1	2822.78	45.23	24	60		26.5	8.13
4506127	ribose-phosphate pyrophosphokinase 1 isoform 1 [Homo sapiens]	25.79	5	4 7	2			5 4.		.186 5	4.9	678.24	25.79	19	24		34.8	6.98
57863298 145386517	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 isoform b [Homo sapiens]	4.29 7.34	17	1 9	3.			2 2.		.157 1	17.6	178.76 384.78	4.29 7.34	15	12	1655	184.7 67.9	7.75 5.40
4758112	phostensin [Homo sapiens] spliceosome RNA helicase DDX39B [Homo sapiens]	28.04	1	3 10	5	7 1.046		1 2.		.008 2	38.0	1379.00	28.04	78	57	428	49.0	5.40
578810779	PREDICTED: ras GTPase-activating protein-binding protein 1 isoform X1 [Homo sapiens]	4.94	1	1 1		6 1.046		2 15		.251 2	11.9	143.84	4.94	20	. 6	466	52.1	5.52
578825985	PREDICTED: proteasome activator complex subunit 2 isoform X1 [Homo sapiens]	63.19	2	1 9	3	9 1.046		1	1	.047 1		1486.84	63.19	27	39	163	18.6	7.99
4506179	proteasome subunit alpha type-1 isoform 2 [Homo sapiens]	60.08	3 1	12 16	8	32 1.046	2	13.		.118 25	6.7	2631.05	60.08	42	82	263	29.5	6.61
12965178	taste receptor type 2 member 13 [Homo sapiens]	2.64	1	1 1		6 1.046		2 1.		.190 2	11.3	62.20	2.64	2	2 6	303	35.1	9.66
4758950 530400291	peptidyl-prolyl cis-trans isomerase B precursor [Homo sapiens]	40.74 16.65	1	8 9	6	6 1.046 11 1.046		5.		.147 17	10.5	1407.04	40.74	26	66		23.7	9.41 5.47
530400291 33239451	PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X9 [Homo sapiens] proliferating cell nuclear antigen [Homo sapiens]	16.65 26.05	11	7 16	4	11 1.046 16 1.046		9 6.		.179 9	10.3	851.84 397.62	16.65 26.05	32	1 16	931	105.6 28.8	5.47 4.69
4885413	histidine triad nucleotide-binding protein 1 [Homo sapiens]	63.49	1	5 4	2			7 9.		.032 3	21.6	865.48	63.49	13	75	126	13.8	6.95
5453599	F-actin-capping protein subunit alpha-2 (Homo sapiens)	48.25	5	5 9	11			6.		.101 10	9.0		48.25	26	113		32.9	5.85
158937236	puromycin-sensitive aminopeptidase [Homo sapiens]	17.41	8 1	12 15	5			4.		.185 17	16.3	1845.57	17.41	40	57		103.2	5.72
5032133	eukaryotic translation initiation factor 1 [Homo sapiens]	25.66	2	1 3		9 1.045		1		.513 1		154.39	25.66	9	9 9	113	12.7	7.44
21361399	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform [Homo sap	27.67	11 1	10 13	4			6.		.283 14	17.3	1615.79	27.67	33	49		65.3	5.11
13027604 4506649	28S ribosomal protein S34, mitochondrial [Homo sapiens] 60S ribosomal protein L3 isoform a [Homo sapiens]	3.21 7.94	3	1 1		1 1.045 18 1.045				.105 1		22.66 68.83	3.21 7.94	1	1 28	218	25.6 46.1	9.98 10.18
4506649 55749431	transcription elongation factor A protein-like 3 [Homo sapiens]	18.00	1	1 6	2			10.		.207 1	5.6	398.25	7.94 18.00	13	26		46.1 22.5	4.92
22202633	prefoldin subunit 5 isoform alpha [Homo sapiens]	32.47	1	1 3		7 1.044		10.		1.698 1	5.0	136.39	32.47	6	7	154	17.3	6.33
325651836	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A membe	7.70	1	1 7	1					.317 1		179.35	7.70	11	16		121.8	8.09
32484979	AP-3 complex subunit beta-1 isoform 1 [Homo sapiens]	9.87	3	2 11	2	7 1.044		2.	0	.926 2	29.3	284.58	9.87	20	27	1094	121.2	6.04
13259510	dynactin subunit 1 isoform 1 [Homo sapiens]	6.34	6	2 9	6			1.		.143 3	2.9	465.29	6.34	22	60		141.6	5.81
578835493	PREDICTED: glycogen phosphorylase, brain form isoform X1 [Homo sapiens]	12.69	1	1 9	5			1		.187 1		1952.14	12.69	24	58		96.6	6.86
350529338	protein sel-1 homolog 1 isoform 2 precursor (Homo sapiens)	15.61	4	1 3		6 1.043		1		.267 1		109.72	15.61	5	6	301	33.5	4.83
7661728 578803042	ragulator complex protein LAMTOR2 isoform 1 [Homo sapiens]  PREDICTED: baculoviral IAP repeat-containing protein 6 isoform X7 [Homo sapiens]	32.00 2.85	2	3 3	2	21 1.043 24 1.043		3 2.		.108 3 .195 1	14.7	263.58 36.64	32.00 2.85	9	21	125 4840	13.5 528.0	5.40 6.13
344179112	scavenger receptor cysteine-rich type 1 protein M130 isoform b precursor [Homo sapiens]	4.46	16	3 5	1			2 12.1		.124 2	39.4	174.92	4.46	11	13		121.5	6.11
33356174	pinin [Homo sapiens]	4.74	1	1 6		9 1.043		1		.093 1	37.4	120.58	4.74	9	9 9	717	81.6	7.14
315259111	NEDD8-MDP1 protein [Homo sapiens]	21.76	4	1 4	2	1.043		1		.872 1		534.26	21.76	9	21	193	22.0	6.37
530362892	PREDICTED: leucine-rich repeat-containing protein 8D isoform X1 [Homo sapiens]	3.15	1	1 3		9 1.043		1		303 1		27.45	3.15	3	9	858	98.1	7.72
82617634	cytoplasmic FMR1-interacting protein 2 isoform a [Homo sapiens]	9.98	5	6 13	4	16 1.043		6.		.285 8	17.3	1006.21	9.98	26	46	1253	145.6	7.05
41406084 195539395	glutathione peroxidase 1 isoform 1 (Homo sapiens)	29.56 16.13	2	4 4	1	15 1.043		5 10.		.200 5	17.8	334.33 279.57	29.56 16.13	12	15	203	22.1	6.55
195539395 564473387	26S protease regulatory subunit 10B (Homo sapiens)	16.13 43.50	1	2 6	1 8			3 14.		.375 2 .115 25	34.7	279.57	16.13 43.50	12	18		45.8 20.4	7.78 8.78
71051616	actin-related protein 2/3 complex subunit 3 isoform 2 [Homo sapiens] uroporphyrinogen decarboxylase [Homo sapiens]	43.50 21.80	2	2 3	8	39 1.042 17 1.042		9.		.115 Z5	15.0		43.50	21	17		20.4 40.8	6.14
523704487	ubiquitin-like-conjugating enzyme ATG3 isoform 2 [Homo sapiens]	7.40	2	2 2		6 1.042		2 8.		.216 2	3.3	322.82	7.40	6		311	35.4	4.79
68509926	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 [Homo sapiens]	6.79	6	5 5	1	18 1.042		7 15.		.200 7	11.4	341.33	6.79	13	18		90.9	7.46
38788353	ragulator complex protein LAMTOR5 [Homo sapiens]	32.95	1	2 4	1	14 1.042		4 3.	7 1	.096 4	7.6	357.75	32.95	8	14	173	18.1	5.50
14574568	allograft inflammatory factor 1 isoform 3 [Homo sapiens]	36.05	17	3 6	2			5 11.		.352 6	8.1	918.08	36.05	14	28		16.7	6.24
4504111	growth factor receptor-bound protein 2 isoform 1 [Homo sapiens]	39.17	2	7 8	5			6.		.263 18	15.1	2305.64	39.17	21	54		25.2	6.32
578837826 336176066	PREDICTED: motile sperm domain-containing protein 2 isoform X2 [Homo sapiens]  RNA-binding protein 39 isoform d [Homo sapiens]	4.00 8.96	4	1 2	2	4 1.042 25 1.042		2 4.		.119 1 .169 2	3.9	157.82 227.44	4.00 8.96	4	25	475	54.5 56.3	5.83 10.04
38327039	heat shock 70 kDa protein 4 (Homo sapiens)	34.40	1 1	1 22	_					.067 24	11.7	3029.01	34.40	54	82		94.3	5.19
219521928	DIS3-like exonuclease 1 isoform 1 [Homo sapiens]	3.04	4	1 4	1			1		.102 1	11.3	20.94	3.04	4	13		120.7	6.54
21450861	attractin isoform 1 preproprotein [Homo sapiens]	9.73	5	8 12	4	14 1.042	1	6.	1 1	.299 13	25.9	1128.30	9.73	30	44	1429	158.4	7.31
388890228	chitotriosidase-1 isoform 2 precursor [Homo sapiens]	11.41	3	3 4	1.			1 3.		.417 4	23.0		11.41	10	12		49.6	6.19
6005846	twinfilin-2 [Homo sapiens]	44.99	1	8 11	4		1	8.		.054 12	25.3	1805.88	44.99	30	47		39.5	6.84
145309300	cyclin-dependent kinase 13 isoform 2 [Homo sapiens]	3.72	93	1 7	9	99 1.041 18 1.041		1 13.		.206 1	12.9	124.03	3.72 17.73	16	99	1452	158.3	9.70 9.88
526253086 578812566	endothelial differentiation-related factor 1 isoform 3 [Homo sapiens]  PREDICTED: SAM and SH3 domain-containing protein 1 isoform X3 [Homo sapiens]	17.73	7	1 3	1	1.041 10 1.041		13.		.340 2 .409 1	12.9	278.23 132.27	17.73 2.43	8	18		15.6 136.0	9.88 7.42
14670392	tyrosine-protein kinase BAZ1B [Homo sapiens]	4.05	2	1 7	3	36 1.041				.060 1		125.60	4.05	11	36	1483	170.8	8.48
530391071	PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X7 [Homo sapiens]	38.95	4 1	15 15	7	78 1.041	2	8.		.163 26	10.4	3024.57	38.95	44	78		48.5	5.92
210147567	glutamate-rich protein 6B [Homo sapiens]	2.30	1	1 2		6 1.041		1	1.	.742 1		37.80	2.30	4	i 6	696	81.6	4.75
62912474	leucine-rich repeat-containing G-protein coupled receptor 6 isoform 3 [Homo sapiens]	1.45	5	1 1		8 1.041		2 14.		.112 2	48.5	106.27	1.45	2	2 8	828	89.2	5.99
194018472	plasma serine protease inhibitor preproprotein (Homo sapiens)	7.64	1	1 3		9 1.040				.506 1		76.06	7.64	6	5 9	406	45.6	9.26
289063395 4507951	pro-interleukin-16 isoform 3 (Homo sapiens)	9.84	7	7 11	3	35 1.040 23 1.040	_	3.		.281 7	22.0	819.46 5522.32	9.84	31	35	1331	141.6 28.2	8.06 4.84
4507951 340138932	14-3-3 protein eta [Homo sapiens] apolipoprotein B receptor [Homo sapiens]	71.95 13.86	1	9 12	22			5 6. 3 3.		.120 26 .182 13	19.8	5522.32 2154.74	71.95 13.86	56	223		28.2 115.6	4.84
530388906	PREDICTED: polyadenylate-binding protein 1 isoform X1 [Homo sapiens]	10.69	5	2 5	1	1.040		3 1.	7 0	.102 13	12.5	540.60	10.69	30	13		70.6	9.50
530424154	PREDICTED: zinc finger protein 319 isoform X1 [Homo sapiens]	2.23	1	1 2		6 1.040		3 1.		.860 3	3.6		2.23	2		582	65.5	8.37
40217847	U5 small nuclear ribonucleoprotein 200 kDa helicase [Homo sapiens]	6.51	1	2 12	2			1 5.		.088 4	26.5		6.51	18	27		244.4	6.06
11056036	tubulintyrosine ligase-like protein 12 [Homo sapiens]	20.34	1	8 10	3	36 1.040		5.		.263 9	30.3	1090.34	20.34	28	36		74.4	5.53
8923541	UPF0587 protein C1orf123 [Homo sapiens]	31.25	1	3 4	1			1.		.047 3	9.1	147.68	31.25	10	15		18.0	5.01
40217843	cartilage oligomeric matrix protein precursor (Homo sapiens)	5.81	1	2 2		6 1.040		2 10.		.961 2	5.4	302.57	5.81	6		757	82.8	4.60
24430151 38016911	26S protease regulatory subunit 4 [Homo sapiens] erythrocyte band 7 integral membrane protein isoform a [Homo sapiens]	14.55 12.85	1	3 6	1			12.		.654 2 .097 4	43.8	359.92 535.02	14.55 12.85	15	15		49.2 31.7	6.21 7.88
401709950	erythrocyte band / integral membrane protein isoform a [Homo sapiens] ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 1 [Homo sapiens]	12.85 25.77	4	4 5	1.			6. 4 0.		.097 4	10.1	363.58	12.85 25.77	12	12		21.9	4.93
578825689	PREDICTED: serpin A11 isoform X1 [Homo sapiens]	6.42	1	1 2		6 1.039		1	1	.050 1		79.02	6.42	4	12	218	24.5	8.16
76880486	activating signal cointegrator 1 complex subunit 3 isoform a [Homo sapiens]	3.77	2	1 7	2			7 4.		.136 7	8.9	214.73	3.77	9	23		251.3	7.09
212276104	leucine-rich repeat flightless-interacting protein 1 isoform 5 [Homo sapiens]	31.25	64 1	18 20	10			6.		.174 30	19.1	4234.81	31.25	57	106		82.6	4.61
578798984	PREDICTED: ubiA prenyltransferase domain-containing protein 1 isoform X1 [Homo sapiens]	11.37	2	1 3	1			2 6.		.501 2	204.2	56.71	11.37	5	10		22.8	7.72
22538467 21237808	proteasome subunit beta type-4 (Homo sapiens)	40.91 2.83	1	6 7	3	9 1.039 9 1.038		9 10.		.110 9	9.7	1233.46	40.91 2.83	19	33		29.2 124.8	5.97
21237808 530417087	SWI/SNF complex subunit SMARCC2 isoform b [Homo sapiens]  PREDICTED: U1 small nuclear ribonucleoprotein 70 kDa isoform X2 [Homo sapiens]	2.83 7.94	7	2 4		9 1.038 11 1.038		2 11.		.071 2	7.6	219.85 101.38	2.83 7.94	9	,	1130	124.8 50.6	5.55 9.89
94536842	ribose-5-phosphate isomerase [Homo sapiens]	7.94 26.05	1	5 7	1	17 1.038		2 12. 5 6.		.044 2	9.9	637.59	7.94 26.05	17	17	428	33.2	9.89 8.54
5454052	14-3-3 protein sigma (Homo sapiens)	43.95	1	5 11	10		1	1 14.		.106 11	7.7	3049.92	43.95	32	108		27.8	4.74

Accession	Description	ΣCoverage	E Σ# Protein	ns Σ# Unique Peptides	Σ# Peptide	es Σ# PSM			A8: 115/114 Variability [%]			A8: 117/116 Variability [%]	Score A(3,6,7	Coverage A(3,6,7) # Peptides A(3,6,7)	r) # PSM A(3,6,7)	# AAs	MW [kDa]	calc. pl
578800460 5031569	PREDICTED: complement factor H-related protein 4 isoform X6 [Homo sapiens] alpha-centractin [Homo sapiens]	2.89		10	1	2	6 1.00 45 1.00		5 51	1.04		5 11.	147.8		4 6	519 376	58.5 42.6	4.94
530411140	PREDICTED: zinc finger protein 207 isoform X3 [Homo sapiens]	6.44		6	1	2	4 1.0		1	1.10		1	126.5		4 4	466	49.6	8.48
151101404	prothymosin alpha isoform 2 [Homo sapiens]	27.27		25	4	5	35 1.03	18 1	0 9.6	1.34	2	9 7.8	1517.58	B 27.27 1	15 35	110	12.1	3.79
67190748	complement C4-A isoform 1 preproprotein [Homo sapiens]	72.36		21	3 1	03 15			0 14.7	0.98		8 95.4			1598		192.7	7.08
530406751	PREDICTED: ubiquitin carboxyl-terminal hydrolase 3 isoform X3 [Homo sapiens]	1.99		7	1	1	1 1.00		1	0.97		1	26.1		1 1	351	40.1	7.75
530420490 189181666	PREDICTED: apolipoprotein L1 isoform X2 [Homo sapiens] beta-hexosaminidase subunit alpha preproprotein [Homo sapiens]	31.05 7.94		1	9		47 1.00 11 1.00		4 9.3	1.09		3 16.9	1687.30		9 11		42.1 60.7	5.80 5.16
295821193	serum amyloid A-1 protein preproprotein [Homo sapiens]	77.05		11	3		31 1.0		5 3.0	1.13		5 22.5			3 131		13.5	6.79
4759212	tubulin-specific chaperone A isoform 2 [Homo sapiens]	66.67		1 1	0	11 -	43 1.03	18 1	4 7.4	1.13	8 1	4 8.1	1668.65	5 66.67	1 43	108	12.8	5.29
222136639	C-1-tetrahydrofolate synthase, cytoplasmic [Homo sapiens]	10.37		1	7		25 1.03		7 2.9	1.11		7 13.0			25 25		101.5	7.30
530397480	PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X19 [Homo sapiens	5.48		26	2	3	11 1.03		3 3.1	1.16		3 3.			7 11		59.7	8.70
578821054 400974227	PREDICTED: protein argonaute 12-like [Homo sapiens]  janus kinase and microtubule-interacting protein 2 isoform 2 [Homo sapiens]	3.00 9.51		1	1	1	2 1.00 25 1.00		4 5.7	1.21		4 7.5	39.8		2 2	233 799	24.2 93.6	11.09 5.97
4505145	NAD-dependent malic enzyme, mitochondrial isoform 1 precursor [Homo sapiens]	5.65		1	1	3	6 1.0		1	1.11		1	291.41		6 6	584	65.4	7.61
530371163	PREDICTED: UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 isoform X1 [Hom	8.23		2	1	2	2 1.03		1	1.03		1	32.3		2 2	328	37.9	8.57
530360487	PREDICTED: protein DJ-1 isoform X1 [Homo sapiens]	89.95		1 1	7	18 2			6 8.8	1.19		6 21.0			52 225		19.9	6.79
148746218	serine/threonine-protein kinase TAO3 [Homo sapiens]	10.13		3	1		53 1.03		1	1.18		1	175.80		17 53		105.3	7.30
4758442 530370277	glia maturation factor beta [Homo sapiens] PREDICTED: 60 kDa heat shock protein, mitochondrial isoform X1 [Homo sapiens]	26.76 7.68		3	1		37 1.00 13 1.00		3 11.1	1.15		1 18.8	1220.35		10 37 10 13		16.7 61.0	5.29 5.87
578837225	PREDICTED: armadillo repeat protein deleted in velo-cardio-facial syndrome isoform X12 [Home	5.49		3	1	4	9 1.0		2 10.0	1.58		2 18.4			5 9	656	71.3	6.24
167234419	thyroid hormone receptor-associated protein 3 [Homo sapiens]	6.07		1	1	6	15 1.03		2 1.0	1.06		2 5.4			12 15	955	108.6	10.15
70980549	protein RRP5 homolog (Homo sapiens)	2.51		2	1	5	11 1.03		1	1.59		1	25.0		5 11		208.6	8.87
28827815	protein S100-A7A (Homo sapiens)	53.47		1	1	5 1	05 1.03		1	1.41		1	2841.74		14 105	101	11.3	7.44
14149627 578836895	ubiquitin carboxyl-terminal hydrolase 15 isoform 2 [Homo sapiens]	7.88 20.22		5	3	9	42 1.03 39 1.03		3 2.2 7 9.9	1.10		3 5.8 7 3.2			19 42	952 445	109.2 51.1	5.15 5.24
4507509	PREDICTED: protein kinase C and casein kinase substrate in neurons protein 2 isoform X5 [Hor metalloproteinase inhibitor 1 precursor [Homo sapiens]	11.11		1	1	2	5 1.0		1 9.9	1.23		1	171.8		5 5	207	23.2	8.10
32313593	olfactomedin-4 precursor (Homo sapiens)	21.18		2 1	0	10	43 1.0	16 1	3 5.2	1.14	0 1	3 9.7			10 43	510	57.2	5.69
532164704	cleft lip and palate transmembrane protein 1 isoform 3 [Homo sapiens]	5.50		1	1	3	8 1.0		2 3.9	1.12		2 5.6			4 8	655	75.1	6.64
195927020	calcium-binding protein 39 [Homo sapiens]	40.47		1	7	12	66 1.0		0 6.2	1.18		0 13.8			13 66		39.8	6.89
6978649 5729953	choline/ethanolamine kinase [Homo sapiens]	3.54 6.95		1	1	1	3 1.0		1	1.66		1	66.8		3 3	395	45.2 38.2	5.49 5.38
5729953 520975489	nuclear migration protein nudC [Homo sapiens] ran-specific GTPase-activating protein isoform 4 [Homo sapiens]	6.95 36.67		6	2	-	11 1.0		3 44	1.15		3 5:			7 11		38.2 17.5	5.38 8.24
520975489	PREDICTED: fructose-bisphosphate aldolase C isoform X3 [Homo sapiens]	48.90		3	9		20 1.0. 68 1.0.		-	1.08		1 5.1			66 168		39.4	6.87
21361794	cullin-associated NEDD8-dissociated protein 1 [Homo sapiens]	19.35		1 1	3		56 1.0			1.08		5 27.			19 56		136.3	5.78
4826659	F-actin-capping protein subunit beta isoform 1 [Homo sapiens]	67.65		5 1	9		93 1.03			1.20		6 19.8			7 193		30.6	6.00
530385095	PREDICTED: src kinase-associated phosphoprotein 2 isoform X1 [Homo sapiens]	25.35		1	8	8	42 1.0		4 7.5	1.23		4 12.3			23 42		41.2	4.69
578838720 5803227	PREDICTED: uncharacterized protein KIAA1210 isoform X1 [Homo sapiens]  14-3-3 protein theta [Homo sapiens]	1.89		2	1	17 1	4 1.00 61 1.00		1 8 10.3	1.24		1 8 14.8	25.04 3 5422.04		4 4	1533 245	167.9 27.7	8.53 4.78
578810593	PREDICTED: calpastatin isoform X11 [Homo sapiens]	27.89		24 1	5		66 1.0			1.17					14 66		78.8	5.05
21040371	ATP-dependent RNA helicase DDX39A (Homo sapiens)	18.74		2	1		46 1.0		1	0.65		1	1099.54		10 46		49.1	5.68
4557323	apolipoprotein C-III precursor (Homo sapiens)	34.34		1	3	3	35 1.03	84 1	3 8.8	1.40	0 1	3 18.	1845.37	7 34.34	9 35	99	10.8	5.41
5902102	small nuclear ribonucleoprotein Sm D1 isoform 1 [Homo sapiens]	54.62		2	4		38 1.0		9 7.8	1.25		9 6.5			12 38		13.3	11.56
56682959	ferritin heavy chain (Homo sapiens)	66.12		1 1	0		05 1.0		-	1.10		0 11.1			105		21.2	5.55
334724455 260436860	acetyl-coenzyme A synthetase, cytoplasmic isoform 3 [Homo sapiens]  AP-1 complex subunit beta-1 isoform b [Homo sapiens]	3.96 17.68		3	4		28 1.01 44 1.01		2 0.9 5 8.5	1.10		2 0.: 5 13.8			8 28 5 44		67.6 103.5	6.15 5.16
401461824	trafficking protein particle complex subunit 3 isoform 3 [Homo sapiens]	5.97		3	1	1	2 1.0		1	1.43		1	31.19		1 2	134	15.0	4.88
530361541	PREDICTED: inaD-like protein isoform X5 [Homo sapiens]	5.57		8	1	9	33 1.03		4 6.6	1.18		4 7.3	268.0		14 33		160.1	4.87
4503507	eukaryotic translation initiation factor 2 subunit 3 [Homo sapiens]	4.24		1	2	3	7 1.03		2 0.5	1.24		2 13.1			7 7	472	51.1	8.40
13569962 530379378	ras-related protein Rab-1B [Homo sapiens]	41.79 4.56		21	2	7	60 1.0		6 3.6	1.18		6 14.			21 60	201 724	22.2 83.5	5.73
530379378 530422933	PREDICTED: phosphatidylinositol 3-kinase regulatory subunit alpha isoform X1 [Homo sapiens] PREDICTED: zinc finger protein 185 isoform X16 [Homo sapiens]	4.56 8.10		10	1	5	9 1.00 10 1.00		1	1.13		1	30.86 92.70		6 9	724 630	83.5 67.2	6.16 7.01
62122917	filaggrin-2 (Homo sapiens)	2.17		1	1	4	8 1.0		1	1.09		1	91.0		6 8	2391	247.9	8.31
578820364	PREDICTED: AP-2 complex subunit alpha-2 isoform X3 [Homo sapiens]	8.71		4	2	7	20 1.0		2 0.6	1.40		2 26.0			14 20		104.3	6.80
62912466	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	23.11		3	5	5	26 1.03		9 2.8	1.40		9 8.5			15 26	251	28.3	5.14
530364287 120433590	PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]	13.03 72.41		3	6	7	31 1.00 45 1.00		9 2.2 3 4.7	1.21		9 19.6 3 13.2			18 31	660	75.3 10.0	6.48
120433590 55770902	acyt-CoA-binding protein isoform 3 [Homo sapiens] opioid growth factor receptor-like protein 1 [Homo sapiens]	15.74		7	4		45 1.00 17 1.00		3 4.7	1.01		3 3.3			18 45		51.2	6.57 6.13
9910460	omega-amidase NIT2 (Homo sapiens)	47.83		1	9		28 1.0		9 3.5	1.11		9 21.			26 28		30.6	7.21
13124873	core-binding factor subunit beta isoform 2 (Homo saplens)	20.88		4	4	4	15 1.03	13	4 5.2	1.08		4 9.3			12 15	182	21.5	6.60
530381587	PREDICTED: FYVE, RhoGEF and PH domain-containing protein 2 isoform X1 [Homo sapiens]	2.74		2	1	2	3 1.00		1				34.76	6 2.74	2 3	620	70.8	7.30
195976777	dysferlin isoform 3 (Homo sapiens)	3.34		16	1	7	26 1.0		3 4.6	1.06		3 1.3			11 26		235.8	5.82
167900484 4503481	pentraxin-related protein PTX3 precursor [Homo sapiens] elongation factor 1-gamma [Homo sapiens]	13.65 45.77		1	3	4	15 1.00 99 1.00		3 3.2	1.08		3 9.3			12 15 12 99		41.9 50.1	5.01 6.67
148536853	coatomer subunit alpha isoform 2 [Homo sapiens]	6.78		3	3	11	60 1.0		3 3.1	1.21		3 24			72 60		138.3	7.66
530406263	PREDICTED: ras-related protein Rab-27A isoform X3 [Homo sapiens]	28.57		2	4	5	19 1.0		6 4.3	1.07		6 11.0			14 19		130.3	5.38
115527062	collagen alpha-2(VI) chain isoform 2C2 precursor [Homo sapiens]	13.35		3	3	9	19 1.03		3 1.7	1.27		3 9.			16 19		108.5	6.21
23110925	proteasome subunit beta type-6 isoform 1 proprotein (Homo sapiens)	4.60		1	1	1	6 1.03		2 6.0	1.22		2 7.3			3 6	239	25.3	4.92
578818376 395455064	PREDICTED: selenide, water dikinase 1 isoform X1 [Homo sapiens] mediator of RNA polymerase II transcription subunit 23 isoform c [Homo sapiens]	14.36 5.81		4	3		10 1.00 18 1.00		3 1.1	1.29 76.12		3 3.5	32.1		10 10 8 18		42.7 155.5	5.97 7.40
395455064 538917488		5.81 48.07		1 1	4	-	18 1.00 00 1.00		9 3.7	76.12		1 15.9			8 18 60 100		155.5 46.6	7.40
538917488	isocitrate dehydrogenase [NADP] cytoplasmic [Homo sapiens] PREDICTED: pericentrin isoform X4 [Homo sapiens]	48.07 5.95		14	1		55 1.00		3.7	1.16		15.5	133.3		9 55		46.6 369.2	5.47
93102375	protein FAM114A2 (Homo sapiens)	4.16		2	2	3	8 1.0		2 0.8	1.04		2 4.0			8 8	505	55.4	4.88
217035154	capZ-interacting protein [Homo sapiens]	29.09		2	6	9	48 1.0			1.06		3 11.4			21 48		44.5	5.40
157502193	26S proteasome non-ATPase regulatory subunit 13 isoform 1 [Homo sapiens]	8.78		2	3	3	10 1.0		4 8.5	1.11		3 6.4			7 10		42.9	5.81
312433960 12667788	NLR family CARD domain-containing protein 4 [Homo sapiens]	9.28 71.48		75 13	3		32 1.00 10 1.00		3 2.1	1.51		3 42.2 4 18.0			18 32		116.1 226.4	6.77 5.60
39995084	myosin-9 [Homo sapiens] integrator complex subunit 3 [Homo sapiens]	4.99		5	1	58 18	7 1.0		0 8.0	1.18		18.0	215.1		i8 1810 7 7	1960	117.9	5.80
7705696	thioredoxin domain-containing protein 12 precursor [Homo saplens]	5.23		1	1	1	3 1.00		1	1.24		1	77.60		3 3	172	19.2	5.40
11321640	beta-1-syntrophin (Homo sapiens)	3.53		2	1	2	4 1.0		1	1.11		1	21.50		2 4	538	58.0	8.63
4759140	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 [Homo saplens]	40.50		1	9	11	67 1.03		0 7.6	1.14		0 20.0			19 67	358	38.8	5.77
14591909 557878612	60S ribosomal protein L5 [Homo sapiens]	20.20		1	5	6	25 1.01 74 1.01		7 4.1	1.22		7 14.5			15 25	297	34.3	9.72 5.57
557878612 7656952	centromere-associated protein E isoform 2 [Homo sapiens] calcyclin-binding protein isoform 1 [Homo sapiens]	8.88 27.63		2	4	7	74 1.00 32 1.00		4 9.0	2.17 1.07		4 2.1	216.9		19 74 17 32	2580 228	301.6 26.2	5.57 8.25
15208660	E3 ubiquitin-protein ligase TRIM21 [Homo sapiens]	5.05		2	2	3	7 1.0		2 15.8	1.07		2 23.			7 7	475	54.1	6.38
157653329	procollagen C-endopeptidase enhancer 1 precursor (Homo sapiens)	16.48		1	5	6	17 1.00		5 7.6	1.10		5 22.4			16 17		47.9	7.43
55770888	early endosome antigen 1 [Homo sapiens]	9.78		12	4	17	71 1.0	31	7 6.9	1.22	3	7 10.1	359.2	9 9.78 3	32 71	1411	162.4	5.66
4502209	ADP-ribosylation factor 5 [Homo sapiens]	42.22		1	1		27 1.03		1	2.45		1	847.1		16 27		20.5	6.79
30795231 4757768	brain acid soluble protein 1 (Homo sapiens)	85.90 46.57		1 2	10		07 1.00		4 5.4 7 7.4	1.13		4 13.8 7 14.4			107		22.7	4.63
4757768 217035150	rho GDP-dissociation inhibitor 1 isoform a [Homo sapiens] inosine-5'-monophosphate dehydrogenase 1 isoform g [Homo sapiens]	46.57 7.36		16	3		21 1.00 14 1.00		7 7.4	1.17		7 14.4			9 121		23.2 52.6	5.11 6.64
578831328	PREDICTED: actin, cytoplasmic 2 isoform X1 [Homo sapiens]	73.93		26	3	40 54			0 10.1	1.12		-					51.2	7.20
7656849	isobutyryl-CoA dehydrogenase, mitochondrial [Homo sapiens]	4.58		1	1	2	4 1.00	10	1				51.9		4 4	415	45.0	7.85
296531349	histone lysine demethylase PHF8 isoform 1 [Homo sapiens]	4.81		8	1	7	25 1.03		2 2.7	1.11		2 7.4			9 25	1060	117.8	8.72
578813343	PREDICTED: thrombospondin type-1 domain-containing protein 7A isoform X4 [Homo sapiens]	1.98		5	1	3	30 1.0		3 0.5	1.19	-	3 24.0			7 30		169.7	7.37
189083844 4507909	dipeptidyl peptidase 1 isoform a preproprotein (Homo sapiens) wiskott-Aldrich syndrome protein [Homo sapiens]	21.38		3	7		44 1.00 42 1.00			1.14					23 44		51.8 52.9	6.99
4507909 530369465	PREDICTED: solute carrier family 35 member F5 isoform X2 [Homo sapiens]	22.71		3	1	2	42 1.0. 10 1.0.		3 0.3	1.20	-	3 1.:			4 10		52.9	9.50
555307405	r reproved. Journal railing 30 member to isolorin Az (nomo sapiens)	2.12		3	*	*	1.0.	~	0.3	1.20		o I.	117.2	2.12	- 10	010	ud. I	7.50

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Accession 119395754	Description keratin, type II cytoskeletal 5 [Homo sapiens]	ΣCoverage 23.05	Σ# Proteins Σ# Unique Pepti	des Σ# Peptides	Σ# PSMs	A8: 115/114 0 1.029	A8: 115/114 Count	A8: 115/114 Variability [%		116 A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7) 1632.39	23.05 Coverage A(3,6,7)	# Peptides A(3,6,7) # PSM A(3,6	,7) #.	AAs M	MW [kDa] ca 62.3	alc. pl 7.74
226443152	alpha/beta hydrolase domain-containing protein 14B isoform 1 [Homo sapiens]	24.76	5	4	7 2	1 1.029		4 4		1.146	5 51.3	379.13	24.76	17	21	210	22.3	6.40
578821106	PREDICTED: EH domain-containing protein 1 isoform X1 [Homo sapiens]	27.15	4	12 1	4 6	8 1.029		1 4		1.191 2	21.5	2015.02	27.15	40	68	534	60.6	6.83
6912586	6-phosphogluconolactonase [Homo sapiens]	69.77	2	12 1	2 5	9 1.029		0 6		1.136	21.1	2177.54	69.77	34	59	258	27.5	6.05
4504483	hypoxanthine-guanine phosphoribosyltransferase [Homo sapiens]	28.90	6	6	6 2			9 8		1.130	17.2	1169.85	28.90	16	29	218	24.6	6.68
20357529	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [Homo sapiens]	17.65	5	3	5 3			2 4		1.760	66.5	514.07	17.65	14	32	340	37.3	6.00
578834138	PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 1 isoform X3 [Homo sa	5.57	2	1	3	5 1.029		1		1.031		143.75	5.57	5	5	754	82.2	4.55
578824247 4885111	PREDICTED: phosphatidylinositol 5-phosphate 4-kinase type-2 gamma isoform X2 (Homo saple calmodulin-like protein 3 (Homo saplens)	6.77	5	1	1	3 1.029 6 1.029		1 6		1.067	1 7	158.69 593.95	6.77	3	3	251 149	28.4	6.13 4.42
4885111 7661882	rho GTPase-activating protein 25 isoform b [Homo sapiens]	24.16 18.50	1	7 1	0 2			2 6 B 8		1.025	7 5.5	691.50	24.16 18.50	9	25	638	72.4	6.07
304555610	EF-hand calcium-binding domain-containing protein 13 isoform A [Homo sapiens]	2 98	8	1	4 3			1		1.165 1.842	0.0	422.57	2 98	8	34	973	110.1	6.07
530365306	PREDICTED: nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 isoform X1 [Ho	13.64	2	2	4 1			2 3		0.955	2 23.2	118.07	13.64	9	12	242	27.2	5.08
33457316	pleckstrin homology domain-containing family O member 2 isoform 1 [Homo sapiens]	9.59	2	4	5 1	3 1.028		4 4	.8	1.220	17.4	499.17	9.59	13	13	490	53.3	5.43
530370925	PREDICTED: X-ray repair cross-complementing protein 5 isoform X1 [Homo sapiens]	35.67	7	15 2	3 13	0 1.028	2	9 8	.3	1.183 29	16.1	5342.84	35.67	59	130	827	93.5	8.10
4504445	heterogeneous nuclear ribonucleoprotein A1 isoform a [Homo sapiens]	53.75	10	13 1	9 15					1.152 30	9.0		53.75	56	156	320	34.2	9.23
12056473	sialic acid synthase [Homo saplens]	11.42	1	3	3	8 1.028				1.357	3 25.3	414.59	11.42	8	8	359	40.3	6.74
530403051	PREDICTED: putative ATP-dependent RNA helicase TDRD9 isoform X1 [Homo sapiens]	4.21	4	1	6 1					1.500	10.3	41.75	4.21	11	19	1330	149.7	7.05
5031593	actin-related protein 2/3 complex subunit 5 isoform 1 [Homo sapiens]	80.13	3	9 1						1.159 29	10.1	3838.50	80.13	29	92	151	16.3	5.67
34147513	ras-related protein Rab-7a [Homo sapiens]	71.98	1	12 1	4 14					1.150 46	15.1	4984.48	71.98	40	143	207	23.5	6.70
262231791 10880979	complement factor H-related protein 3 isoform 2 precursor [Homo sapiens] lymphocyte-specific protein 1 isoform 1 [Homo sapiens]	16.36 50.44	3	11 1	4 /	9 1.028 7 1.027	2	6 12 1 6		1.385 ! 1.119 3'	8.1	1436.05 4759.62	16.36 50.44	11	79 107	269 339	30.7 37.2	7.78 4.74
140972063	neurabin-2 [Homo sapiens]	3.43	8	2	2 10	8 1.027	3	1		1.063	17.7	133.62	3.43	8	8	817	89.3	4.97
117320537	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 [Homo sapiens]	9.88	1	5	9 2			5 10		1.094	6.7	700.25	9.88	22	23	1265	147.8	6.64
14251209	chloride intracellular channel protein 1 [Homo sapiens]	76.76	8	14 1			5			1.201 49	20.1	5836.57	76.76	41	162	241	26.9	5.17
354983501	protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 1 [Homo sapiens]	53.33	5	9 1	1 7	4 1.027				1.261 20	16.1	2240.38	53.33	29	74	285	30.3	7.52
530393565	PREDICTED: insulin-degrading enzyme isoform X4 [Homo sapiens]	1.48	3	1	1 :	2 1.026		1				47.52	1.48	2	2	609	69.9	6.89
530403615	PREDICTED: DNA-(apurinic or apyrimidinic site) lyase isoform X1 [Homo sapiens]	55.03	2	16 1	8 8	5 1.026	2	6 3		1.133 26	17.2	3438.31	55.03	51	85	318	35.5	8.12
22538465	proteasome subunit beta type-3 [Homo sapiens]	31.71	1	5	5 3	0 1.026		0 6		1.154	10.4	919.84	31.71	15	30	205	22.9	6.55
513126877	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	13.21	5	4	6 2					1.299	32.0	407.50	13.21	15	22	386	44.0	7.71
578834433 194018537	PREDICTED: uncharacterized protein C19orf68 isoform X3 [Homo sapiens]	6.12	6	1	8 1:	8 1.026 4 1.026		3 8		1.803	26.5	54.42	6.12	12	18	947	104.7 42.4	8.40 8.47
194018537 300360515	phosphoribosyl pyrophosphate synthase-associated protein 1 [Homo sapiens] actin-related protein 2/3 complex subunit 1A isoform 2 [Homo sapiens]	7.79	1	1	1	4 1.026 2 1.026		1		1.358 n.960		116.88 41.64	7.79	4	4	385 356	42.4 39.6	8.47 8.22
121114302	actin-related protein 2/3 complex subunit 1A isoform 2 [Homo sapiens]  cullin-4B isoform 2 [Homo sapiens]	11.17	6	1	8 2					1 137		186.99	3.37	14	27	356 895	39.6 102.2	7.94
530384039	PREDICTED: utrophin isoform X7 [Homo sapiens]	6.13	7	1 2	6 20			1		1.450		973.26	6.13	50	205	3424	393.2	5.33
530380347	PREDICTED: glucosamine-6-phosphate isomerase 1 isoform X1 [Homo sapiens]	25.16	9	5	7 2			7 3		1 202	7.6		25.16	19	27	318	36.1	7.61
4557587	fumarylacetoacetase (Homo sapiens)	18.38	1	6	6 2			В 3	.3	1.111 8	15.6	455.20	18.38	17	25	419	46.3	6.95
55741719	iporin [Homo sapiens]	3.10	2	1	4 1	9 1.026		3 5	.9 2	1.362	51.5	43.86	3.10	4	19	1516	161.1	6.62
7657069	ERO1-like protein alpha precursor [Homo sapiens]	16.03	1	3	7 1	5 1.025		3 0	.7	1.076	1.7	482.55	16.03	15	15	468	54.4	5.68
41281453	STE20-like serine/threonine-protein kinase [Homo sapiens]	13.28	17	6 1	6 4			5 4		1.050	17.8	855.10	13.28	37	45	1235	142.6	5.15
24430132	WW domain-binding protein 2 [Homo sapiens]	8.81	1	1	-	8 1.025		1		1.068		98.26	8.81	7	8	261	28.1	5.91
71773110	apolipoprotein A-IV precursor [Homo sapiens]	61.36	1	23 2						1.265 58	16.3	5910.78	61.36	73	200	396	45.3	5.38
24430192	keratin, type I cytoskeletal 16 [Homo sapiens]	38.90	20	6 2	1 7			B 7		1.136	11.0		38.90	56	75	473	51.2	5.05
344030204	ras-related protein Rab-6A isoform c [Homo sapiens]	11.43	19	1	2	9 1.025		1 9		1.118	20.5	335.11	11.43	6	238	175 394	19.9 44.7	5.07 6.74
5031571 256222019	actin-related protein 2 isoform b [Homo sapiens] ras-related protein Rab-10 [Homo sapiens]	61.17 25.50	25	16 2	0 23 5 3			5 5		1.221 59 1.405 5	20.5	8489.39 1619.89	61.17 25.50	56	34	200	44.7 22.5	8.38
8051584	ficolin-1 precursor (Homo sapiens)	24.85	20	6	6 3	0 1.025	1			1.046	13.4	1020.75	24.85	18	30	326	35.1	6.86
4504061	N-acetylglucosamine-6-sulfatase precursor [Homo sapiens]	14.67	1	6	8 2			В 3		1.211	13.3	965.34	14.67	20	26	552	62.0	8.31
34577063	adenylosuccinate synthetase isozyme 2 (Homo sapiens)	39.25	4	14 1	7 9	0 1.025				1.176 26	25.4	2651.68	39.25	45	90	456	50.1	6.55
4757826	beta-2-microglobulin precursor (Homo sapiens)	49.58	2	4	4 2	6 1.025		В 2	.7	1.142 8	8.3	1084.87	49.58	12	26	119	13.7	6.52
4507949	14-3-3 protein beta/alpha [Homo sapiens]	81.30	1	9 2	1 26	0 1.025	4	7	.1	1.205 39	18.6	8374.54	81.30	59	260	246	28.1	4.83
4503477	elongation factor 1-beta [Homo sapiens]	42.22	1	4	7 2	6 1.025		7 1		1.235	12.0	908.14	42.22	17	26	225	24.7	4.67
530392285	PREDICTED: sickle tail protein homolog isoform X14 [Homo sapiens]	3.28	30	1	7	9 1.025		1		1.229		33.21	3.28	7	9	1770	194.6	6.95
530380865	PREDICTED: CREB3 regulatory factor isoform X1 [Homo sapiens]	4.91	2	2	4	7 1.025		2 11		1.940	39.1	36.02	4.91	7	7	631	71.3	4.87
578834710 4757900	PREDICTED: spectrin beta chain, non-erythrocytic 4 isoform X1 [Homo sapiens]	7.81 74.34	3	1 2				2 1		1.380 2 1.116 5	2 2.9	306.49 6259.99	7.81 74.34	40	61	2394	270.1 48.1	5.67 4.44
4757900 197382664	calreticulin precursor (Homo sapiens)	74.34	1	21 2	3 18.	2 1.025 6 1.024				1.116 54 1.080 3		6259.99 235.06	74.34 14.41	64	182	417 118	48.1 13.3	5.78
4504901	eukaryotic translation initiation factor 4E type 3 isoform b [Homo sapiens]	6.33	2	1	1	6 1.024		2 7		1.080	5.2	235.06	6.33	3	6	118 521	13.3	4.96
4504701	ras GTPase-activating-like protein IQGAP1 [Homo sapiens]	54 44	5	63 7	0 40			2 6		1.168 117	7 18.0	15836.30	54.44	198	400	1657	189 1	6.48
156616294	N-acetylmuramoyl-L-alanine amidase precursor [Homo sapiens]	34.55	2	11 1						1 186 20	17.4	2939.96	34.55	32	70	576	62.2	7.55
47132620	keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	19.41	27	3 1	3 7	3 1.024		4 7	.9	1.058	10.8	1598.28	19.41	39	73	639	65.4	8.00
4757818	V-type proton ATPase subunit G 1 [Homo saplens]	35.59	1	3	4 1	7 1.024		5 3	.0	1.095	9.4	589.90	35.59	11	17	118	13.7	8.79
19923497	echinoderm microtubule-associated protein-like 4 isoform a [Homo sapiens]	6.63	6	2	7 1-	4 1.024		2 3	.4	1.123	14.7	167.40	6.63	12	14	981	108.8	6.32
33519455	methionine adenosyltransferase 2 subunit beta isoform 2 [Homo sapiens]	5.88	2	1	2 3	3 1.024		1		0.920	1	52.30	5.88	6	33	323	36.4	6.65
4507651	tropomyosin alpha-4 chain isoform 2 [Homo sapiens]	53.23	14	5 2				6 1		1.046	5.5	3983.62	53.23	64	152	248	28.5	4.69
578809860	PREDICTED: serine/threonine-protein kinase NIM1 isoform X1 [Homo sapiens]	6.42	2	1		8 1.024				1.039	5.8		6.42	3	8	436	49.6	8.35
9257257	WD repeat-containing protein 1 isoform 1 [Homo sapiens]	59.74	3	27 3				4 5		1.166 83		11149.75	59.74	90	284	606 93	66.2	6.65 4.93
13775198 530366190	SH3 domain-binding glutamic acid-rich-like protein 3 [Homo sapiens]  PREDICTED: lamin-B receptor isoform X1 [Homo sapiens]	76.34 8.38	1	6	6 12					1.161 30 1.171 12	8.8 2 19.0	3086.89 879.68	76.34 8.38	18	125	573	10.4 65.9	9.45
57863257	T-complex protein 1 subunit alpha isoform a [Homo sapiens]	33.99	11	12 1	5 5					1.171 1.		1460.98	33.99	43	50	556	60.3	6.11
88999583	myosin light polypeptide 6 isoform 2 (Homo sapiens)	84.77	4		2 21					1.204 69	9 19.2	8829.13	84.77	36	213	151	17.0	4.55
578821456	PREDICTED: nuclear mitotic apparatus protein 1 isoform X9 [Homo sapiens]	8.19	2		8 4					1.205	2.0	334.43	8.19	28	47	2101	236.4	5.80
217330646	activated RNA polymerase II transcriptional coactivator p15 [Homo sapiens]	23.62	1	3	3 1	1 1.023		4 3	.7	1.104	6.9	369.57	23.62	8	11	127	14.4	9.60
387527974	dynactin subunit 2 isoform 3 [Homo sapiens]	21.95	3	4	6 1	9 1.023				1.299	25.5	624.79	21.95	14	19	401	44.2	5.21
304571975	L-xylulose reductase isoform 2 [Homo sapiens]	10.74	2	2	2	6 1.023				1.186	31.9	275.63	10.74	6	6	242	25.7	8.10
530374793	PREDICTED: DCN1-like protein 1 isoform X1 [Homo sapiens]	15.16	2	2	4 1	8 1.023				1.195	4.9	572.54	15.16	11	18	244	28.3	4.98
70778918	inter-alpha-trypsin inhibitor heavy chain H2 precursor (Homo sapiens)	38.16	1	22 2	6 21			4 9		1.185 6	17.8	7826.99	38.16	73	216	946	106.4	6.86
5729991 530368016	26S protease regulatory subunit 6B isoform 1 [Homo sapiens]	24.64	2	4	7 3			9 2		1.144 8	9.2	702.03	24.64	16	33	418	47.3	5.21
530368016 5031595	PREDICTED: striatin isoform X1 [Homo sapiens]	7.27	2	1	5 1	4 1.023		1		1.614	2/ 2	113.52	7.27	10	14	743	81.6 19.7	5.12
5031595 13569901	actin-related protein 2/3 complex subunit 4 isoform a [Homo sapiens]  TSC22 domain family protein 4 [Homo sapiens]	73.21 17.47	1	11 1	2 13			5 7 2 4	-7	1.196 42 1.195	2 26.3	4767.73 348.30	73.21 17.47	33	139	168 395	19.7 41.0	8.43 7.21
9966827	PEST proteolytic signal-containing nuclear protein [Homo sapiens]	17.42	1	1	3	5 1.023		1		1.417	0.7	63.24	17.42	4	5	178	18.9	7.49
578830918	PREDICTED: DNA ligase 3 isoform X3 (Homo saplens)	4.18	4	2	5	9 1.023		2 8		1.163	2.4	130.25	4.18	9	9	958	107.1	9.22
578801388	PREDICTED: 60 kDa SS-A/Ro ribonucleoprotein isoform X1 [Homo sapiens]	6.96	5	1	5 1			1		1.184	2.5	156.60	6.96	11	16	560	63.1	8.38
89903012	cell division control protein 42 homolog isoform 1 precursor [Homo sapiens]	52.88	6	6	7 6					1.287 16	28.2	2365.79	52.88	21	69	191	21.2	6.55
22035620	apoptosis-associated speck-like protein containing a CARD isoform b [Homo sapiens]	69.89	2	10 1	1 6					1.261	18.8		69.89	30	65	176	20.0	5.95
153070260	myristoylated alanine-rich C-kinase substrate [Homo sapiens]	58.13	1	-	8 4					1.126 12		2053.79	58.13	24	49	332	31.5	4.45
20070125	protein disulfide-isomerase precursor (Homo sapiens)	64.17	1	26 3						1.091 6			64.17	90	202	508	57.1	4.87
110611218	ribosome-binding protein 1 [Homo sapiens]	8.09	4	3	8 3			4 1		1.173	41.5	395.46	8.09	14	34	977	108.6	5.54
302318952	PML-RARA-regulated adapter molecule 1 [Homo sapiens]	37.61	2	12 1				6 4		1.162	9.3	1304.24	37.61	45	62	670	73.9	9.67
82546830 530361117	exocyst complex component 4 isoform a [Homo sapiens]  PREDICTED: heterochromatin protein 1-binding protein 3 isoform X5 [Homo sapiens]	5.24 25.05	3	1 10 1	6 1 3 5			1 4 4		1.092 1.102	1 10.0	130.18 1042.22	5.24 25.05	13	17 58	974 515	110.4 57.2	6.49 9.76
31542984	inter-alpha-trypsin inhibitor heavy chain H4 isoform 1 precursor [Homo sapiens]	25.05 58.92	11	1 4				4		1.102 14	10.0	19384.38	25.05 58.92	122	573	930	103.3	6.98
542133174	liprin-alpha-2 isoform   [Homo sapiens]	7.34	21	1 1				1		1.040		31.02	7.34	18	25	1104	125.8	6.58
22027655	AP-1 complex subunit sigma-2 isoform 2 [Homo sapiens]	15.29	1	1	2	6 1.022		2 11	.0	0.750	28.1	345.84	15.29	4	6	157	18.6	5.47
567315950	THAP domain-containing protein 5 isoform 3 [Homo sapiens]	3.00	3	1	1	6 1.022		2 11		1.053	10.9	145.30	3.00	3	6	233	26.5	4.92
58761500	obg-like ATPase 1 isoform 1 [Homo sapiens]	14.65	2	4	5 1	6 1.022				1.020	13.5	600.97	14.65	13	16	396	44.7	7.81
20986512	mitogen-activated protein kinase 14 isoform 2 [Homo sapiens]	44.72	47	10 1	1 5		1			1.090 12		1324.46	44.72	30	52	360	41.3	5.78
4506671	60S acidic ribosomal protein P2 [Homo sapiens]	70.43	1	4	5 2	2 1.021		6 9	.3	1.078	46.4	750.70	70.43	13	22	115	11.7	4.54

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Accession 4502565	Description  calgain small subunit 1 [Homo sagiens]	ΣCoverage 48.88	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/114 5 1.0		A8: 115/114 Variability [%		16 AB: 117/116 Count .149 2	A8: 117/116 Variability [%]	Score A(3,6,7) 2669.60	Coverage A(3,6,7) 48.88	# Peptides A(3,6,7) # PS	SM A(3,6,7)	# AAs M\ 268	V [kDa] 28.3	calc. pl 5.20
355594753	clusterin preproprotein [Homo sapiens]	41.65		2 1	3 14	13			23 a 40 5		.251 3	7 16.9	5046.73	41.65	39	134	449	52.5	6.27
73747917	antigen peptide transporter 2 isoform 2 [Homo saplens]	8.12		3	1 6	1					119	2 2445.6	100.16	8.12	9	19	653	72.0	7.84
5453597	F-actin-capping protein subunit alpha-1 [Homo sapiens]	68.18		5 10	0 13	21	2 1.0	21	16 9		.247 4	2 29.0	8308.36	68.18	38	212	286	32.9	5.69
530376754	PREDICTED: acyl-CoA synthetase family member 4 isoform X6 [Homo sapiens]	3.93		В	1 4	3	4 1.0	21	6 5	.5 1	.108	6 3.5	351.49	3.93	9	34	789	89.0	7.97
21313638	leucine-rich repeat LGI family member 2 precursor (Homo sapiens)	1.28		1	1 1		2 1.0		1		.214	1	38.44	1.28	2	2	545	62.3	6.93
4507145	sorting nexin-4 (Homo sapiens)	2.00		1	1 1		2 1.0		1		.079	1	47.05	2.00	2	2	450	51.9	5.99
156151392	heterogeneous nuclear ribonucleoprotein R isoform 4 (Homo sapiens)	10.71		7 :	2 6	2					.192	2 3.7	610.14 901.24	10.71	18	24	532 341	59.6 38.7	9.16
197927454 573014819	protein DEK isoform 2 [Homo sapiens]	21.41		3	5 8 5 17	3					.134	8 16.6	901.24	21.41 32.38	21	32	341 559		8.15
573014819	X-ray repair cross-complementing protein 6 isoform 3 [Homo sapiens] PREDICTED: tyrosine-protein kinase For isoform X1 [Homo sapiens]	32.38		7 1	n 17						.113 1	6 16.3	1465.40	32.38 34.03	47 34	60	529	64.2 59.4	9.28 5.59
154759259	spectrin alpha chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	38.03	2	0 6	2 75	-					.186 8	6 16.5	10470.93	38.03	200	291	2472	284.4	5.35
4504523	10 kDa heat shock protein, mitochondrial [Homo sapiens]	18.63	_	1	2 2		9 1.0				.002	3 3.5	195.69	18.63	6	9	102	10.9	8.92
4503977	starch-binding domain-containing protein 1 [Homo sapiens]	3.63		1	1 2		3 1.0	20	1		.167	1	31.67	3.63	3	3	358	39.0	5.73
4502133	serum amyloid P-component precursor (Homo sapiens)	34.53		1 1	8 8	8	9 1.0	20	30 5	.4 1	.386 2	9 15.1	2992.18	34.53	23	89	223	25.4	6.54
530389297	PREDICTED: GDP-L-fucose synthase isoform X2 [Homo sapiens]	13.61		4 .	4 7	1	7 1.0	20	4 3	1.5 1	.127	4 8.8	337.81	13.61	17	17	441	48.3	6.79
60097902	filaggrin (Homo sapiens)	16.55		1 1	4 21	10	0 1.0	20	23 11		.081 2	3 8.3	2590.94	16.55	47	100	4061	434.9	9.25
578803915	PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform X4 [Homo sapiens]	30.51		6	7 11						.152 1	5 6.1	1971.90	30.51	32	84	331	35.4	9.17
530406069	PREDICTED: transient receptor potential cation channel subfamily M member 7 isoform X3 [Ho			6	1 7	2					.145	2 3.2	101.93	4.29	14	27	1864	212.5	7.88
6806898 5031877	alpha-synuclein isoform NACP112 (Homo sapiens)	19.64 52.05		4 :	2 2	11	8 1.0 4 1.0				.005	3 8.8	373.94 4715.70	19.64 52.05	5	114	112 586	11.4	8.29
4758484	lamin-B1 isoform 1 [Homo sapiens] qlutathione S-transferase omega-1 isoform 1 [Homo sapiens]	52.05 85.06		2 2	1 27 B 23				53 6		.163 3	9 13.7	4715.70 5142.34	52.05 85.06	12	114	241	27.5	5.16 6.60
530381195	PREDICTED: docking protein 3 isoform X2 [Homo sapiens]	7.95		5	23	19	6 1.0		2 5		.165	2 31.5	234.22	7.95	6	191	440	47.6	7.61
10947139	arginase-1 isoform 2 [Homo sapiens]	61.80		7 1	4 16	9					.196 2	6 16.6	2738.86	61.80	48	92	322	34.7	7.21
14702180	eukaryotic translation initiation factor 4H isoform 2 [Homo sapiens]	18.42		2	2 2		9 1.0				.902	3 19.5	323.96	18.42	6	9	228	25.2	8.09
19923142	importin subunit beta-1 isoform 1 [Homo sapiens]	22.49		2 16	6 17	6	6 1.0				.185 2	1 12.1	2020.35	22.49	48	66	876	97.1	4.78
530384863	PREDICTED: probable palmitoyltransferase ZDHHC4 isoform X1 [Homo sapiens]	6.40		1	1 2		9 1.0	20	1	1	.144	1	23.87	6.40	2	9	344	39.8	7.36
530384472	PREDICTED: chromobox protein homolog 3 isoform X1 [Homo sapiens]	49.73		3	6 7	3	8 1.0		13 13	1.8 1	.120 1	1 36.1	1114.49	49.73	19	38	183	20.8	5.33
5453990	proteasome activator complex subunit 1 isoform 1 [Homo sapiens]	63.05		4 1	4 15	8			23 5		.283 2	3 17.3	2625.39	63.05	41	87	249	28.7	6.02
40353734	nucleophosmin isoform 2 [Homo sapiens]	36.98		5	7 8	4					.130 1	5 11.9	2153.29	36.98	22	46	265	29.4	4.61
18375644 578830584	tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Homo sapiens]	9.35 13.63		4	2 4	1 3	0 1.0		2 11		.348	2 13.1 5 26.2	168.38 909.55	9.35 13.63	9 23	10 35	460 1071	52.8 120.6	7.44 6.40
578830584 12025678	PREDICTED: protein unc-13 homolog D isoform X1 [Homo sapiens] alpha-actinin-4 [Homo sapiens]	13.63 75.08		3 ! 5 3:		-					.012	5 26.2 8 19.7	909.55 25500.34	13.63 75.08	23 163	35 692	911	120.6	5.44
375331941	dipeptidyl peptidase 3 isoform 2 [Homo sapiens]	14 29		3.	3 50	3					150	8 23.0	1433.71	14.29	19	33	707	79.3	5.44
5902072	serpin B3 (Homo sapiens)	35.64		2 1	n 14	-			15 16		042 1	5 4.7	1615.74	35.64	37	56	390	44.5	6.81
14790115	caspase-3 preproprotein (Homo sapiens)	11.55		1 :	3 4		9 1.0				178	3 81	183.83	11.55	9	9	277	31.6	6.54
87196339	collagen alpha-1(VI) chain precursor [Homo sapiens]	11.58		2	9 10	4	2 1.0	19	14 9	.9 1	.072 1	4 7.7	1416.33	11.58	28	42	1028	108.5	5.43
17149844	peptidyl-prolyl cis-trans isomerase FKBP2 precursor [Homo sapiens]	14.79		1 .	1 2	1	0 1.0	19	3 0	1.1 1	.045	3 9.5	133.26	14.79	4	10	142	15.6	9.13
4501891	alpha-actinin-1 isoform b [Homo saplens]	78.59	4	0 4	1 65	95	3 1.0	19 1	59 7	.9 1	.166 16	4 18.2	34229.23	78.59	194	953	892	103.0	5.41
10863927	peptidyl-prolyl cis-trans isomerase A [Homo sapiens]	74.55	2	0 1:	2 13	43	6 1.0	19 1	17 8	1.8 1	.191 11	6 19.8	14043.41	74.55	39	436	165	18.0	7.81
109689695	transient receptor potential cation channel subfamily M member 8 (Homo sapiens)	2.72		1	1 4	1			1		.351	1	43.45	2.72	7	14	1104	127.6	7.24
4506613	60S ribosomal protein L22 proprotein [Homo sapiens]	20.31		1 '	1 1		6 1.0		2 1		.473	2 38.3	409.64	20.31	3	6	128	14.8	9.19
530372330	PREDICTED: Golgin subfamily A member 4 isoform X7 [Homo sapiens]	5.83	1	D '	1 16				1		.062	1	56.80	5.83	26	54	2214	259.0	5.36
4507555 4557797	thymopoletin isoform alpha [Homo sapiens]	16.28		5	7 8	4					.206 1	3 8.0 2 24.4	2129.17	16.28	22	43	694 152	75.4 17.1	7.66 6.19
4557797 58218968	nucleoside diphosphate kinase A isoform b [Homo sapiens]	53.29 81.21		2	1 8	1 14			2 4 38 11		.154 .176 3	2 24.4 8 14.5	3126.20 5582.30	53.29	23	98 140	149		4.22
7661920	calmodulin [Homo sapiens] eukaryotic initiation factor 4A-III [Homo sapiens]	14.11		1	0 13	1 14			1		.009	1 14.5	143.53	81.21 14.11	10	140	411	16.8 46.8	6.73
530385393	PREDICTED: nicotinamide phosphoribosyltransferase isoform X1 [Homo sapiens]	69.86		1 2	6 27	30			37 6		.234 8	7 20.0	9255.69	69.86	79	302	491	55.5	7.15
23110939	proteasome subunit alpha type-3 isoform 2 [Homo sapiens]	24.19	2	1	7 7	4					.180 1	2 11.6	1418.61	24.19	21	41	248	27.6	5.33
156231037	kininggen-1 isoform 1 precursor (Homo sapiens)	48.91		1 .	4 34						.230	9 17.6	15980.92	48.91	94	510	644	71.9	6.81
4502261	antithrombin-III precursor (Homo sapiens)	65.95		2 3	2 33	46	7 1.0	18 1	28 9	.1 1	.131 12	6 12.9	13604.88	65.95	94	467	464	52.6	6.71
153791507	leucine-rich repeat neuronal protein 3 precursor [Homo sapiens]	3.25		1	1 3		4 1.0		1		.182	1	35.42	3.25	3	4	708	79.4	7.83
50593002	U2 small nuclear ribonucleoprotein A' [Homo sapiens]	25.49		1 :	3 5	1			3 0		.324	3 13.4	475.51	25.49	12	12	255	28.4	8.62
5174735	tubulin beta-4B chain [Homo sapiens]	55.73		4 4	4 20				11 5		.232 1	1 22.4	6804.17	55.73	56	195	445	49.8	4.89
530410446	PREDICTED: alpha-2-antiplasmin isoform X6 [Homo sapiens]	40.73		7 1	1 13						.153 2		3088.17	40.73	35	83	464	51.7	6.29
194248072	heat shock 70 kDa protein 1A/1B [Homo sapiens] gamma-interferon-inducible lysosomal thiol reductase preproprotein [Homo sapiens]	71.61	6	1 3	0 40		2 1.0 8 1.0		96 9	.4 1	.195 18	2 17.4	29008.35 105.76	71.61	114	802	641 250	70.0 27.9	5.66 4.88
13489054	gamma-interreron-inducible lysosomal thiol reductase preproprotein [Homo sapiens]  dual specificity mitogen-activated protein kinase kinase 2 [Homo sapiens]	17.75		1	1 1	2			2 0		125	2 0.0	105.76 503.77	11.60	3	23	400	44.4	4.88 6.55
166235148	osteoclast-stimulating factor 1 [Homo sapiens]	38.79		4 .	6 6	5					252 1		2118 26	38.79	18	56	214	23.8	5.68
166197660	complement component C8 gamma chain precursor [Homo sapiens]	55.94			7 7	4						4 90	1476.33	55.94	20	48	202	22.3	8.31
21624607	coactosin-like protein [Homo sapiens]	78.87		1 1	1 12						.173 3		2794.79	78.87	35	105	142	15.9	5.67
14141161	heterogeneous nuclear ribonucleoprotein U isoform b (Homo sapiens)	22.70		2 1:	3 17	12	1 1.0	17	28 9	.0 1	.213 2	8 22.5	4097.87	22.70	45	121	806	88.9	5.78
71565154	alcohol dehydrogenase class-3 (Homo sapiens)	6.42		1 :	3 4	1	4 1.0	17	3 5	.1 1	.227	3 4.6	249.31	6.42	10	14	374	39.7	7.49
55956788	nucleolin [Homo sapiens]	23.10		1 1	2 17	7	6 1.0	17	21 8	1.3 1	.115 2	1 14.4	2754.22	23.10	43	76	710	76.6	4.70
578825752	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isoform X2 [Homo sapiens]	35.49		7 10								3 17.3	2158.36	35.49	35	78	293	32.3	5.08
578822169	PREDICTED: heat shock cognate 71 kDa protein isoform X1 [Homo sapiens]	56.04		2 2	2 38				39 6		.182 8	9 14.5	16380.28	56.04	107	516	646	70.9	5.52
530368014	PREDICTED: spectrin beta chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	28.03		5 31	9 58						.233 4	9 24.5	5762.35	28.03	146	184	2351	272.7	5.64
530416136	PREDICTED: protein LSM14 homolog A isoform X2 [Homo sapiens]	12.62		3	. 6	2					.316 .178 4	3 19.0 0 16.6	196.17 5592.58	12.62	8	20	428 215	47.1	9.13 5.74
530402312 21361302	PREDICTED: high mobility group protein B1 isoform X1 [Homo sapiens]  kallistatin isoform 2 precursor [Homo sapiens]	53.49 5.15		2 10	2 2	20	0 1.0 6 1.0		2 0		.178 4	2 1.1	153.37	53.49 5.15	49	200	427	24.9 48.5	7.75
11056061	thymosin beta-4 [Homo sapiens]	56.82		1	7 8	12					.125 3	7 11.9	3039.58	56.82	22	120	44	5.0	5.06
31377468	dedicator of cytokinesis protein 2 [Homo sapiens]	6.34		2	4 13				4 0	1.5 1	.230	4 16.0	375.66	6.34	21	29	1830	211.8	6.87
11128019	cytochrome c [Homo sapiens]	45.71		1 .	4 5	2					.149	7 12.3	630.90	45.71	13	22	105	11.7	9.57
52632383	heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]	47.37		2 1	2 15	6					.155 1	7 28.8	2687.55	47.37	39	65	589	64.1	8.22
56676393	rho GDP-dissociation inhibitor 2 [Homo sapiens]	87.06		9 19	9 21						.151 12		12128.91	87.06	61	379	201	23.0	5.21
530402335	PREDICTED: plastin-2 isoform X2 [Homo sapiens]	91.87		4 5	3 56	126			52 8		.218 34	9 20.0	43324.29	91.87	165	1264	627	70.2	5.43
4885165	cystatin-A (Homo sapiens)	27.55		1 '	1 2		9 1.0		1		.371	1	212.97	27.55	6	9	98	11.0	5.50
67782305	superoxide dismutase [Mn], mitochondrial isoform A precursor [Homo sapiens]	39.19		2 (	6 7	4					.076 1	5 8.3	1721.07	39.19	20	46	222	24.7	8.25
66932947 578820749	alpha-2-macroglobulin precursor (Homo sapiens)	77.82 2.88	2	83	2 97	320	9 1.0 4 1.0				.232 76 .853	2 23.4 2 56.1	127785.40 62.18	77.82 2.88	285	3209	1474 451	163.2 48.6	6.42
578820749 578838657	PREDICTED: tubby protein homolog isoform X2 [Homo sapiens]  PREDICTED: septin-6 isoform X3 [Homo sapiens]	2.88		4 '	1 1	3					.853	2 56.1 4 8.8	62.18 480.56	2.88	2	32	451 427	48.6	9.36 6.81
578838657 7661922	PREDICTED: septin-6 isoform X3 [Homo sapiens] ras-related protein Rab-21 [Homo sapiens]	28.10	1:	1	3 2	1 1					.048	4 8.8 5 10.9	480.56 498.33	28.10	22	32 17	427 225	48.8	7 94
46049114	kinesin-like protein KIF20B isoform 2 [Homo sapiens]	7.36	2	1	1 18				2 21		.180	2 0.9	169.31	7.36	31	78	1780	206.0	5.77
21536326	heterogeneous nuclear ribonucleoprotein U-like protein 1 isoform a [Homo sapiens]	15.65	1	D !	5 12						.290	7 5.4	708.21	15.65	28	39	856	95.7	6.92
23065544	glutathione S-transferase Mu 1 isoform 1 [Homo saplens]	55.96		В 1	1 12						.221 1		1983.53	55.96	34	50	218	25.7	6.70
332205939	ras-related protein Rab-11A isoform 2 [Homo sapiens]	26.45		3	4 4	3	5 1.0	16	11 2	1.5 1	.192 1	1 4.8	1113.67	26.45	12	35	155	17.6	8.85
156616273	pleckstrin (Homo sapiens)	35.43		1 4	B 10	4	9 1.0	16	13 5	i.0 1	.108 1	3 22.1	1389.01	35.43	25	49	350	40.1	8.28
530380590	PREDICTED: prefoldin subunit 1 isoform X1 [Homo sapiens]	18.26		2	2 2		6 1.0				.108	2 31.1	195.09	18.26	6	6	115	13.2	6.32
112421122	dnaJ homolog subfamily C member 13 [Homo sapiens]	3.74		2	2 9	3					.493	2 51.7	198.30	3.74	19	35	2243	254.3	6.74
31542319	coatomer subunit epsilon isoform a [Homo sapiens]	22.73		3	3 5	2			3 1		.189	3 0.3	536.99	22.73	14	23	308	34.5	5.12
100913206	ATP-dependent RNA helicase A [Homo sapiens]	5.28			4 8	2			3 1		.174	3 7.8	449.68	5.28	16	21	1270	140.9	6.84
530385906 15149476	PREDICTED: leucine-rich repeat and calponin homology domain-containing protein 4 isoform X			4	1 4		6 1.0 6 1.0		1		.651	1 3 22.4	23.73 310.03	6.76	4	6	621	66.4	7.58 6.68
15149476 4505763	argininetRNA ligase, cytoplasmic [Homo sapiens] phosphoglycerate kinase 1 [Homo sapiens]	10.91 80.58		2 3	3 8	68					.073		310.03 22381.97	10.91 80.58	16	16 686	660 417	75.3 44.6	6.68 8.10
33589854	phosphogrycerate kinase 1 [Homo sapiens] biliverdin reductase A precursor [Homo sapiens]	35.14		1 3	6 R	1 3					.141 20	0 8.4	954.29	80.58 35.14	22	37	296	33.4	6.44
4758648	kinesin-1 heavy chain [Homo sapiens]	12.67		3	4 12	4			4 5		.955	4 3.6	367.89	12.67	19	45	963	109.6	6.51
431822408	heat shock protein HSP 90-beta isoform c [Homo sapiens]	46.50	1	3 1	4 35		2 1.0	15	26 4	.3 1	.135 2	5 23.7	9083.63	46.50	102	262	714	82.3	5.06
10863977	U6 snRNA-associated Sm-like protein LSm2 [Homo sapiens]	54.74		1 :	3 4		9 1.0		3 0		.203	2 10.6	256.50	54.74	9	9	95	10.8	6.52

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Accession 19923106	Description	ΣCoverage 55.21	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116		A8: 117/116 Variability [%] 0 40.0	Score A(3,6,7) 5024.35	Coverage A(3,6,7) 55.21	# Peptides A(3,6,7) # PSM A(3,6,7)	# AAs 4 355	MW [kDa]	calc. pl
19923106 4759160	serum paraoxonase/arylesterase 1 precursor [Homo sapiens] small nuclear ribonucleoprotein Sm D3 [Homo sapiens]	26.19	- 1	2 11	12	114	9 1.01	3.	9.9	1.35		0 40.0	138 17	26.19	36 T	4 355 9 126		5.22 10.32
68799814	AP-2 complex subunit mu isoform b [Homo sapiens]	8.31		2	5		9 1.01		1.8			2 3.5	107.38	8.31	9	9 433		9.54
38201644	homeodomain-interacting protein kinase 1 isoform 4 [Homo saplens]	2.08	1	1 1	2		3 1.015			1.35		1	29.41	2.08	2	3 816		8.59
10834978	interleukin-8 precursor (Homo sapiens)	25.25	1	1 2	2		9 1.015		3.8			2 10.9		25.25	6	9 99		8.84
31742503 23110962	histone H3.2 (Homo sapiens) cathepsin S isoform 1 preproprotein (Homo sapiens)	58.82 34.44	3	3 1	11 11				13.1			4 12.7 3 14.2		58.82 34.44		2 136		11.27 8.34
74136549	AT-rich interactive domain-containing protein 5B isoform 1 (Homo sapiens)	2.78		2 1	4	7	6 1.01		0.0	2.07		1 14.2	29.80	2.78	4	6 1188		8.72
21956645	myotrophin (Homo sapiens)	61.86	1	1 7	7	55			5.7			8 11.0		61.86	20	5 118		5.52
578828075	PREDICTED: pyrin isoform X1 [Homo sapiens]	9.62	3	3	7	2			1.6			2 3.3		9.62		780		7.94
5454158	valinetRNA ligase (Homo sapiens)	8.86	3	3 6	8	2			1.2	1.18	5	6 24.0		8.86	21	1264		7.59
112790163 5031863	metal regulatory transcription factor 1 [Homo sapiens] galectin-3-binding protein precursor [Homo sapiens]	1.20	1	1 1	1 10	45	8 1.014 5 1.014		3.7	1.24	3 1	5 33.4	68.75 1788.59	1.20 24.79	3	8 753 5 585		5.30 5.27
21735621	malate dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	24.77		3 6	6	25			3.7			8 20.2	979.89	24.79		5 338		8.68
40254866	charged multivesicular body protein 2b isoform 1 (Homo sapiens)	21.13		2 1	5		9 1.014			1.14		1	127.79	21.13	9	9 213		8.76
4506549	non-secretory ribonuclease precursor [Homo saplens]	19.88	1	1 3	3	35	5 1.014	1:	12.8	1.22	5 1:	2 22.5	1479.42	19.88	9	161		8.73
157276599	bactericidal permeability-increasing protein precursor (Homo sapiens)	59.14	1	7 19	21	250							7690.95	59.14	63 29			9.38
153251270 222352151	calcineurin-like phosphoesterase domain-containing protein 1 isoform a [Homo sapiens]	55.41	-	2 13	14				5.8			6 9.1	2085.40	55.41		314		6.20 7.09
4503471	poly(rC)-binding protein 1 [Homo sapiens] elongation factor 1-alpha 1 [Homo sapiens]	29.49 56.71	1	2 1	1 18	20			5.4			5 17.7 7 13.1	671.63 7118.03	29.49 56.71		0 356 0 462		7.09 9.01
8923110	nuclear distribution protein nudE homolog 1 [Homo sapiens]	8.66		3 1	4	13				1.22		1	164.37	8.66		3 335		5.15
402478626	low affinity immunoglobulin gamma Fc region receptor III-B isoform 4 [Homo sapiens]	31.94	9	9 6	8	21			5.5			8 24.1	812.75	31.94	19	9 216		6.71
4506695	40S ribosomal protein S19 (Homo sapiens)	6.21	1	1 1	1	21	9 1.014			1.21		1	167.90	6.21	3	145		10.32
223890219 530402176	RNA-binding motif protein, X-linked-like-3 [Homo sapiens]	4.69 6.30		2 1	5	25	5 1.014 0 1.014		3.1	0.93		1 11.0	574.27 567.97	4.69 6.30		1067 10 1445	114.9 164.3	9.10 8.43
4557894	PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X2 [Homo sapiens]  lysozyme C precursor [Homo sapiens]	72.30		1 12	1 12	479								72.30		9 148		9.16
55743122	retinol-binding protein 4 precursor (Homo sapiens)	76.12		2 11	12	239			6.9				8428.62	76.12		9 201		6.07
58533161	PDZ and LIM domain protein 5 isoform e [Homo sapiens]	6.54	1	7 1	1		2 1.01			0.98	4	1	44.82	6.54	2	2 214	23.8	9.92
38016914 530398067	deoxynucleoside triphosphate triphosphohydrolase SAMHD1 [Homo sapiens]	15.97 86.89	2	2 3	8	31	8 1.01: 7 1.01:		2.0			5 9.2	923.34	15.97 86.89	16	8 626	72.2 30.8	7.14
530398067 578837549	PREDICTED: apolipoprotein A-I isoform X1 [Homo sapiens] PREDICTED: DEP domain-containing protein 5 isoform X10 [Homo sapiens]	86.89 3.83	35	31	36	1347							43488.15 78.09	86.89 3.83	106 13	7 267		5.76 6.80
170016081	protein XRP2 [Homo sapiens]	8.29	1	1 4	4	1:						4 9.5		3.83 8.29		3 350		5.12
167234422	hematopoietic lineage cell-specific protein isoform 1 [Homo sapiens]	25.51		2 12	14	9:	3 1.01:	2	6.2	1.11	5 2	5 9.0	2406.12	25.51		3 486	54.0	4.81
578809106	PREDICTED: immunoglobulin J chain isoform X1 [Homo sapiens]	41.51	1	1 6	6	8:							2362.56	41.51		159		5.24
4506629	60S ribosomal protein L29 [Homo sapiens]	18.87	1	1 1	3	- 1	8 1.01		4.9			2 1.0		18.87	5	8 159		11.66
75709200 578832788	phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform A precursor [Homo s PREDICTED: thioredoxin-like protein 1 isoform X2 [Homo sapiens]	18.27 27.06	3	3 1	4	1	8 1.01: 2 1.01:		4.0	1.34		4 3.3	56.28 643.72	18.27 27.06	8	8 197 2 255		8.37 4.83
4505753	phosphoglycerate mutase 1 [Homo sapiens]	84.65	23	3 13	20									84.65		3 254		7.18
578804376	PREDICTED: bifunctional purine biosynthesis protein PURH isoform X1 [Homo sapiens]	19.14		2 1	8	44			6.6			9 6.8		19.14		6 533		6.84
39812055	beta-arrestin-2 isoform 2 [Homo sapiens]	12.94	1	7 3	4	22	2 1.01		4.3	1.13	9	6 3.5	783.55	12.94	12	2 394	44.4	7.88
5032059	protein S100-A12 [Homo sapiens]	91.30	10	9	10				11.3			6 28.2		91.30	29 6			6.25
530379653	PREDICTED: chromodomain-helicase-DNA-binding protein 1 isoform X1 [Homo sapiens]	4.62	23	3 1	10				9.0	1.76		1	30.47	4.62		4 1798		7.23
47271443 62420888	serine/arginine-rich splicing factor 2 [Homo sapiens] dipeptidyl peptidase 2 preproprotein [Homo sapiens]	18.55 8.74	- :	2	5 5	14	4 1.013 8 1.013		9.0			4 13.5 2 10.2		18.55 8.74	11	4 221 8 492		11.85
55749932	desmin [Homo sapiens]	14.89	-	1 1	9	129			1.0	1.19		1 10.2	1543.77	14.89	22 1:	9 470		5.27
530407832	PREDICTED: protein CLEC16A isoform X7 [Homo sapiens]	6.05	8	3 1	7	10				1.18		1	91.12	6.05		6 925		6.51
6912388	grancalcin (Homo sapiens)	44.70		5 9	9	65						1 21.3		44.70	26	5 217		5.21
530376092	PREDICTED: protein phosphatase 2, regulatory subunit B, gamma isoform X3 [Homo sapiens]	5.26	- 6	5 1	2		9 1.01:		2.5			2 16.0	168.17	5.26	6	9 342		6.95
4503689 4506185	fibrinogen alpha chain isoform alpha-E preproprotein [Homo sapiens] proteasome subunit alpha type-4 isoform 1 [Homo sapiens]	51.15 44.44	52	2 47	49	1390	0 1.01: 1 1.01:		7.6		7 39	5 16.9 4 9.6	33979.80 1364.77	51.15 44.44	145 13	0 866 11 261		6.01 7.72
530409962	PREDICTED: WD repeat-containing protein 16 isoform X2 [Homo sapiens]	3.58		2	2	4	2 1.01.		0.0	0.80		4 9.6	27.86	3.58	2/	2 531		7.42
4507793	ubiquitin-conjugating enzyme E2 N [Homo sapiens]	34.87		2 4	4	2			5.5			6 12.7	698.40	34.87	12	152		6.57
4502317	V-type proton ATPase subunit E 1 isoform a [Homo sapiens]	36.28	4	1 5	7	2			6.0			4 22.0	692.50	36.28		226		8.00
578831314	PREDICTED: transcription elongation factor SPT6 isoform X3 [Homo sapiens]	5.68	2	2 1	9	2	7 1.01:		1.5			3 4.8	146.13	5.68	15	1603		5.11
66932916 209862911	mitogen-activated protein kinase 1 [Homo sapiens] periostin isoform 2 precursor [Homo sapiens]	27.50 45.57	21	7	8	204	6 1.012 4 1.012					1 44.1 4 29.2	925.50 6831.68	27.50 45.57	23	16 360 14 779		6.98 7.81
32483377	thioredoxin-dependent peroxide reductase, mitochondrial isoform b [Homo sapiens]	39.08	- 5	2 6	6 6	204			8 4.7			8 9.1	880.19	45.57 39.08		13 238		7.46
10645195	histone H2A type 1-B/E [Homo saplens]	60.00		5 1	6	70	0 1.012		1.2			2 9.6	2076.11	60.00		0 130		11.05
4506505	regulator of G-protein signaling 10 isoform b [Homo sapiens]	7.19	- 2	2 1	1		3 1.012			1.25		1	239.31	7.19	3	3 167	19.6	5.87
377520143	protein FAM49B [Homo sapiens]	70.06	q	16	18	108			9.7			4 22.0	4234.79	70.06		324	36.7	6.06
4503987 194394158	gamma-glutamyl hydrolase precursor (Homo sapiens)	27.99 54.83	1	1 8	8 8	4'								27.99		11 318 12 538		7.11
194394158	nicotinate phosphoribosyltransferase isoform 1 [Homo sapiens] mitochondrial peptide methionine sulfoxide reductase isoform a precursor [Homo sapiens]	54.83 21.70	-	2 17	18	82			7.7		7 2	4 19.7	3262.18 339.64	54.83 21.70		2 538		5.68 8.09
189163532	alpha-1-antitrypsin precursor (Homo sapiens)	81.10	+ 3	2 40	43									81.10	124 36			5.59
148596990	copper homeostasis protein cutC homolog (Homo sapiens)	10.62	1	1	2	-	6 1.012			8.94	1	1	242.79	10.62	6	6 273	29.3	8.18
260166612	hydroperoxide isomerase ALOXE3 isoform 1 precursor [Homo sapiens]	2.37	2	2 1	2		2 1.01			0.88		1	27.45	2.37	2	2 843		7.75
11545817	G-protein-signaling modulator 3 (Homo saplens)	14.37	1	1 1	1		2 1.01			1.14		1	113.39	14.37	2	2 160		4.97
4507521 578815882	transketolase isoform 1 [Homo sapiens] PREDICTED: t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]	71.11	22	3 40	44	78			7.3	1.13		2 15.3	34995.56 44 93	71.11		6 878		7.66 8.92
4503291	PREDICTED: t-SNAKE domain-containing protein 1 isoform X2 [Homo sapiens]  D-dopachrome decarboxylase [Homo sapiens]	43.22		5	5 5	4			14.8			3 16.8		43.22		11 118		7.30
578818836	PREDICTED: gamma-tubulin complex component 2 isoform X1 [Homo sapiens]	3.10		2	3		9 1.01		14.0	1.13		1	205.94	3.10	7	9 902		6.84
85362735	oxysterols receptor LXR-beta isoform 1 [Homo sapiens]	1.74	1	1 1	1 1		2 1.01		5.1			2 12.7	24.03	1.74	1	2 461		7.74
4502107	annexin A5 (Homo sapiens)	80.00	1	1 20	25									80.00	71 2			5.05
33239445 110735433	eukaryotic translation initiation factor 3 subunit B [Homo sapiens]  CD177 antiqen precursor [Homo sapiens]	7.37 4.58	1	1 3	3 7	10	6 1.01° 9 1.01°		5.6 5.2			3 8.1 3 5.8	391.77 241.50	7.37 4.58	15	6 814 9 437		5.00 6.01
4503521	eukaryotic translation initiation factor 3 subunit E [Homo sapiens]	14.61			5 5	1			3.1			3 13.3		14.61	11	2 445		6.04
578826850	PREDICTED: tropomodulin-3 isoform X1 [Homo sapiens]	42.90		2 6	11	40			7.0			8 13.8		42.90		0 352		5.19
4502511	complement component C9 precursor (Homo sapiens)	45.08	14	1 21	24	234	4 1.01	5	10.1	1.21	4 5.	3 19.6	5597.76	45.08	67 2			5.59
62198235	drebrin-like protein isoform b (Homo sapiens)	26.98		5 8	10	61			9.2			9 26.1	2540.22	26.98		6 430		5.05
15431310 6598323	keratin, type I cytoskeletal 14 (Homo sapiens)	43.22 68.31	21	1	24	107		1.	3.3			2 6.7	2936.52 9300.85	43.22 68.31		7 472 8 445		5.16 6.47
6598323 63162572	rab GDP dissociation inhibitor beta isoform 1 [Homo sapiens] T-complex protein 1 subunit gamma isoform a [Homo sapiens]	68.31 26.24	10	20	30	278	8 1.01° 4 1.01°	6	6.1			1 11.9 8 15.9	9300.85 1822.98	68.31 26.24		8 445 i4 545		6.47
6005764	gamma-aminobutyric acid receptor-associated protein [Homo sapiens]	21.37	3	3 2	3		8 1.01		8.2			2 10.9	143.01	21.37	5	8 117		8.79
217330598	glyoxalase domain-containing protein 4 [Homo sapiens]	33.22		2 8	10	31	8 1.010	1	3.9	1.17	6 1	1 14.0		33.22	28	18 298	33.2	5.60
14141193	40S ribosomal protein S9 [Homo sapiens]	11.34	20	2	2 3		7 1.010	)	1.8			2 1.1	139.54	11.34	7	7 194		10.65
384475554	histidinetRNA ligase, cytoplasmic isoform 3 [Homo sapiens]	11.66	8	3	8	19	9 1.010		6.1			3 6.0		11.66		9 489		5.54
578813850 469608407	PREDICTED: actin-related protein 2/3 complex subunit 1B isoform X1 [Homo sapiens] transgelin-2 isoform b [Homo sapiens]	44.35 75.88	1	1 14	1 14	178		4	7.6			5 10.0 0 24.3		44.35 75.88	42 1	8 372 2 199		8.35 8.25
459508407	transgelin-2 isoform b [Homo sapiens]  lumican precursor [Homo sapiens]	75.88 44.67	2	1 12	12	110		3	i 8.7			0 24.3 5 9.5	3691.54 4063.56	75.88 44.67	42 1	0 338		6.61
40068518	6-phosphogluconate dehydrogenase, decarboxylating (Homo sapiens)	66.25	2	2 30	31	460		14						66.25		0 483		7.23
10880134	beta-arrestin-1 isoform B [Homo sapiens]	14.88		3	5	26	6 1.010		7.8	0.71	5	2 51.6	321.74	14.88	13	6 410	46.3	6.34
530393298	PREDICTED: cytosolic purine 5'-nucleotidase isoform X8 [Homo sapiens]	15.98		5 6	6	20			10.1			7 19.8	878.55	15.98		532		5.74
530394583	PREDICTED: TATA-binding protein-associated factor 172 isoform X1 [Homo sapiens]	4.68	3	1	7	1	7 1.010			1.15		1	37.33	4.68		7 1646		6.70
530398051 4557367	PREDICTED: porphobilinogen deaminase isoform X1 [Homo sapiens] bleomycin hydrolase [Homo sapiens]	14.24	4		5	15	5 1.010		7.5			2 42.1	146.51 489.06	14.24 11.43		5 344 5 455		7.39 6.27
578828107	PREDICTED: polycystin-1 isoform X9 [Homo sapiens]	1.80	12	2	7	11			3.3			3 7.0		1.80		8 4279		6.70
530375987	PREDICTED: transforming acidic coiled-coil-containing protein 3 isoform X2 [Homo sapiens]	10.37	4	1	6	1			2.0	1.12		1	31.61	10.37		7 482		5.44
401709935	IST1 homolog isoform d [Homo sapiens]	7.76	1	7 1	3		7 1.010			1.45	8	1	92.03	7.76	7	7 335	36.6	5.44

	9 21 22 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	9 154 29 301 17 273 18 273 18 270 7 139 9 239 17 320 33 577 24 253 33 577 24 253 33 53 577 24 656 18 337 77 4666 18 337 18 477 18 483 20 483 20 483 20 483	16.6   16.6   16.6   16.6   16.6   16.6   16.6   16.1   16.6   16.1   16	calc. pl 6.58 5.31 7.81 5.48 6.38 9.99 5.73 10.18 6.40 7.71 6.43 5.20 8.32 6.811 7.17
September   Sept	18 2 18 3 19 41 5 30 5 100 47 115 15 11 15 11 16 12 21 22 22 23 7 6 15 1 1 25 30 6 15 1 25 30 6 17 37 8 37 8	29 301 11 314 318 270 7 139 17 239 17 239 17 239 17 320 18 270 17 320 18 270 17 320 18 270 18 270 18 270 18 277 466 18 277 466 18 277 466 18 277 466 18 47 10 337 10 337 10 348 11 4337 10 483 10	35.1 28.9 36.2 30.6 15.3 27.4 33.7 67.8 27.0 59.8 100.1 20.8 53.6 30.4 37.5 97.1 47.0	5.31 7.81 5.48 6.38 9.99 5.73 10.18 6.40 7.71 6.43 5.20 5.78 5.12 8.32
SEATONING   PRESCRIPTION - STANDARD - STAN	18 2 18 3 19 41 5 30 5 100 47 115 15 11 15 11 16 12 21 22 22 23 7 6 15 1 1 25 30 6 15 1 25 30 6 17 37 8 37 8	11 314 316 37 139 39 239 17 320 33 577 24 24 253 33 554 33 554 31 88 477 466 818 277 41 337 33 847 41 41 337 33 847 41 41 337 42 432 41 41 337 438 438 447	36.2 30.6 15.3 27.4 33.7 67.8 27.0 59.8 100.1 20.8 53.6 30.4 37.5 97.1 47.0	5.48 6.38 9.99 5.73 10.18 6.40 7.71 6.43 5.20 5.78 5.12 8.32 6.81 7.17
Section   Processing   Proces	18 2 18 3 19 41 5 30 5 100 47 115 15 11 15 11 16 12 21 22 22 23 7 6 15 1 1 25 30 6 15 1 25 30 6 17 37 8 37 8	38 270 7 7 139 39 239 17 320 33 577 24 253 33 577 24 253 33 53 54 53 908 18 277 466 18 277 466 18 277 41 337 31 22 432 16 413 32 32 36 36 37 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 37 38 38 38 38 38 38 38 38 38 38 38 38 38	30.6 15.3 27.4 33.7 67.8 27.0 59.8 100.1 20.8 53.6 30.4 37.5 97.1 47.0	6.38 9.99 5.73 10.18 6.40 7.71 6.43 5.20 5.78 5.12 8.32 6.81 7.17
1975    1975	18 2 18 3 19 41 5 30 5 100 47 115 15 11 15 11 16 12 21 22 22 23 7 6 15 1 1 25 30 6 15 1 25 30 6 17 37 8 37 8	7 139 39 239 17 320 31 577 24 24 253 33 577 33 534 54 184 64 184 67 466 18 277 41 337 33 847 12 432 12 432 10 483 10 483 10 483 10 483 10 483 10 483	15.3 27.4 33.7 67.8 27.0 59.8 100.1 20.8 53.6 30.4 37.5 97.1 47.0	9.99 5.73 10.18 6.40 7.71 6.43 5.20 5.78 5.12 8.32 6.81
Mathematical Continues and Principles against agai	18 2 18 3 19 41 5 30 5 100 47 115 15 11 15 11 16 12 21 22 22 23 7 6 15 1 1 25 39 6 12 37 8 37 8	39 239 320 33 577 24 253 33 534 53 908 54 184 77 466 18 277 413 337 33 847 12 432 16 432 16 433 20 483 23 487	27.4 33.7 67.8 27.0 59.8 100.1 20.8 53.6 30.4 37.5 97.1 47.0	5.73 10.18 6.40 7.71 6.43 5.20 5.78 5.12 8.32 6.81
EMPSIZED   Programmer Section Deproposition (from support)	18 2 18 3 19 41 5 30 5 100 47 115 15 11 15 11 16 12 21 22 22 23 7 6 15 1 1 25 39 6 12 37 8 37 8	33 577 24 253 33 534 53 908 54 184 77 466 18 277 466 18 277 11 337 103 847 12 432 16 413 20 483 20 483 28 376 28 497	67.8 27.0 59.8 100.1 20.8 53.6 30.4 37.5 97.1 47.0	6.40 7.71 6.43 5.20 5.78 5.12 8.32 6.81 7.17
Section   Continue	18 2 18 3 19 41 5 30 5 100 47 115 15 11 15 11 16 12 21 22 22 23 7 6 15 1 1 25 39 6 12 37 8 37 8	24 253 33 534 534 908 54 184 77 466 18 277 41 337 33 847 112 432 16 413 20 483 376 53 497	27.0 59.8 100.1 20.8 53.6 30.4 37.5 97.1 47.0	7.71 6.43 5.20 5.78 5.12 8.32 6.81 7.17
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2577162 265 protessorm non-Affrese regulatory submit 2 section 1 phonon supplied 94.23 3 1 1 15 5 1 1,00° 17 7 9 1.111 17 31.4 219.26 94.25 21.00° 17 17 18 17 1.111 17 31.4 219.26 94.25 21.00° 17 18 18 17 1.111 17 18 1.11	30 5 105 47 105 115 11 105 115 11 105 115 11 105 115 11	184 177 466 18 277 41 337 33 847 112 432 116 413 20 483 228 376 53 497	20.8 53.6 30.4 37.5 97.1 47.0 47.3	5.20 5.78 5.12 8.32 6.81 7.17
STREETER   PREDICTED representation for the Disconnection of the Computer System   1.00   1	105 47 15 11 15 95 44 151 151 16 1. 18 22 21 22 37 6. 15 17 4 125 39 6 537 88	777 466 18 277 41 337 93 847 12 432 16 413 220 483 376 53 497	53.6 30.4 37.5 97.1 47.0 47.3	5.12 8.32 6.81 7.17
25.99   25.9	15 11 95 44 95 44 95 44 95 131 140 150 150 150 150 150 150 150 150 150 15	18 277 41 337 03 847 12 432 16 413 220 483 376 53 497	30.4 37.5 97.1 47.0 47.3	8.32 6.81 7.17
Page	95 44 131 40 141 151 152 152 152 152 153 154 155 155 155 155 155 155 155 155 155	411 337 333 847 12 432 16 413 20 483 28 376 63 497	37.5 97.1 47.0 47.3	6.81 7.17
PREDICTED procesponder associated with glycosphogogape arthord microcommism 1 lineary 6 .64	6 1. 1. 18 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.	12 432 16 413 20 483 28 376 63 497	47.0 47.3	
PRIDICTIC profise-series Processing products in Surface   15.00   5   5   7   16   1.00°   5   6.0°   1.42°   5   37.5°   207.40   15.05   1	16 8 22 37 6 6 6 15 1 125 36 6 6 37 8 8 37 8 8	16 413 20 483 28 376 63 497	47.3	
SERDICTED probable AP Despendent PNA Incloses DONE obtem XI [Homo spiern]   12.84   2   2   4   20   1.009   5   14.0   1.151   5   16.0   60.01   70.000	8 2 21 21 37 6 6 1 15 1 4 1 25 36 6 37 8 3 3	20 483 28 376 63 497		4.65
1314-2080   buts contracting (Nerro supering)   22,33   2   2   8   20   1.009   3   0.4   2.229   3   7.79   651.70   26.31   26.5171070   7.70	21 21 37 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	28 376 63 497		5.45 8.66
	6 15 1 1 4 4 1 1 1 2 5 3 6 6 6 1 3 7 8 8		42.3	6.40
221316414   extracellatar marker protein 1 bottom: procuracy [Pienon supplems]   14.81   3   5   6   17   1,000   5   10.6   1,122   4   1,03   80   3.72   15146191   heat shock protein 15°P 0-alights bottom: 2 [Pienon supplems]   51.09   11   24   43   349   1,000   59   7.5   1,172   50   16.6   12°Pa.52   51.09   2.5   1.05	6 37 81 3		54.1	5.31
S0039774   PREDICTID: nuclear GPIPAGE SUPPAGE Notion xalpiening   51.07   1.72   1   4   9   1.009   1   1.173   1   50.00   3.72   3.75   3	6 37 81 3	6 224 17 540	25.2 60.6	9.28 6.71
13.59971999   ras-related protein Rab-Za kotomb [Homo saplems]   14.36   4   2   2   6   10.09   2   4.4   1.185   2   6.9   44.30   14.35   34.22   3.854326   APP-ribosyl-pytrase-lytemos saplems]   34.22   3   13   3   3   10   10.09   25   5.11   15   2   26.85   3.34.22   3.854326   APP-ribosyl-yytrase-lytemos saplems]   4.79   5   1   1   1   8   10.09   3   9.5   1.248   3   16.6   104.91   2.67   3.854326   APP-ribosyl-yytrase-lytemos saplems]   4.79   5   1   1   1   8   10.09   3   9.5   1.248   3   16.6   104.91   2.67   3.854326   APP-ribosyl-yytrase-lytemos saplems]   4.79   5   1   1   1   8   10.09   3   9.5   1.248   3   16.6   104.91   2.67   3.854326   APP-ribosyl-yytrase-lytemos saplems]   53.79   1   3   3   3   62   10.08   21   6.1   1.242   21   13.1   266.607   35.79   3.1	6 37 81 3	9 672	76.8	8.40
2007.77441   Physion-bunding globulin preciver [Homo saplers]   34.22   3   13   13   80   1.009   25   5.1   1.157   25   1.12   22.68.13   34.22   3   3.16.6   10.99   2.67   3.1   3   1.009   3   9.5   1.24   3   1.009   2.67   3.1   1.008   4   2.5   1.204   4   2.12   68.86   4.75   3.000   2.0	6 37 8 3		84.6	5.02
Sale-State   App-retory (values/vgke APP-retory (values/vgk APP-retory (values/vgk APP-retory (values/vgk APP-retory (values	37 8	6 188 80 415	20.8 46.3	6.11
Specific District D	12 2	8 300	46.3 34.3	6.30 7.66
Post		21 1564	184.8	9.47
12449425   profiteration-associated proteins 244 Merons appliers  36.55   1   10   13   61   1.008   18   7.2   1.102   7   6.2   1346, 2   346, 4   46, 4   46, 4   4   5.3011349   PREDICTID: complement 1 a subcomponent saukuril Bullow Informa Spiems   46, 4   6, 4   6   7   1   1   4   8   1.008   2   14.2   1.217   2   10.5   42.95   6.85   1.008   1   1   1   1   4   8   1.008   2   14.2   1.217   2   10.5   42.95   6.85   1.008   1   1   1   1   1   1   1   1   1	9 6		11.4	6.86
S03011334   PRETICITE: conspiented C1 subcomponent Submit Biothern X1 (Homo sapiens)   46.64   1   8   10.01   13.3   1.008   32   9.0   1.273   31   22.6   3746.24   46.64   1   8   10.00   2   14.2   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   3.01   12.7   2   10.3   3.01   12.7   2   10.3   3.01   12.7   3.01   12.7   2   10.3   3.01   12.7   3.01   12.7   3.01   12.7   3.01   12.7   3.01   12.7   3.01   12.7   3.01   12.7   3.01   12.7   3.01   3.	9 1	11 295	32.8 43.8	4.87 6.55
SB702793   Sastring recursor [Floron saplers]   4-90   1   3   11   1.008   1   2.147   1   296.71   4-90   1   1   3   11   1.008   1   2.147   1   296.71   4-90   27.68   1   5   5   2.6   1.008   7   3.6   1.180   7   7.6   6.980   27.68   1   5   5   2.6   1.008   7   3.6   1.180   7   7.6   6.980   27.68   1   5   1.008   7   3.6   1.180   7   7.6   6.980   27.68   1   1.008   7   2.08   27.68   1   1.008   7   2.08   27.68   1   1.008   7   2.08   27.68   1   1.008   7   2.08   27.68   1   1.008   7   2.08   27.68   1   1.008   7   2.08   27.68   1   1.008   7   2.08   27.68	35 6 29 13:		43.8 26.7	8.63
197148608   ubiquim thoisterne OTUBI   Homo suplems   27.68   1   5   5   26   1.008   7   3.6   1.180   7   7.6   698.03   27.68   27.78	4	8 496	54.9	9.51
STITE   STIT		11 673 26 271	71.7 31.3	7.39 4.94
22331211   actin-related protein 23 complex subunit 2 [Horno saplems]   74.00   2   23   24   314   1.008   97   6.6   1.184   66   1.35   1098.5 4   74.00	14 39		75.6	9.79
	70 31		34.3	7.36
123173757   Robunskoprofein PTB-binding   Homo saplers    1.72   1   1   3   1.008   1   1.033   1   1.053   1   1.008   1	34 5		26.7	5.20
196979323   encyl-Cab Myrdatake, mitschandrial [Morro sapiens]   12.07   1   2   2   4   1.008   2   13.4   1.582   2   0.1   135.01   12.07   12.07   12.07   12.07   13.5   13.07   13.5   13.07   13.5   13.07   13.5   13.07   13.5   13.07	14 2	22 277 3 756	30.2 79.5	5.26 8.92
ABZA700   neterogeneous nuclear ribonucleogrother [ Horros spalen]   21.45   2   3   7   30   1.008   5   3.8   1.074   5   2.2   855.98   21.45   22.48339   3.243399   3.243	4	4 290	31.4	8.07
28905.417   AMP dearmines 3 Isoform 4 (Normo spiens)   215.5   6   10   12   41   1.008   12   9.0   1.197   12   16.9   122.100   215.5   17.8   1	19 3	30 415	45.6	5.58
578810352 PREDICTED: regulator of G-protein signaling 7-binding protein isoform X2 (Homo sapiens) 3.43 3 1 1 1 1 1.008 1 1.108 1 1.161 1 20.33 3.43 222772553 alidestypic deshydrogenase family 16 member A1 Isoform 2 (Homo sapiens) 13.18 2 4 6 20 1.008 4 4.1 1.358 4 11.6 56.47 13.138 5 50.316.55 confilin-1 (Homo sapiens) 1 1.008 1 1 1 1.008 1 1 1 1.008 1 1 1 1 1 1.008 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	30 4	46 524 41 608	58.0 71.2	5.96 6.99
223972553 alidestryked eichydrogensase Family 16 member A1 koform 2 (Homo sapiens) 13.18 2 4 6 20 1.008 4 4.1 1.358 4 11.6 564.71 13.18 50316.55 codin-1 (Homo sapiens) 12.52 80.12 20 22 23 389 1.008 119 6.7 1.190 119 119 119 125.52 80.12 25918200 serime/Threen/ine-protein phosphatase 6 regulatory subunit 3 koform 3 (Homo sapiens) 1.26 16 1 1 1 1.008 1 1 1 1.008 1 1 1 1.008 1 1 1 1.008 1 1 1 1 1.008 1 1 1 1 1 1.008 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	1 204	22.7	7.36
25919200 serime/Threorine-protein phosphatase 6 regulatory subunit 3 isoform 3 (Homo sapiens) 1.26 16 1 1 1 1.008 1	16 21	20 751	79.9	7.58
11863154 coatomer subunit delta isoform 1 [Homo sapiens] 12.52 3 5 7 24 1.008 7 9.4 1.120 7 18.2 817.24 12.52 42822872 riboruolesse inhibitor [Homo sapiens] 48.59 1 12 15 90 1.008 27 3.8 1.111 27 9.8 4056.96 48.59	66 38	1 791	18.5 88 9	8.09 4.58
42822872 ribonuclease inhibitor (Homo sapiens) 48.59 1 1 12 15 90 1.008 27 3.8 1.111 27 9.8 4056.96 48.59	19 20		88.9 57.2	4.58 6.21
530373049 PREDICTED: biotinidase isoform X4 (Homo saplens) 6.69 4 3 3 11 1.008 4 8.0 1.095 4 6.1 520.82 6.69	41 9	90 461	49.9	4.82
	8 1	11 523	58.9	5.85
199011728 kinesin light chian 2 boform 2 [Nemo sapiers] 8.44 4 1 7 12 1.008 1 3.563 1 43.55 8.44 4 1 7 12 1.008 1 1.119 1 3.127 6.57 1 3 7 1.008 1 1.119 1 3.127 6.57 1 3 7 1.008 1 1.119 1 1 3.127 6.57 1 3 7 1.008 1 1.119	12 1:	12 545 7 350	60.0 38.5	7.28 6.15
188497671 serum amyloid A-2 protein isoform a precursor (Homo sapiers) 77.31 11 4 11 117 1.007 19 6.9 1.111 19 28.0 3984.90 71.31	32 11		13.5	9.14
58530845 zywin [Homo sapiens] 17.13 3 6 6 42 1.007 12 2.8 1.091 12 11.6 1335.70 17.13	18 4		61.2	6.67
21654847 protien-sprinte deliminate lippe-4 [homo sapiens] 57.01 5 27 34 362 1.007 97 6.9 1.158 94 1.66 9906.90 57.01 1.20 1.007 35 4.9 1.148 34 28.0 484.70 52.48 1 13 16 113 1.007 35 4.9 1.348 34 28.0 484.70 52.48 1 1.007 35 4.9 1.007 35 4.9 1.007 35 4.9 1.007 35 4.0 1.007 35	91 36: 44 11:		74.0 42.6	6.58 8.46
7706423 U6-snRNA-associated Sm-like protein LSmr [Homo spiens] 65.05 1 2 4 13 1.007 3 3.9 1.013 3 21.3 225.39 65.05	10 1:		11.6	5.27
7657603 heme-binding protein 2 (Homo sapiens) 32.68 1 6 6 29 1.007 9 6.0 1.178 9 10.0 1188.05 32.68	18 2	29 205	22.9	4.63
S30417131   PREDICTID: vasculator-stimulated phosphogroties in follow XI (Nono saplems)   53.83   3   15   16   149   1.007   40   7.7   1.210   36   8.5   5040.61   53.83   54.6   54.7   5	47 14 <sup>4</sup> 61 26i		39.7 34.2	8.94 6.05
4503377   Zinc. alpha-2-ghopogrotein precursor [Homo sapiems]   5940   1   19   21   266   1,007   85   5.9   1,229   81   16.2   924.782   594.0   595.0   595.0   1,219   10   10   1,007   10   10   1,007   10   10   1,007   10   1,007   10   1,007   10   1,007   1,0	61 26i 18 3		43.1	4.84
578804845 PREDICTED: WAS/WASL-interacting protein family member 1 isoform X1 (Homo sapiens) 27.44 1 6 8 43 1.007 11 5.4 1.043 11 27.0 1049.17 27.44	19 4		51.2	11.47
7657532 protein \$100-A6 (Homo sapiens) 66.67 33 9 10 100 1.007 30 7.6 1.169 28 10.4 1781.11 66.67	30 10		10.2	5.48
387598071   thioredouin reductase 1, cytoplasmic lostorm 5 (Horno saplem)   15.40   5   4   5   13   1.007   4   4.6   1.378   3   12.3   36.118   15.40   17.879849   17.879849   17.879849   17.8799	13 1:	13 461 57 889	50.8 96.1	6.62
Talastration Transaction Configuration Engineery (under vir) (second as from a separation of the configuration of	51 12		267.1	5.02
S30372380 PREDICTED: acytemino-acids releasing enzyme tooform X1 (Homo saplens) 14.58 3 9 9 30 1.007 10 4.0 1.157 10 14.9 904.12 14.58	26 31	30 686	76.2	5.96
4557014 catalase (Homo sapiens) 84.25 4 39 41 640 1.007 186 8.7 1.115 178 11.9 20955.71 84.25 2 6 5.0059032 2 6 5.0059032 6 5.00 5 5 209 2 2 1.796 1.007 5 5 6.9 1.327 5 2 6 5.6464.00 5 5 0.00 5 5 209 2 2 1.796 1.007 5 5 6 5.0059032 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	120 641 644 179		59.7 515.2	7.39 7.05
105/H9/22 approprietine 1-100 precursor (Hermo sapients) 5 2/09 223 1/99 1.007 1 1.009 1 5-258 6-564-00 -59/00	7	9 1407	151.6	6.18
77361688 myeloblastin precursor [Homo saplens] 46.09 1 7 7 156 1.007 41 5.9 1.266 41 27.8 3399.64 46.09	21 15	56 256	27.8	8.35
307/09/12/5 clashrin interactor 1 Bodomn 3 [Homo sapiens] 8.00 3 4 1 12 1.007 4 2.4 1.359 4 11.7 445.58 8.00	12 1:		68.1	6.42
345441758 MAP kinas-activated protein kinase 2 [kinon sapiens] 5.50 1 1 2 5 1.006 1 1.205 1 187.61 5.50 1 1 2 5 1.006 1 1.205 1 1 1 2 5 1.7.4 4002.43 51.44 1 1 15 16 141 1.006 35 7.2 1.211 35 17.4 4002.43 51.44 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 14	5 382 41 418	43.0 46.3	7.28 6.38
28302131 hemoglobin subunit gamma-1 [Homo sapiers] 76.87 1 1 1 0 280 1.006 3 7.7 1.032 3 7.8 5986.32 76.87	30 28	80 147	16.1	7.20
4502149 apolipoprotein A-II preproprotein (Homo sapiens) 74.00 7 10 10 320 1.006 96 9.2 1.151 91 16.1 9734.72 74.00	30 32		11.2	6.62
530027543 PREDICTED: ubiquith-like modifier-activating enzymer Isoform X3 (Mono saplens) 46.41 3 30 32 193 1.006 61 7.0 1.160 60 18.5 8121.95 46.43 3 5.2 193 1.006 61 7.0 1.160 60 18.5 8121.95 46.43 3 5.2 48.73	93 193	93 1058 13 700	117.8 80.0	5.76 4.98
15/28/WUD calignari_catasync_subunit scoron   [16/07 Sajpers]	19 2		332.9	4.98 5.53
157168362 purine nucleoside phosphorylase (Homo sepiens) 73.36 1 16 18 109 1.006 32 6.7 1.120 32 10.3 3673.58 73.36	52 10	289	32.1	6.95
13569879 addit leuisin-rich nuclear phosphoproprolein 22 family member E koform 1 (Homo sapiens) 40.67 9 8 10 36 10.06 9 13.0 1.167 9 13.8 906.59 40.67 9 13.0 1.167	28 30		30.7	3.85
578816051 PREDICTID plectin ledorm X12 (Phono suplers) 13.05 21 19 63 190 1.006 20 4.4 1.146 20 7.4 1728.54 13.05 (27379186 complement fator bit hisform a procurse) (Hono suplers) 6.57.2 5 56 65 12.6 1.006 34 8.1 1.211 339 20.8 39887.56 65 12.6 10.06 10.0 10.0 10.0 10.0 10.0 10.0 1	133 199 191 1210		513.8 139.0	5.77 6.62
02.73*100 Configerini radio in Tradition in Faculti from Capital in a pression from Capital in a press	5	8 953	101.3	4.68
4506901 serine/arginine-rich splicing factor 3 [Homo saplens] 29.27 1 3 4 11 1.006 3 0.1 1.323 3 4.0 243.40 29.27	11 1	104	19.3	11.65
4507.05 annesin At (Horno sapters) 70.09 2 18 23 145 1.006 37 6.7 1.158 36 12.8 5865.19 70.09 4603843 elimpation factor (Horno sapters) 48,14 3 32 34 220 1.006 70 6.5 1.196 70 17.7 709.55 48,14	66 149 99 221		36.1 95.3	6.13
40.144.5 elongistion factor 2 (yenon saperes) 48.14 3 32 34 220 1 10.006 1 1.205 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1 1.205 1 1 8.89.9 2.38 (2.00 1.1006 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	10 1		95.3 241.5	6.83
578825417 PREDICTED: epidddymal secretory protein E1 isoform X1 [Homo sapiens] 37.36 2 2 5 17 1.005 4 8.6 1.280 4 16.9 554.65 37.36	11 1	17 174	19.2	8.44
24119203 tropomyosini alpha-3 chain lostioma 2 (Homo saglens) 75.81 29 20 36 300 1.005 56 11.2 1.145 55 12.4 9499-65 75.81 29 20 36 300 1.005 56 11.2 1.145 55 12.4	104 30		29.0	4.78
1486/12838 uncharacterized protein KMA2026 (Homo saplems) 3.28 62 1 9 34 1.005 1 1.086 1 341.56 1.28 101051 1 1 1 8.5 788.62 68.25 23 2 12 24 1.005 13 5.3 1.117 13 8.5 788.62 68.25	15 3- 36 24 <sup>4</sup>	34 2103 49 126	227.9 13.9	9.04 10.32
390517020 Inosine triphosphate pyrophosphatase isoform c [Homo sapiens] 9.15 3 1 1 2 1.005 1 1.220 1 35.59 9.15	2	2 153	16.8	7.18
40254982 protein PAMIOTR Soform In [Femous agients] 18.95 2 5 8 24 1.005 7 12.7 1.205 91 18.57 1				
153265611 beta-2-glycoprotein 1 precursor (Homo sepiens) 60.29 7 18 18 324 1.005 96 9.7 1.205 94 18.7 8781.61 60.29	18 2- 53 32-	24 306	34.7 38.3	7.18 7.01 7.97

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Accession 4503971	Description	ΣCoverage 40.27	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]			A8: 117/116 Variability [%]	Score A(3,6,7) 3403.24	Coverage A(3,6,7) 40.27	# Peptides A(3,6,7) # PSM A(3,6,7)		MW [kDa] 7 50.6	calc. pl 5.14
612407849	rab GDP dissociation inhibitor alpha [Homo sapiens] integrin alpha-8 Isoform 2 preproprotein [Homo sapiens]	1.72	2	1	1 2	2 8	9 1.005 B 1.005		4.	2 1.12 3.76		10.9	26.67	1.72	2	8 1048		5.14
4826643	annexin A3 (Homo sapiens)	81.11	2	29	32									81.11	89 5			5.92
525342616 306922420	acyl-protein thioesterase 1 isoform 6 (Homo sapiens)	21.08 9.42	7	2	3 3	13	3 1.005 B 1.005		7.			3 0.2	365.32 35.10	21.08 9.42	9	13 16s 8 383		5.06 8.27
306922420 4507791	trophoblast glycoprotein-like precursor [Homo sapiens]  NEDDB-conjugating enzyme Ubc12 [Homo sapiens]	12.02	1	1	) 3	8 8	9 1.005		5.			2 16		12.02	9	9 183		7.69
41393561	cytosol aminopeptidase (Homo sapiens)	11.75	1	-	1 5	17			10.			4 8.2		11.75	13	17 519		7.93
4503303	neutrophil defensin 4 preproprotein [Homo sapiens]	5.15	1	1	1 1	1 2	2 1.005			1.21		1	28.57	5.15	2	2 9		8.02
11968182 530390795	40S ribosomal protein S18 [Homo sapiens]  PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]	23.03 17.06	1		2 4	1 10			6.			2 22.0 7 14.8		23.03 17.06		10 153 35 55		10.99 5.24
381342476	heterogeneous nuclear ribonucleoprotein H [Homo sapiens]	17.06	8		5 8	3 38			6.			9 16.4		19.82		88 449		6.30
578829418	PREDICTED: piezo-type mechanosensitive ion channel component 1 isoform X2 (Homo sapiens	1.16	8		2 4	1 8	B 1.005		2.	1.19	15	2 8.9	47.53	1.16	8	8 2497	7 283.9	7.43
7669492	glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Homo sapiens]	91.64	3	4	1 27									91.64	81 28			8.46
4758638 63055049	peroxiredoxin-6 [Homo sapiens] phosphoglucomutase-2 [Homo sapiens]	74.55 40.20	1	16	5 16				8.1 i 5.1			10 12.3 25 13.2		74.55 40.20	46 1:	24 224		6.38
260099723	L-lactate dehydrogenase A chain isoform 3 [Homo sapiens]	67.04	10	25										67.04	83 50			8.43
4557325	apolipoprotein E precursor [Homo sapiens]	55.84	2	15									7419.73	55.84		317		5.73
115298678 4557351	complement C3 precursor [Homo sapiens]	88.51	5	153	3 160	5899								88.51 5.32	468 58			6.40 7.42
530397403	cholinesterase precursor [Homo sapiens]  PREDICTED: cleavage and polyadenylation specificity factor subunit 7 isoform X5 [Homo sapier	5.32 12.07	2		2 2		6 1.004 4 1.004		3.	3 1.25 1.88		3 50.3	295.19 172.06	12.07	4	6 602 4 38		7.42 9.57
508772599	annexin A11 isoform 2 [Homo sapiens]	39.19	6	17	7 17	97	7 1.004	3				12.1	3752.64	39.19	51	97 47:		7.66
583966148	isocitrate dehydrogenase [NADP], mitochondrial isoform 2 [Homo sapiens]	21.25	3		5 9	44	4 1.004		5.			7 9.0	1004.83	21.25	20	14 400 35 1048		7.75
319918873 530372834	CORO7-PAM16 protein [Homo sapiens] PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit isoform X1 [Hom	9.73 13.12	8		2 5	5 23	5 1.004 3 1.004		11.:			7 25.0 5 7.2		9.73 13.12	19	23 404		6.33 5.07
21071008	transcobalamin-1 precursor [Homo sapiens]	28.18	1		3 8	3 31	1 1.004	1	5.			10 11.1	1264.12	28.18	23	31 43		5.03
578818421	PREDICTED: amyloid beta A4 precursor protein-binding family B member 1-interacting protein	18.92	1	ç	9 11		9 1.004	1:	4.			4 15.2		18.92	29	59 666	6 73.1	5.59
385251392 546232005	minor histocompatibility protein HA-1 isoform 2 precursor (Homo sapiens)	4.60 5.21	11		2 7	1 12			2.			2 7.4		4.60 5.21		1152		6.05
546232005	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 isoform 3 [Homo sapiens] PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3 isoform X3 [Homo sapiens]	34.41	6	16	5 24				6.			2 0.5		34.41		18 898		5.91
21071030	alpha-1B-glycoprotein precursor [Homo sapiens]	59.39	1	17	7 18	499	9 1.004	14	7.	1.25	9 14	26.0	15923.34	59.39	54 4	99 499	5 54.2	5.86
4504067	aspartate aminotransferase, cytoplasmic [Homo sapiens]	39.71	30	ç	11				6.			9 23.7		39.71		14 41:		7.01
388240801 162809334	lamin-B2 (Homo sapiens)	17.42 26.86	1		5 12				6.			7 19.9 26 35.1		17.42 26.86	90 6	11 620		5.59 6.38
162809334 7524346	pregnancy zone protein precursor [Homo sapiens] adenylate kinase 2, mitochondrial isoform b [Homo sapiens]	26.86 44.40	1	16	33	8 608			6.			8 35.1 8 15.0		26.86 44.40		1482 31 232		6.38 7.88
15431301	60S ribosomal protein L7 [Homo sapiens]	16.94	4		2 4	1 11			2.1			3 11.6		16.94		11 241		10.65
55743106	collagen alpha-3(VI) chain isoform 5 precursor [Homo sapiens]	12.05	8	19								26 12.7		12.05		11 297		7.30
578811455 4506381	PREDICTED: leukocyte elastase inhibitor isoform X1 [Homo sapiens] ras-related C3 botulinum toxin substrate 2 [Homo sapiens]	58.84 52.60	5	19	9 22				7.			60 8.3 13 31.5		58.84 52.60		52 379 93 193		6.28 7.61
52487191	endoplasmic reticulum resident protein 44 precursor [Homo sapiens]	13.55	1		3 5	16			4.			4 19.4		13.55		16 40		5.26
578822199	PREDICTED: neutrophil collagenase isoform X1 [Homo sapiens]	38.29	2	13	3 13	188	B 1.003	6	5.	7 1.18	00 6	0 16.8	7784.50	38.29	39 11	88 44		6.16
4502315	V-type proton ATPase subunit C 1 [Homo sapiens]	6.54	1	-	2 2	2 6	6 1.003		24.			2 14.1	268.32	6.54	6	6 382		7.46
578813531 6912396	PREDICTED: MAGUK p55 subfamily member 6 isoform X3 [Homo sapiens] qlyoxylate reductase/hydroxypyruvate reductase [Homo sapiens]	6.67 36.89	5	1	1 4	1 22			3.	1.00 I 1.32		1 6 27.3	44.19 861.75	6.67 36.89		20 328		6.18 7.39
530400688	PREDICTED: rho GTPase-activating protein 9 isoform X4 [Homo sapiens]	10.03	8		3 5	12			0.			3 17.0		10.03		12 791		8.07
4557361	BH3-interacting domain death agonist isoform 2 [Homo sapiens]	38.46	3		5 6	5 28	B 1.003		9.	1.21	15	9 20.1		38.46	16	28 19	5 22.0	5.44
5730023	ruvB-like 2 [Homo sapiens]	8.86	1	1	1 4	1 13				1.30		1	183.54	8.86	6	13 463		5.64
41327764 133778974	aflatoxin B1 aldehyde reductase member 2 [Homo sapiens] transketolase-like protein 2 [Homo sapiens]	18.38	1	3	3 5	5 11	1 1.003 5 1.003		2.	1 0.91		3 9.3	487.60 33.33	18.38 4.31	11	5 620		7.17 6.33
530428415	PREDICTED: proteasome subunit beta type-8 isoform X1 [Homo sapiens]	49.79	3		3 8	3 48			3.			14 13.9		49.79	24	18 24		7.18
260436922	suprabasin isoform 1 precursor (Homo sapiens)	26.10	3		5 6	27	7 1.003		5.			9 7.9		26.10	18	27 590	0 60.5	7.01
315075331	SAA2-SAA2 protein precursor [Homo sapiens]	42.79	3		5 10	149			3.			20.8		42.79	28 1	19 201		8.98
11761621	mannose-1-phosphate guanyltransferase beta isoform 2 [Homo sapiens] dedicator of cytokinesis protein 11 [Homo sapiens]	10.56 2.60	2	3	3 4	1 17	7 1.003 0 1.003		4.	1.18		5 9.8	397.60 26.17	10.56 2.60	11	17 360 10 2073	0 39.8 3 237.5	6.79 7.74
530370210	PREDICTED: mannose-1-phosphate guanyltransferase alpha isoform X4 [Homo sapiens]	9.05	3		3 3	3 9	9 1.003		4.			3 7.9		9.05	9	9 420		7.74
165905601	proline-serine-threonine phosphatase-interacting protein 2 (Homo sapiens)	14.67	1	2	3 5	5 13			0.			3 29.6		14.67	12	13 33		8.48
45439306	aspartatetRNA ligase, cytoplasmic isoform 1 [Homo sapiens]	18.56	2		5 9	21	1 1.003		11.			5 10.7	186.04	18.56	18	21 50		6.55
540344555 4507725	complement C2 isoform 5 [Homo sapiens] transthyretin precursor [Homo sapiens]	40.11 77.55	6	21										40.11 77.55		27 723 96 143	3 80.1 7 15.9	7.46 5.76
6005942	transitional endoplasmic reticulum ATPase [Homo sapiens]	61.29	6	35										61.29	111 2	17 80		5.26
5901998	U6 snRNA-associated Sm-like protein LSm6 [Homo sapiens]	77.50	1		4 5	5 26	6 1.003		5.	3 1.38	10	6 31.7	682.98	77.50	13	26 80	0 9.1	9.58
4505227	myeloid cell nuclear differentiation antigen (Homo sapiens)	74.20	57	_										74.20		11 40		9.76
530368148 11386147	PREDICTED: macrophage-capping protein isoform X1 [Homo sapiens]  prosaposin isoform a preproprotein [Homo sapiens]	77.01 28.63	2	13								19 16.4 18 12.0		77.01 28.63		341 30 524		6.19 5.17
503774159	sorting nexin-2 isoform 2 (Homo sapiens)	14.93	7		2 5	12			1.			2 0.5		14.93		12 40		7.24
543583725	prostaglandin E synthase 3 isoform f [Homo sapiens]	19.27	8		2 3	3 14			12.			6 24.2		19.27		14 10		5.59
145309326	laminin subunit gamma-1 precursor (Homo sapiens)	4.60	1		2 8	3 24			3.			2 10.8		4.60		160		5.12
291575128 4507115	L-lactate dehydrogenase B chain [Homo sapiens] fascin [Homo sapiens]	51.50 6.29	4	14	1 16	141	1 1.002 6 1.002		7.			11.5 2 27.8		51.50 6.29	48 1	11 334 6 493		6.05 7.24
40317626	thrombospondin-1 precursor [Homo sapiens]	6.15	1	3	3 7	7 15			3.			3 4.1		6.15	12	15 1170		4.94
4557795	merlin isoform 1 [Homo sapiens]	10.25	2	1	1 7	7 11	1 1.002		3.			2 13.5		10.25		11 599		6.47
145275213 39930541	coagulation factor XII precursor [Homo sapiens] uncharacterized protein C9orf142 [Homo sapiens]	24.55 8.82	1	11	1 12	2 51	1 1.002 4 1.002		5	2 1.12		9.5	1593.11 143.87	24.55 8.82	32	4 20		7.74 5.48
39930541 148539876	uncharacterized protein C9orf142 [Homo sapiens] beta-adrenergic receptor kinase 1 [Homo sapiens]	8.82 19.30	1		1 2	1 51			4.			1 17.3		8.82 19.30	28	4 204		5.48 7.28
530379292	PREDICTED: transportin-1 isoform X2 [Homo sapiens]	5.31	3		2 5	5 58	B 1.002			1.03	34	1	175.40	5.31		86	6 98.6	4.97
530377342	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	7.30	7		2 4	1 9	9 1.002		0.			2 0.3		7.30	9	9 534		7.91
4504183 73858564	glutathione S-transferase P (Homo sapiens) corticosteroid-binding globulin precursor (Homo sapiens)	91.90 38.27	1	15	5 16							78 22.2 17 19.2		91.90 38.27		3 210		5.64 6.04
223029410	talin-1 [Homo sapiens]	47.74	1	72										47.74		3 254		6.04
530434751	PREDICTED: LOW QUALITY PROTEIN: double homeobox protein 4-like [Homo sapiens]	3.35	3	1	1 2	2 26	6 1.002		4.	7 1.37	70	7 9.3	264.80	3.35		26 418	B 44.9	8.53
325652118	probable aminopeptidase NPEPL1 isoform 3 [Homo sapiens]	9.05	3	1	1 2	2 9	9 1.002			1.22		1	121.23	9.05	4	9 47		6.52
66347875 4827036	complement C1r subcomponent precursor [Homo sapiens] peptidoglycan recognition protein 1 precursor [Homo sapiens]	42.84 53.06	2	23	3 24	187		5	6.1			66 24.2 86 44.8	6306.50 5105.05	42.84 53.06		709		6.29 8.59
4827036	vinculin isoform VCL [Homo sapiens]	68.86	4	50	2 60	352		10						68.86	18 1			6.09
4506773	protein S100-A9 [Homo sapiens]	91.23	1	16	5 17	6295	5 1.001		8.	1.20	169	5 18.3	182454.26	91.23	51 62	95 114	4 13.2	6.13
41393602	complement C1s subcomponent precursor [Homo sapiens]	45.06	1	19	22	133		4	8.1			10 26.3		45.06	59 1:			4.96
186700623 530366456	rab-like protein 6 isoform 1 [Homo sapiens]	3.16 55.78	2	1	3	3 362	5 1.001 2 1.001	~	7.	1.48		1 17.8	79.70 8487.60	3.16 55.78	5	5 729		5.22 7.30
530366456	PREDICTED: C4b-binding protein alpha chain isoform X2 [Homo sapiens]  cAMP-dependent protein kinase type I-alpha regulatory subunit isoform a [Homo sapiens]	33.33	4	28	3 11			9	1.			73 17.8 15 14.2		33.33		19 38		7.30 5.35
156119625	inter-alpha-trypsin inhibitor heavy chain H1 isoform a precursor [Homo sapiens]	36.99	3	17	7 21	207	7 1.001		7.	1.21	3 6	i3 16.7	9160.36	36.99	58 29	91	1 101.3	6.79
530418095	PREDICTED: glutathione synthetase isoform X2 [Homo sapiens]	13.92	1	2	2 6	14			3.1			2 50.0		13.92		474		5.92
46397403 4758018	centrin-3 isoform 2 [Homo saplens]	16.77 39.16	1	1	. 5	5 12 3 73			6		-	4 2.6 18 20.4	0.1102	16.77 39.16		12 167 73 309		4.74 7.33
148806869	calponin-2 isoform a [Homo sapiens] transmembrane protein 251 isoform 2 [Homo sapiens]	5.34	2	1	1 1	1 4	4 1.001		4.	1.08		1	2784.94	39.16 5.34	21	73 309 4 131		7.83
167857790	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	49.75	1		7 12	1638	B 1.001	44		1.29	14 42		57139.16	49.75	36 16	38 20	1 23.5	5.11
374081861	ras-related protein Rab-18 isoform 4 [Homo sapiens]	18.13	4		2 3	3 8	B 1.001		4.1			2 7.7	267.26	18.13	8	8 182		5.00
4506205 578818938	proteasome subunit beta type-9 proprotein [Homo sapiens]  PREDICTED: cytochrome c oxidase assembly protein COX15 homolog isoform X2 [Homo sapien	43.84	1	4	1 5	5 25	5 1.001 1 1.001		3.1	1.20		7 10.6	1097.71	43.84	13	25 219		5.03 9.52
34365783	visual system homeobox 2 [Homo sapiens]	2.68	1		1 1	1 22			5.			6 45.0		2.68	2	22 36		7.55

Accession	Description	ΣCoverage	Σ# Proteins Σ# Unique	Peptides Σ# Peptide	s Σ# PSMs	A8: 115/114	A8: 115/114 Count	A8: 115/114 Variability [%]	AB: 117/116	A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)		# AAs	MW [kDa]	calc. pl
	PREDICTED: complement factor I isoform X4 [Homo sapiens]	42.75	5	21	26 179			52 8.5	1.231	52	16.4		42.75	72	179	531	60.0	7.93
39995109	ganglioside GM2 activator isoform 1 precursor [Homo sapiens]	18.65	1	2	3 10	1.00		3 13.1	1.050	3	5.3		18.65	7	10	193	20.8	5.31
19923973	BTB/POZ domain-containing protein KCTD12 [Homo sapiens]	28.92	2	8	9 32			9 2.9		9	11.3		28.92	27	32	325	35.7	5.64
194688133	high mobility group protein B2 (Homo sapiens)	60.77	1	10	17 241			51 4.2		51	14.4		60.77	51	241	209	24.0	7.81
530410617	PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]	61.67	2		20 158			18 7.2	1.124	38	16.5		61.67	60	158	240	27.4	4.89
530412282	PREDICTED: ATP-citrate synthase isoform X1 [Homo sapiens]	35.15	4	26	30 133			13 8.2		43	15.0		35.15	81	133	1155	126.1	8.18
4504981	galectin-1 (Homo sapiens)	35.56	1	5	5 17			6 4.5		6	7.7		35.56	14	17	135	14.7	5.50
530397175	PREDICTED: signal-induced proliferation-associated protein 1 isoform X1 [Homo sapiens]	5.37	30	1	6 13			1	1.525	1		68.45	5.37	9	13	1042	112.1	6.60
530364900	PREDICTED: ubiquitin-fold modifier-conjugating enzyme 1 isoform X1 [Homo sapiens]	22.13	2	3	3 9	1.000	D	3 0.2		3	12.4		22.13	9	9	122	14.6	5.59
21361621	phosphoglucomutase-1 isoform 1 [Homo sapiens]	68.33	3	23	27 181			51 5.8		48	17.0		68.33	72		562	61.4	6.76
54792071	small ubiquitin-related modifier 2 isoform b precursor [Homo sapiens]	36.62	5	2	2 15			3 1.9	1.100	3	13.0		36.62	6	15	71	8.1	5.41
4506925	SH3 domain-binding glutamic acid-rich-like protein [Homo sapiens]	68.42	1	8	8 67			9.2	1.186	21	15.2		68.42	24	67	114	12.8	5.25
515869342	hsc70-interacting protein isoform 2 [Homo sapiens]	18.11	2	5	7 24	1.000		6 8.2	1.070	6	7.7	687.69	18.11	21	24	359	40.1	5.30
325652048	transcription elongation factor B polypeptide 1 isoform b [Homo sapiens]	42.71	2	3	3 15	1.000	D	5 2.2	1.201	5	13.4	740.40	42.71	9	15	96	10.8	5.36
530391028	PREDICTED: gelsolin isoform X6 [Homo sapiens]	70.45	10	37	41 975	1.000	D 26	64 8.4	1.161	257	19.5	34080.66	70.45	121	975	731	80.6	5.85
73858566	heparin cofactor 2 precursor [Homo sapiens]	62.73	2	22	24 226	1.000	D 7	11 5.9	1.284	69	20.0	6434.13	62.73	68	226	499	57.0	6.90
47132622	S-methyl-5'-thioadenosine phosphorylase [Homo sapiens]	26.86	1	4	6 15			4 3.2		4	7.7		26.86	15	15	283	31.2	7.18
16418467	leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	52.74	1	14	15 194			52 9.0	1.148	48	23.4		52.74	44		347	38.2	6.95
530376957	PREDICTED: sulfotransferase family cytosolic 1B member 1 isoform X3 [Homo sapiens]	21.66	3	2	5 12			3 0.4		3	30.7		21.66		12	277	32.7	6.62
	adenylyl cyclase-associated protein 1 [Homo sapiens]	82.32	3	36	39 613					186	16.4		82.32	113		475	51.6	8.02
375493534	casein kinase 2, alpha 1 polypeptide-like [Homo sapiens]	8.18	3	30	4 21			6 6.8		100	15.8		8.18	113		391	45.2	8.50
222144229	ubiquitin-like modifier-activating enzyme ATG7 isoform c [Homo sapiens]	10.43	,	3	5 18			5 5.2			18.4		10.43	12	18	623	68.6	6.30
4502163	apolipoprotein D precursor (Homo sapiens)	37.57	8	3	8 128			16 8.2			21.2		37.57	11	128	189	21.3	5.15
			1	8	8 128			16 8.2		45	21.2			24	128			
574584836	mannose-6-phosphate isomerase isoform 2 [Homo sapiens]	9.41	3	1	1 2	1.000		1	1.100	1		47.37	9.41	2	2	287	31.9	6.74
348041314	cathelicidin antimicrobial peptide preproprotein [Homo sapiens]	54.91	1	11	12 141			11 4.6	1.248	41	11.4		54.91	34	141	173	19.6	9.41
384367993	COP9 signalosome complex subunit 4 isoform 2 [Homo sapiens]	29.26	31	3	8 16			3 7.9		3	5.5		29.26	16	16	352	40.2	6.95
30581135	structural maintenance of chromosomes protein 1A isoform 1 [Homo sapiens]	20.60	30	8	26 84			8 7.7	1.334	8	21.3		20.60	56	84	1233	143.1	7.64
296080770	platelet-activating factor acetylhydrolase IB subunit beta isoform d [Homo sapiens]	25.76	4	2	2 12			4 8.7	1.271	4	32.4		25.76	6	12	132	14.9	5.10
345197264	tumor protein D54 isoform h [Homo sapiens]	14.11	10	2	2 6	0.999		2 4.3	1.179	2	3.8		14.11	6	6	163	17.5	6.60
	major vault protein isoform 3 [Homo sapiens]	46.19	3	27	30 125			5.9	1.101	35	14.9		46.19	82	125	827	91.9	5.41
60279268	splicing factor U2AF 65 kDa subunit isoform b [Homo sapiens]	13.16	3	5	5 16	0.999		5 6.7	1.121	5	35.5		13.16	13	16	471	53.1	9.09
530380257	PREDICTED: core histone macro-H2A.1 isoform X3 [Homo sapiens]	47.28	6	13	13 114			5.4	1.192	36	11.6		47.28	39	114	368	39.0	9.80
4826898	profilin-1 [Homo sapiens]	75.00	4	11	11 912			9.6	1.184	285	16.6	34773.89	75.00	33	912	140	15.0	8.27
77404397	staphylococcal nuclease domain-containing protein 1 [Homo sapiens]	12.75	1	7	11 25			7 5.3		7	12.6		12.75	25	25	910	101.9	7.17
530410036	PREDICTED: eukaryotic translation initiation factor 5A-1 isoform X5 [Homo sapiens]	71.43	4	8	8 48			14 13.4	1.115	13	5.6		71.43	24	48	154	16.8	5.24
578846043	PREDICTED: editaryone translation initiation factor swin solitim to (Homo sapiens)	7.52	2	1	3 333			10 6.9	1.402	10	24.0		7.52	24	333	359	39.1	8.47
18104989	tyrosine-protein phosphatase non-receptor type 6 isoform 1 [Homo sapiens]	45.21	4	22	24 164			18 8.5	1.148	48	16.9		45.21	71	164	595	67.5	7.78
4502119	membrane primary amine oxidase isoform 1 [Homo sapiens]	43.21	3	1	4 4	0.77		1	1.294	1	10.9	25.36	4 19	/1	104	763	84.6	6.52
	prothrombin preproprotein (Homo sapiens)	60.29	2	24	29 235			5 66		73	21.1		60.29	90	235	622	70.0	5.90
5453555	GTP-binding nuclear protein Ran isoform 1 [Homo sapiens]	40.74	- :		11 82			6 5.3		73	13.7		40.74	00	82	216	24.4	7.49
4557581		40.74 65.93	1	10	9 88					26	13.7		40.74	31	82	135	24.4 15.2	7.49
	fatty acid-binding protein, epidermal [Homo sapiens]		1	8						21				26				
4504301	histone H4 (Homo sapiens)	59.22	1	7	8 246			8 6.0		78	21.9		59.22	24	246	103	11.4	11.36
4506691	40S ribosomal protein S16 [Homo sapiens]	29.45	2	2	5 25			2 3.4		2	0.3		29.45	11	25	146	16.4	10.21
9951915	adenosylhomocysteinase isoform 1 [Homo sapiens]	37.04	2	15	16 75			24 6.7	1.178	23	19.2		37.04	46	75	432	47.7	6.34
48762920	6-phosphofructokinase, liver type isoform b [Homo sapiens]	33.59	12	16	20 64			18 7.3		18	14.0		33.59	55	64	780	85.0	7.50
5453567	craniofacial development protein 1 [Homo sapiens]	7.02	1	1	3 12	0.999	9	1	1.161	1		38.45	7.02	4	12	299	33.6	4.81
578806371	PREDICTED: protein kinase C delta type isoform X2 [Homo saplens]	15.09	13	4	11 31			6 2.0	1.211	6	18.1		15.09	21	31	676	77.5	7.75
4506203	proteasome subunit beta type-7 proprotein [Homo sapiens]	18.77	1	3	4 16		9	4 6.7	0.997	4	5.8	338.64	18.77	12	16	277	29.9	7.68
4885385	histone H3.3 [Homo sapiens]	58.82	3	1	11 106	0.999		5 8.2	1.418	3	2.6		58.82	33		136	15.3	11.27
	D-3-phosphoglycerate dehydrogenase [Homo sapiens]	5.25	1	3	3 12	0.999		4 5.9	1.166	4	10.5		5.25	9	12	533	56.6	6.71
6912494	microtubule-associated protein RP/EB family member 1 [Homo sapiens]	46.64	8	9	12 58			7 5.3	1.186	17	12.2		46.64	30	58	268	30.0	5.14
	glutaredoxin-1 (Homo sapiens)	80.19	3	7	7 237			16 10.4	1.123	44	18.4		80.19	21	237	106	11.8	8.09
35493701	vacuolar protein sorting-associated protein 13B isoform 1 [Homo sapiens]	0.90	3		E 14	0.998		1	1.038			94.95	0.90	12	16	3997	445.7	6.46
4826762	haptoglobin isoform 1 preproprotein [Homo sapiens]	78.08	8	10	38 5608			9.5		908	29.8		78.08	111		406	45.2	6.58
293332611	tyrosine-protein kinase SYK isoform Syk(S) [Homo sapiens]	14.38	0		9 25			7 4.3	1.153	700	26.0		14.38		25	612	69.5	7.56
578823780	PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X10 [Homo sapiens	25.58	2		4 20			6 4.8	1.069	,	28.7		25.58	19	25	215	23.4	4.56
7657315	U6 snRNA-associated Sm-like protein LSm3 [Homo sapiens]	20.08	- '	4	3 12			3 6.3			37.3		25.56	12	12	102	11.8	4.50
				- '						3								
112293277	dnaJ homolog subfamily C member 8 (Homo sapiens)	21.74	1	3	4 14			4 7.2		4	4.6		21.74	11	14	253	29.8	9.06
578813467	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X5 [Homo sapiens]	43.13	10		21 173			5.1		36	13.5		43.13	61	173	313	33.9	9.03
5174447	guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sapiens]	37.85	1	-	10 32			7 5.6		7	17.8		37.85	24		317	35.1	7.69
	proteasome subunit alpha type-7 [Homo sapiens]	51.61	8		13 80			8.4		20	9.2		51.61	39	80	248	27.9	8.46
116284394	myosin-14 isoform 2 [Homo sapiens]	15.39	92	1	35 154	0.998	В	1	0.952	1		3023.50	15.39	75	154	1995	227.7	5.60
5032057	protein S100-A11 [Homo sapiens]	88.57	1	9	9 181	0.998	B 5	55 7.7	1.260	54	16.9	6657.37	88.57	27	181	105	11.7	7.12
578821773	PREDICTED: fermitin family homolog 3 isoform X1 [Homo sapiens]	45.10	4	22	24 102	0.998	В 3	4.3	1.160	30	16.3	3350.88	45.10	67	102	663	75.4	6.77
578821284	PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) is	6.93	4	2	3 7	0.998	В	2 7.3	1.202	2	19.8	139.09	6.93	6	7	505	51.9	6.81
255918077	versican core protein isoform 3 precursor (Homo sapiens)	1.74	4	2	5 11	0.998		2 10.0	1.207	2	1.3		1.74	8	11	2409	264.9	4.54
528078313	neutrophil cytosol factor 1 [Homo sapiens]	76.15	3	22	25 251	0.998	в 8	80 8.1	1.220	77	23.9	9500.96	76.15	71	251	390	44.7	9.13
70906437	fibrinogen gamma chain isoform gamma-A precursor [Homo sapiens]	82.84	4		36 3219					719	24.7		82.84	107	3219	437	49.5	6.09
	PREDICTED: copine-3 isoform X1 [Homo sapiens]	37.99	18	13	17 110			18 9.6		28	21.3		37.99		110	537	60.1	5.85
5031573	actin-related protein 3 isoform 1 [Homo sapiens]	72.49	11		25 326			0 7.3	1.212	108	18.9		72.49	69	326	418	47.3	5.88
296040505	glycogenin-1 isoform 2 [Homo sapiens]	29.13	3	7	8 62					21	10.9		29.13	22	62	333	37.5	5.40
47519798	neutrophil cytosol factor 4 isoform 1 [Homo sapiens]	57.82	4	17	20 135			7.0	1.228	37	21.7		57.82	57	135	339	39.0	6.83
4505029	leukotriene A-4 hydrolase isoform 1 (Homo sapiens)	67.43	7		40 337				1.225	103	22.2		67.43	118		611	69.2	6.18
451172106	coronin-1C isoform b [Homo sapiens]	48.73		50	20 77				1.173	103	14.1		48.73	EA	77	474	53.2	7.08
11386183	wiskott-Aldrich syndrome protein family member 2 isoform 1 [Homo sapiens]	8.63	7		4 25			4 2.6		10	14.1		8.63	54	25	474	54.3	5.53
70906435		79.02	2	40	4 25				1.405	4	24.3		79.02	10		498	55.9	
70906435 38708321	fibrinogen beta chain isoform 1 preproprotein [Homo sapiens]  DNA helicase INO80 [Homo sapiens]	79.02 5.08	2	40	40 3302 9 47			9.2 4 1.8		808	24.3		79.02 5.08	119	3302	491 1556	55.9 176.6	8.27 9.50
			1	2						3				9				
16579888	fructose-1,6-bisphosphatase 1 [Homo sapiens]	18.34	3	4	4 15			6 6.0		6	10.1		18.34	11	15	338	36.8	6.99
4503571	alpha-enolase isoform 1 (Homo sapiens)	82.03	16		34 1656					439	19.8		82.03	99	1656	434	47.1	7.39
530380520	PREDICTED: annexin A6 isoform X2 [Homo sapiens]	74.51	1	1	46 437			2 11.0		2	8.4		74.51	133	437	667	75.2	5.67
	PREDICTED: serine/threonine-protein kinase Nek9 isoform X3 [Homo sapiens]	3.40	4	1	4 7	0.99		1	1.135	1		85.54	3.40	6	7	971	106.3	5.73
578826266				23	29 149	0.99	7 4	10 6.0	1.106	40	13.1	4985.78	60.00	79	149	505	56.7	6.35
578826266 21361657	protein disulfide-isomerase A3 precursor (Homo sapiens)	60.00			6 43	0.99	7	1	1.235	1		121.86	20.23	11	43	257	29.3	9.39
21361657 4505469	protein disulfide-isomerase A3 precursor [Homo sapiens] neurotrophin-3 isoform 2 preproprotein [Homo sapiens]	60.00 20.23	2	1	6 43				1.123		16.7							
21361657 4505469 530413446	protein disulfide-isomerase A3 precursor [Homo sapiens]		2 2	1 2	3 25	0.99	7	6 5.0	1.123		10.7	821.54	21.43	9	25	196	20.5	9.86
21361657 4505469	protein disulfide-isomerase A3 precursor [Homo sapiens] neurotrophin-3 isoform 2 preproprotein [Homo sapiens]	20.23	2 2	1 2 6				6 5.0		32	20.5		21.43 41.88	9	25 146	196 160	20.5 18.4	9.86
21361657 4505469 530413446	protein disulfide-isomerase A3 precursor [Homo sapiens] neurotrophin-3 isoform 2 preproprotein [Homo sapiens] PREDICTED: THO complex subunit 4 isoform X1 [Homo sapiens]	20.23 21.43	2 2 1 8	1 2 6 5	3 25	0.99	7 3		1.191	32 15		3631.53		9 21 58				
21361657 4505469 530413446 45243507 29788785	protein disulfide-formerane AT procursor (Homo sapiens) neurotrophin-3 bostom 2 preproprotein (Homo sapiens) PREDICTED: THO complex suburnit 4 bostom XT (Homo sapiens) ecisinophil autitoric protein precursor (Homo sapiens) icolanophil autitoric protein precursor (Homo sapiens) lucium beta chain lasform (I) (Homo sapiens)	20.23 21.43 41.88 59.23	2 2 1 8	1 2 6 5	3 25 7 146	0.99	7 3	52 6.3 5 5.3	1.191 1.175	32 15 24	20.5 27.2	3631.53 7334.84	41.88 59.23	9 21 58 25	146 207	160 444	18.4 49.6	10.02 4.89
21361657 4505469 530413446 45243507 29788785 4885371	protein disulfide-isomerase A3 precursor (Homo sapiens) neurotrophin-3 soform 2 preproprotein (Homo sapiens) PREDICTED: THO complex suburult 4 soform X1 (Homo sapiens) eosinophic autionic protein precursor (Homo sapiens) ubulin beta chain isoform b (Homo sapiens) histone H1.0 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11	2 2 2 1 8 4	1 2 6 5 8	3 25 7 146 21 207	0.99	7 3 7 1 7 2	52 6.3 15 5.3 24 5.4	1.191 1.175 1.146	15	20.5 27.2 13.8	3631.53 7334.84 2192.74	41.88 59.23 37.11	9 21 58 25	146 207	160 444 194	18.4 49.6 20.9	10.02 4.89 10.84
21361657 4505469 530413446 45243507 29788785 4885371 223671861	protein disulfide-formerane AB procursor (Homo sapiens) neurotrophin-3 isoform 2 preproprotein (Homo sapiens) PREDICTED: THO complex suburnit 4 isoform XT (Homo sapiens) ecisinophil cutionic protein precursor (Homo sapiens) tutulum beta chain isoform (D (Homo sapiens) histone H10 (Homo sapiens) histone H10 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91	2 2 2 1 1 8 4 1	1 2 6 5 8 6	3 25 7 146 21 207	0.997 0.997 0.997	7 3 7 1 7 2	52 6.3 5 5.3	1.191 1.175 1.146 1.154	15	20.5 27.2	3631.53 7334.84 2192.74 972.06	41.88 59.23 37.11 17.91	9 21 58 25	146 207 81 26	160 444 194 469	18.4 49.6 20.9 51.2	10.02 4.89 10.84 7.90
21361657 4505469 530413446 45243507 29788785 4885371 223671861 4759000	protein disulfide-isomerase AS precursor (Homo sapiens) neutrotophin Johom preproprotein (Homo sapiens) PREDICTED. 14th Complex subunit 4 isoform XT (Homo sapiens) ensimplications protein precursor (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) properdin precursor (Homo sapiens) properdin precursor (Homo sapiens) properdin precursor (Homo sapiens) rar-related protein Rab-30 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74	2 2 2 1 1 8 8 4 1 1 22	1 2 6 5 8 6 1 1 25 6	3 25 7 146 21 207 9 81 6 26 5 18	0.997 0.997 0.997 0.997 0.997	7 3 7 1 7 2 7	62 6.3 15 5.3 24 5.4 8 6.1	1.191 1.175 1.146 1.154 1.023	15	20.5 27.2 13.8 12.9	3631.53 7334.84 2192.74 972.06 444.44	41.88 59.23 37.11 17.91 23.74	9 21 58 25 18	146 207 81 26 18	160 444 194 469 219	18.4 49.6 20.9 51.2 24.3	10.02 4.89 10.84 7.90 4.93
21361657 4505469 530413446 45243507 29788785 4885371 223671861 4759000 50845386	protein dauffide-locemerase AS procursor (Homo sapiens)  neutrotophin Jaborno 2 preproportein (Homo sapiens)  PREDICTED: THO complex subunit 4 bottom XT (Homo sapiens)  eosinophic autionic protein precursor (Homo sapiens)  lutulum beta chain insofrum (Dimon sapiens)  histone H1.0 (Homo sapiens)  ras-related protein Rab-30 (Homo sapiens)  ras-related protein Rab-30 (Homo sapiens)  ras-related protein Rab-30 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27	2 2 1 8 4 1 22 2	1 2 6 6 5 8 6 6 1 1 25 5	3 25 7 146 21 207 9 81 6 26 5 18 27 149	0.997 0.997 0.997 0.997 0.997	7 3 7 1 7 2 7 7	52 6.3 15 5.3 24 5.4	1.191 1.175 1.146 1.154 1.023	15	20.5 27.2 13.8	3631.53 7334.84 2192.74 972.06 444.44 4995.54	41.88 59.23 37.11 17.91 23.74 72.27	9 21 58 25 18 15	146 207 81 26 18	160 444 194 469 219 339	18.4 49.6 20.9 51.2 24.3 38.6	10.02 4.89 10.84 7.90 4.93 7.75
21361657 4505469 530413446 45243507 29788785 4885371 223671861 4759000 50845386 530385665	protein disulfici-isomerana AD precursor (Homo sapiens) neutrotophin Johom 2 preproprotein (Homo sapiens) PREDICTED. 1140 complex subunit 4 isoform XT (Homo sapiens) ecinophic attoring protein precursor (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) properdin precursor (Homo sapiens) properdin precursor (Homo sapiens) are-related protein Rab-30 (Homo sapiens) amenin AZ isoform 2 (Homo sapiens) amenin AZ isoform 2 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27 4.77	2 2 1 8 4 1 1 22 2	8 6 1 25	3 25 7 146 21 207 9 81 6 26 5 18 27 149 6 28	0.99 0.99 0.99 0.99 0.99 0.99	7 3 7 1 7 2 7 2 7 4	12 6.3 15 5.3 14 5.4 18 6.1 17 6.1	1.191 1.175 1.146 1.154 1.023 1.086 2.049	15	20.5 27.2 13.8 12.9 9.9	3631.53 7334.84 2192.74 972.06 444.44 4995.54 72.00	41.88 59.23 37.11 17.91 23.74 72.27 4.77	18 15 78 6	146 207 81 26 18 149 28	160 444 194 469 219 339 1761	18.4 49.6 20.9 51.2 24.3 38.6 193.4	10.02 4.89 10.84 7.90 4.93 7.75 6.35
21361657 4505469 4505469 45243807 29788785 4885371 223671861 475900 50845386 53085665 578804832	protein dauffide-loamerase AS procursor (Homo sapiens) mountrophin-3 bottom 2 prereprotein (Homo sapiens) PREDICTED: THO complex subunit 4 bottorm X1 (Homo sapiens) ecalnophic autionic protein precursor (Homo sapiens) ludulin beda chain bottorm 10 (Homo sapiens) histone H1 D (Homo sapiens) properdim precursor (Homo sapiens) rax-related protein Rab-3D (Homo sapiens) properdim precursor 2 (Homo sapiens) pramein Az bottorn 2 (Homo sapiens) PREDICTED: Ilaminin subunit beta-4 bottorm X1 (Homo sapiens) PREDICTED: Ilaminin subunit beta-4 bottorm X1 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93	2 2 1 8 4 1 22 2 2 1 35	8 6 1 25	3 25 7 146 21 207 9 81 6 26 5 18 27 149 6 28 21 450	0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99;	7 3 7 1 7 2 7 7 7 7 7 4	12 6.3 5.3 5.3 5.4 5.4 6.1 1 1 7 6.1 1 7 2.4	1.191 1.175 1.146 1.154 1.023 1.086 2.049	15 24 8 1 47 1 6	20.5 27.2 13.8 12.9 9.9	3631.53 7334.84 2192.74 972.06 444.44 4995.54 72.00 668.75	41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93	9 21 58 25 18 15 78 6	146 207 81 26 18 149 28 450	160 444 194 469 219 339 1761 35484	18.4 49.6 20.9 51.2 24.3 38.6 193.4 3935.9	10.02 4.89 10.84 7.90 4.93 7.75 6.35 6.43
21361657 4505469 530413446 45243507 29788785 4885371 223671861 4759000 50845386 530385665 573804832 4502101	protein disulfici-isomerase AD precursor (Homo sapiens) meutrotiphin Johom 2 preproprotein (Homo sapiens) PREDICTED. 1140 complex subunit 4 isoform XT (Homo sapiens) enciphical taction protein precursor (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) properdin precursor (Homo sapiens) properdin precursor (Homo sapiens) arra-related protein Rab-30 (Homo sapiens) amenin AZ isoform 2 (Homo sapiens) PREDICTED: Intinin isobunit beta-4 soform XT (Homo sapiens) PREDICTED: tithin isoform XS (Homo sapiens) PREDICTED: tithin coform XS (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57	2 2 1 1 8 4 1 1 22 2 2 1 35	8 6 1 25	3 25 7 146 21 207 9 81 6 26 5 18 27 149 6 28 21 450 30 467	0.999 0.999 0.999 0.999 0.999 0.999 0.999	7 3 7 1 7 2 7 7 7 4 7 4 7 6 6 15	12 6.3 5.3 5.3 5.4 5.4 5.4 5.4 6.1 7.7 6.1 7.7 2.4 9.9 9.4	1.191 1.175 1.146 1.154 1.023 1.086 2.049 1.187	15	20.5 27.2 13.8 12.9 9.9	3631.53 7334.84 2192.74 972.06 444.44 4995.54 72.00 668.75 20132.96	41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57	18 15 78 6	146 207 81 26 18 149 28 450 467	160 444 194 469 219 339 1761 35484	18.4 49.6 20.9 51.2 24.3 38.6 193.4 3935.9 38.7	10.02 4.89 10.84 7.90 4.93 7.75 6.35 6.43
21361657 4505469 530413446 45243507 29788785 4885371 223671861 4759000 50845386 530385665 578804832 4502101 23943880	protein dauffide-loamerase AS procusor (Homo sapiens) mountrophin-3 softom 2 preproprotein (Homo sapiens) PREDICTED: 1100 complex subunit 4 softom X1 (Homo sapiens) ecsinophia cationic protein precursor (Homo sapiens) luctum beta chain softom 8 (Homo sapiens) histore Int IO (Homo sapiens) properdin precursor (Homo sapiens) rax-related protein Rab-3D (Homo sapiens) prepending precursor 2 (Homo sapiens) prepending precursor 3 (Homo sapiens) prepending precursor 3 (Homo sapiens) amenia A1 (Homo sapiens) amenia A1 (Homo sapiens) amenia A1 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48	2 2 1 8 4 1 1 22 2 1 35 7	8 6 1 25	3 25 7 146 21 207 9 81 6 26 5 18 27 149 6 28 21 450 30 467 1 31	0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99;	7 3 7 1 7 2 7 7 7 4 7 4 6 5 6 15	12 6.3 6.3 1.3 1.4 1.5 1.4 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5	1.191 1.175 1.146 1.154 1.023 1.086 2.049 1.187 1.160	15 24 8 1 47 1 6	20.5 27.2 13.8 12.9 9.9 15.2 14.3	3631.53 7334.84 2192.74 972.06 444.44 4995.54 72.00 668.75 20132.96	41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48	18 15 78 6	146 207 81 26 18 149 28 450 467 31	160 444 194 469 219 339 1761 35484 346	18.4 49.6 20.9 51.2 24.3 38.6 193.4 3935.9 38.7 34.5	10.02 4.89 10.84 7.90 4.93 7.75 6.35 6.43 7.02 5.69
21361657 4505464 45043507 29788785 4885371 223671861 4759000 50845386 530385665 57804832 4502101 23943880 554790349	protein disulfide-isomerase AD precursor (Homo sapiens) meutrotiphin Johann 2 preproprotein (Homo sapiens) PREDICTID: 1140 complex subunit 4 isoform XT (Homo sapiens) enciphical tostice protein precursor (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) properdin precursor (Homo sapiens) properdin precursor (Homo sapiens) arre-related protein Bab-30 (Homo sapiens) amenin AZ isoform 2 (Homo sapiens) PREDICTED: Intinin subunit beta-4 isoform XT (Homo sapiens) PREDICTED: tithin isoform XS (Homo sapiens) methythinoribose-1-phosphate isomerase isoform 2 (Homo sapiens) methythinoribose-1-phosphate isomerase isoform 2 (Homo sapiens) indelydinoribose-1-phosphate isomerase isoform 2 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48 16.55	2 2 1 1 8 4 4 1 1 2 2 2 2 1 1 3 5 5 7 2 2 6 6	8 6 1 25	3 25 7 146 21 207 9 81 6 26 5 18 27 149 6 28 21 450 30 467 1 31 3 25	0.99 0.99 0.99 0.99 0.99 0.99 0.99 0.99	7 3 7 1 7 2 7 7 7 4 7 7 6 6 15	12 6.3 5.3 5.3 5.3 5.3 5.4 6.5 5.4 6.1 1.1 1.1 7.7 6.1 1.7 7.2.4 9.9 9.4 4.5 3.3 2.2 10.00	1.191 1.175 1.146 1.154 1.023 1.086 2.049 1.187 1.160 1.444	15 24 8 1 47 1 6	20.5 27.2 13.8 12.9 9.9 15.2 14.3 23.4	3631.53 7334.84 2192.74 972.06 444.44 4995.54 72.00 668.75 20132.96 37.77 35.79	41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48 16.55	18 15 78 6	146 207 81 26 18 149 28 450 467 31	160 444 194 469 219 339 1761 35484 346 322	18.4 49.6 20.9 51.2 24.3 38.6 193.4 3935.9 38.7 34.5	10.02 4.89 10.84 7.90 4.93 7.75 6.35 6.43 7.02 5.69 6.58
21361657 4505469 4505469 45243507 29788785 4885371 223671861 475900 50845386 530385665 578004832 4502101 23943880 5405591	protein dauffide-loomerase AF procusor (Homo sapiens) neutroliphia Salomor pergreprotein (Homo sapiens) PREDICTED: 110 complex subunit 4 kolorm XT (Homo sapiens) ecsinophia cationic protein precursor (Homo sapiens) lubulin beta chain kolormo (Homo sapiens) histore HT IO (Homo sapiens) properdin precursor (Homo sapiens) rax-related protein Rab-3D (Homo sapiens) praperdin Peruson 2 (Homo sapiens) preperdin precursor 2 (Homo sapiens) preperdin precursor 2 (Homo sapiens) preperdin Peruson 2 (Homo sapiens) preperdin precursor 2 (Homo sapiens) preperdin precursor 3 (Homo sapiens) preperdin precursor 3 (Homo sapiens) amenia A1 to Homo sapiens) amenia A1 (Homo sapiens) preperdin precursor 3 (Homo sapiens) colied-coli domain-containing protein 908, milochondrial isoform e (Homo sapiens) colied-coli domain-containing protein 908, milochondrial isoform e (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48 16.55 46.73	2 2 2 1 1 8 4 1 1 2 2 2 2 2 2 1 1 3 3 5 7 2 2 6 6 3 3	8 6 1 25	3 25 7 146 21 207 9 81 6 26 5 18 27 149 6 28 21 450 30 467 1 31 3 25 9 64	0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99; 0.99;	7 3 7 1 7 2 7 7 7 4 7 6 6 15 6 15	122 6.3 6.3 6.3 6.3 6.1 6.1 6.1 6.1 6.1 6.1 6.1 6.1 6.1 6.1	1.191 1.175 1.146 1.154 1.023 1.086 2.049 1.187 1.160 1.444 1.258	15 24 8 1 47 1 6	20.5 27.2 13.8 12.9 9,9 15.2 14.3 23.4 16.1	3631.53 7334.84 2192.74 972.06 444.44 4995.54 72.00 668.75 20132.96 37.77 35.79 2034.97	41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48 16.55 46.73	18 15 78 6	146 207 81 26 18 149 28 450 467 31 25 64	160 444 194 469 219 339 1761 35484 346 322 139	18.4 49.6 20.9 51.2 24.3 38.6 193.4 3935.9 38.7 34.5 16.2 22.1	10.02 4.89 10.84 7.90 4.93 7.75 6.35 6.43 7.02 5.69 6.58 8.13
21361657 4505464 45043507 29788785 4885371 223671861 4759000 50845386 530385665 57804832 4502101 23943880 554790349	protein disulfici-isomerase AD precursor (Homo sapiens) meutrotiphin Johom 2 preproprotein (Homo sapiens) PREDICTID: 1140 complex subunit 4 isoform XT (Homo sapiens) enciphic attoring protein precursor (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) lubulin beta chain isoform b (Homo sapiens) properdin precursor (Homo sapiens) properdin precursor (Homo sapiens) arra-related protein Bab-30 (Homo sapiens) amenia AZ isoform 2 (Homo sapiens) PREDICTED: Intinin isobumit beta-4 isoform XT (Homo sapiens) PREDICTED: tithin isoform XS (Homo sapiens) methythinoribos-1-phosphate isomerase isoform 2 (Homo sapiens) methythinoribos-1-phosphate isomerase isoform 2 (Homo sapiens) indelydinoribos-1-phosphate isomerase isoform 2 (Homo sapiens)	20.23 21.43 41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48 16.55	2 2 1 1 8 4 1 1 22 2 2 1 1 3 5 7 7 2 6 6 3 3 3 3 3	8 6 1 25	3 25 7 146 21 207 9 81 6 26 5 18 27 149 6 28 21 450 30 467 1 31 3 25	0.99 0.99 0.99 0.99 0.99 0.99 0.99 0.99	7 3 7 1 7 2 7 7 7 4 7 6 6 5 6 15 6 15	12 6.3 5.3 5.3 5.3 5.3 5.4 6.5 5.4 6.1 1.1 1.1 7.7 6.1 1.7 7.2.4 9.9 9.4 4.5 3.3 2.2 10.00	1.191 1.175 1.146 1.154 1.023 1.086 2.049 1.187 1.160 1.444 1.258 1.077	15 24 8 1 47 1 6	20.5 27.2 13.8 12.9 9.9 15.2 14.3 23.4	3631.53 7334.84 2192.74 972.06 444.44 4995.54 72.00 668.75 20132.96 37.77 35.79 2034.97 558.52	41.88 59.23 37.11 17.91 23.74 72.27 4.77 2.93 74.57 2.48 16.55	18 15 78 6	146 207 81 26 18 149 28 450 467 31	160 444 194 469 219 339 1761 35484 346 322	18.4 49.6 20.9 51.2 24.3 38.6 193.4 3935.9 38.7 34.5	10.02 4.89 10.84 7.90 4.93 7.75 6.35 6.43 7.02 5.69 6.58

Month			E o	F		F . P	F - 0011		T			[			[ ]				. fr m . 1	
Marke   Mark	Accession	Description  Without proton ATRoco cultural P. Proto inform (Home conton)	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs			A8: 115/114 Variability [%			A8: 117/116 Variability [%]	Score A(3,6,7)		A(3,6,7) # PS	SM A(3,6,7)			calc. pl
Series of the file of the control of				1	25	29	25			18 7			17 11 3			79	257			
Series of the se		malate dehydrogenase, cytoplasmic isoform 2 [Homo sapiens]		3	11	12										32				
SMEAN SECTION AND ALTER ASSESSMENT ASSESSMEN	333470717	basic leucine zipper and W2 domain-containing protein 1 isoform 1 [Homo sapiens]	20.05	5	5 4	. 6	1	6 0.99	6							15	16	419		
Series of the series and the series of the s	530393496	PREDICTED: hexokinase-1 isoform X1 [Homo saplens]	7.92	6	. 4	9	2	8 0.99	6	4 3	1.0 1	.224	4 34.1			22	28		106.9	6.98
See		non-histone chromosomal protein HMG-17 [Homo saplens]		1	4	9										22	85			
Marching and and an interpretation of the continue of the cont				42	2	2 8	1			2 6			2 3.0			17	18			
Control   Cont				1		1				1			1			3	3			
See				33												10	16			
Marche of the stand of the stan		SH3 domain-containing kinase-binding protein 1 isoform b [Homo sapiens]		6		7										16				
March	83700220		5.00	1		. 2		7 0.99	5	1		.590	1	32.79	5.00	4	7	300	34.8	6.14
Manuface plane and plane	156523970		54.77	1	14	14	44	3 0.99	5 13	12 8	1.6 1	.236 12	7 24.2	14123.93	54.77	42	443	367	39.3	5.72
Selection of the property of t	4501987		54.92	2	22	26	21	9 0.99	5 6	8 5	i.9 1	.225 6	6 24.2	7085.17	54.92	72	219	599	69.0	5.90
Seminar Seminar segment and and antimate characterises of the seminar segment and antimate chara				1	16															
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Mary Mary Mary Mary Mary Mary Mary Mary				12	1											26				
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Seedle Se				1		5 5										15				
Series of sear selected programs for sequency of the series of the serie	48255891		20.95	6	5 6	8	3	4 0.99	5 1	12 4	.0 1	.137 1	12.2	1303.66	20.95	23	34	525	59.1	4.42
STRIES ST		vitamin K-dependent protein S preproprotein [Homo sapiens]	41.57	2	17	24				86 8	1.8 1	.209 3	15.7	4444.64	41.57	65			75.1	5.67
Service of service ser	38455402			1	16									15936.06		47				
Seement of the proposal of the				4	14											42				
Ministry		vitamin D-binding protein isoform 1 precursor [Homo sapiens]		12	35											122				
Series of the proposed control programment of the proposed control		complement component C7 precursor [Homo sapiens]		1	22	24							1 24.2			69	158			
Section   Process   Proc		plasma protease C1 inhibitor precursor (Homo sapiens)		41	21	73							2 6.1			66	340			
Part				1	21											26				
Series Se				2		3	-			1			1			6				
Marce of separate freedom free grown of the separate freedom f			13.24	1	1	1				1			1			3	3		7.3	9.85
Memory   M		glutamate-rich protein 5 isoform 1 [Homo sapiens]	3.21	1	1	1				1			1			1	1			
State   Personal Pe				5	17											50				
March   Marc		lactotransferrin isoform 1 precursor (Homo sapiens)		21	63															
March   Separate the water international tentral plant regions   Line				10	3															
Mathematical   Math				1		12														
Septimone September 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				9	15	15														
Second   Process   Proce				5		. 9														
March   Marc				5	27	28														
Second Content   1	194097330	hexokinase-3 [Homo sapiens]	59.05	7	24	35	19	9 0.99	4 5	1 7	.1 1	.246 4	19 28.7	6924.50	59.05	97	199	923	99.0	5.40
June   1   1   1   1   1   1   1   1   1	116063573	filamin-A isoform 1 [Homo sapiens]	52.10	2	89	101	85	4 0.99	4 24	19 9	.1 1	.152 24	14 13.3	34211.11	52.10	296	854		279.8	
				5	1	1 2				1			1			5	5			
Service of the following service and of the f				5	19	25														
Margin   Margin comprises of glown expense of glown expenses   170   2   2   3   5   7   68   1   1   2   1   1   1   1   1   1   1				6		8										20				
Secondary				3		6	3			7 2			7 19.6			18	33			
Margine   Margine skart again skart agai				2	25	3	27						1 10.2			104	272			
March   Marc		hemoglobin subunit ensilon (Homo sapiens)		1		30										9				
Marting   Marting prints grown seems   23				6		9										26				
March   Marc		RNA-binding protein 20 (Homo sapiens)		1		4										7				
Second Content   Processing   Content   Pro	4506195	proteasome subunit beta type-2 isoform 1 [Homo sapiens]		3		8				9 6	.3 1		9 10.0							
Mary				7	4	1 26	31	7 0.99		6 5	.9 1									
1965  1966   1				54	69	72														
Second Second Person Spring   Second Person		PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV40R15-8-	30.97	1	1 2	4										12				
SECURITY				3	1	1										2				
1997    Section from Express grown of Section 7   1990   6   7   2   4   60   90   2   6   1133   2   17   70   70   90   6   6   10   70   50   6   10   70   50   6   10   70   50   10   70   70   70   70   70   70   7						, 9										21				
Security   Ministry				5		, ,										4	4			
Second				7		4	1									10	10			
Section   Sect	58219054	bcl-2-like protein 15 [Homo sapiens]	13.50	1	1	2	1	2 0.99	3	3 5	.3 1	.161	3 36.2	211.13	13.50	6	12	163	17.7	4.41
STREAM   PRESENTE DEPLACEMENT Photosophen Action The Deplace appropriate Natural Photosophen Action The Deptace appropriate Natural Photosophen Action The Deptace appropriate Natural Photosophen Action The Deptace approximation and the Natural Natural Photosophen Action The Deptace approximation and the Natural Natural Photosophen Action The Deptace approximation and the Natural Natural Photosophen Action The Deptace approximation and the Natural Photoso			73.41	3	1	15			3 1			.179 1		4240.51	73.41	44	154			8.92
March   Marc				1	4	4				4 5			4 14.9			12				
1332979    subtriped calcular landorm a precursor (plemo supering)   15.79   2   2   2   2   2   2   2   2   2				4	1	5				1			1			7				
Separation   Part and magne informal Partiewn separating   15.77   2   2   2   5   6.073   2   4.5   1.05   2   3.1   1.14, 1.15, 1.17   8   10   2.7   3.2   8.19				4	1	4				1			1							
## PERDICTED proceamsgering   10.77   2   2   3   10   0.979   2   6.1   1.192   2   16.6   10.277   8   10   277   3.12   8.19				2		8	3									22	37			
## STATES OF A PROMOTOR PART OF THE PART O				2		2	1									8	10			
2014/1979   care   febror support				1	13	15										42				
64992   Cythorhome J-25 Ready Chain   Homo saplems   6.49   1   1   3   6   0.992   1   1.126   1   2.310,59   6.49   6   6   570   6.53   8.61	21614499	ezrin [Homo sapiens]	57.68	64	17	41	37	9 0.99	2 3	13 5	.4 1	.155 3	15.7	8558.79	57.68		379	586	69.4	6.27
18571112   Tructone-beliphopeuher addesses Authorn   Homo sapiems    42,58   2   23   27   3   0.992   188   0   0   1.166   179   201   23157.49   92.88   94   94   743   344   39.6   87.9   1971124   19				4	1 2	4	1			3 14	.8 1		3 55.1			8	13			
19913424   V-yape proton APPase catalysis subark A (Horno sapiens)   55.62   1 1 6 19 115 0.092   30 7.6 1.185   30 16.7 3578.16 35.82   52 116 67 6.3 3 5.52   52 117 6 2.3 1.51 5154206 (Auge multivesculared body proton 15 (Horno sapiens)   41.07 7 7 1 1 19 0.092   52 7.2 1.207 5 1 1.8 1.57 3 1.0 2 1 190 0.092   52 7.2 1.207 5 1 1.8 1.0 21 190 0.092 1 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1				1	1	3				1	1		1			6	6			
S145206   charged multiresiculate body proteins Tife from sagering   14.07   1   1   4   17   0.992   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1.157   1   1   1   1   1   1   1   1   1				2	23	32							79 20.1			94				
Street   S				1	16	19				7			16.7			52				
Section   Sect				1		4				1 2			1 1/0			21				
Profession   Pro				1		, ,										18				
9REDICTID: putative coaster-extates cAPR Isoform 3 [Horno sapiens] 11.42 5 3 6 13 0.992 1 1.50 5 3 6 3 0.992 1 1.50 5 5 73 6 6.21 9.42 11.078508 1 1.07850				1		, ,										17				
Page				5		6										13				
Part		histone-binding protein RBBP7 isoform 1 [Homo sapiens]		2	1	6	1			1			1			15	15			
4557141 plated-schwarfspector active/purchase its subcruit alpha (Norw ageins) 15.85 1 6 7 26 0.992 7 1.3 1.098 7 15.2 6.38.75 15.85 20 26 4107 46.36 174 366 107 20.00 4 1390.01 12 20.00 110 20.00 4 1390.01 14 366 107 37 70 15.2 6.38.75 15.85 20 20.00 10.00 10.00 10.00 10.00 11.00		pantothenate kinase 4 [Homo sapiens]		1	1	3				1			1			5	5			
201947   Complement C5 pregrogate in Home saglems   46.36   1.56   46.52   2.04   11590,77   46.36   176   188.2   6.52   2.04   5.54				6	47	51														
252-64-65-55 colled-coll domain-containing protein 166 [Norm aspiers] 3 90 4 2 38 73 0.991 2 6.4 1.658 2 28.7 80.45 3.00 50 73 708 80.14 8.79 80.016-6229 81.016-6229 81.016-629				1		7														
S20161/229   PEBDICTED: glacose- de-phosphate loomerase looform 32 [Namo saplems]   85.48   7 36 40 873 0.99 21 7.7 1.208 207 20.1 25/55.66 8.48 116 873 5.58 6.31 8.32 8.51 1.51 1.7 2.3 1.51 1.51 1.7 2.3 1.52 1.52 1.52 1.52 1.52 1.52 1.52 1.52		complement C5 preproprotein [Homo sapiens]		1	56															
1850  1734   Integrin splay-M kolomn 2 precursor [Horno splenn]   28.56   3   19   28   82   0.991   23   8.1   1.099   23   15.6   250.137   28.56   67   82   1157   1.73   1.74   1.75   1				4																
1761624 suppressor of tumorigenicity 7 protein follown aspiens) 3.79 2 1 1 2 4 0.99 1 1 1.317 1 1 23.8 3.79 2 4 5.56 6.34 7.56 1.5000000000000000000000000000000000000				7	36															
SEAUTIVE   SLAV-like protein   Homo sapiens   6.75   1 2 2 9 0.991   3 1.9 1.172   3 4.3 242.99 6.75   6 9 3.26 24.74 6.75				3	. 19	28	8			1			15.6			2	4			
23110944 protessome subural alpha types-biodorm a [bloom sapiens] 43.90 3 8 10 50 0.99! 16 7.8 1.07! 16 21.2 1815.48 43.90 25 50 24 27.4 6.76 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.0				1		2 2				3 1			3 43			6	9			
5304020102   PREDICTED - Principal popular sulfurtandersease bofform XI [Horno sapiens]   6.73   3   2   2   6   0.991   2   8.3   1.244   2   18.1   179.07   6.73   6   6   2.795   2.795   2.50383107   2.50383107   2.50482333   NieS-like protein's 15040012   2.5048001				3		10	5			16	.8 1					25	50			
2546/2833 NHS-like protein 2 [Homo sapiers] 6.45 2 1 5 12 0.99! 1 1.075 1 1.075 1 1.033 6.45 7 12 1225 133 2 7.77 53036065 PREDICTED protein LZC footom X5 [Homo sapiers] 15.79 2 2 2 6 0.99! 2 0.2 1.039 2 30.9 327.66 15.79 6 6 6 190 21.5 4.94 2.0149498 [rentin light chain [Homo sapiers] 43.43 1 5 6 45 0.99! 14 9.1 1.104 1 5.1 2081.85 43.43 18 45 175 20.0 57.8 37.89	530420102	PREDICTED: 3-mercaptopyruvate sulfurtransferase isoform X1 [Homo sapiens]		3		2 2		6 0.99	1	2 8	1.3 1	.234	2 18.1	179.07	6.73	6	6	297	33.2	6.60
\$30360665 PREDICTED: protein LZIC isoform X5 [Homo sapiens] \$15.79 2 2 2 6 0.991 2 0.2 1.039 2 30.9 327.66 15.79 6 6 6 190 21.5 4.94   20144948 [Fertifi light chian [Homo sapiens] 43.43 1 5 6 45 0.991 14 9.1 1.104 14 5.1 2081.85 43.43 18 45 175 20.0 5.78   2012199392 Provincedous? [Homo sapiens] 87.88 1 1 14 15 183 0.991 54 6.6 1.062 54 8.5 663.50 87.88 45 183 193 193 193 193 193 193 193 193 193 19				4	1	9				2 0			2 17.6			21	31			
2014/9498 [ferritin light chain [Horno sapiers] 43.43 1 5 6 45 0.991 14 9.1 1.104 14 5.1 2081.85 43.43 18 45 175 20.0 5.78 3218/9392 peroxiredxxin-2 [Horno sapiers] 87.88 1 1 14 15 183 0.991 54 6.6 1.062 54 8.5 6453.90 87.88 45 183 198 21.9 5.97				2	2	5	1			1			1			7	12			
32189992 perouriedoxin-2 (Homo sapiens) 87.88 1 14 15 183 0.991 54 6.6 1.062 54 8.5 6453.90 87.88 45 183 199 21.9 5.97				2		2 2				2 0	1.2 1					6	6			
				1		6								2081.85		18				
0.9 1.601 0017 66.7 101.0 0017 66.7 311 69.79 007 07.3 0.60				20	14	15														
	T-02-02-7		12.70	30	91	107	2709	0.99	925				. 22.9	1042/02.27	72.70	3.7	27074	007	07.3	5.20

	5	F.o.			F													
Accession 557878742	Description [long-chain-fatty-acidCoA ligase 1 isoform d [Homo sapiens]	ΣCoverage	Σ# Proteins Σ# Unique Peptide	s Σ# Peptides	Σ# PSMs	A8: 115/114 0 0.991	A8: 115/114 Count	A8: 115/114 Variability [%]		116 A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7) 221.26	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa] 58.5	calc. pl 7.53
5453880	acidic leucine-rich nuclear phosphoprotein 32 family member A [Homo sapiens]	37.35	4	4 1	0 8	6 0.991	1	7 11.		1.268 1	4 11.0		37.35	30	86	249	28.6	4.09
16933542	fibronectin isoform 3 preproprotein (Homo sapiens)	49.34	27	80 81	0 100		28			1.184 27		33251.20	49.34	240	1001		259.1	5.73
4885381	histone H1.5 (Homo sapiens)	50.88	2	15 20	0 32	4 0.991	8	9 7.		1.204 8	9 17.5		50.88	59	324		22.6	10.92
578808622	PREDICTED: multifunctional protein ADE2 isoform X1 [Homo sapiens]	13.40	3	6 1.				B 6.		1.290	8 30.6		13.40	24	30		93.9	8.06
7662502	malignant T-cell-amplified sequence 1 isoform 1 [Homo sapiens]	30.94	2	4	4 1-		)	5 1.		1.259	5 7.0		30.94	11	14		20.5	8.82
578814728	PREDICTED: uncharacterized aarF domain-containing protein kinase 2 isoform X1 (Homo saple	6.83	2	1 .	4	4 0.990		7 5		.246	7 14.9	23.47	6.83	4	4	542	60.0	9.31
149999611	signal recognition particle 14 kDa protein [Homo sapiens] histidine-rich glycoprotein precursor [Homo sapiens]	27.21 43.24	1	17 1	3 2			7 5. n 7		1.188	7 14.9	1070.62 6954.80	27.21 43.24	9	22		14.6 59.5	10.04 7.50
392307009	receptor-type tyrosine-protein phosphatase C isoform 2 precursor [Homo sapiens]	23.41	2	15 2	-					1.100 0	8 20.3		23.41	54	61		131.0	6.33
578808863	PREDICTED: eukaryotic translation initiation factor 4E isoform X1 [Homo sapiens]	24.49	6	4 1	6 1			4 2.		1.011	4 12.4		24.49	16	16		28.5	8.12
10716563	calnexin precursor (Homo sapiens)	23.65	1	11 13	2 6.	2 0.990	1	В 7.	.3	1.118 1	8 12.6	2135.56	23.65	33	62	592	67.5	4.60
295844834	N-acetyl-D-glucosamine kinase [Homo sapiens]	40.51	3	12 1:	3 5	9 0.990	1	7 5.	.9	1.307 1	7 23.1	1818.47	40.51	37	59	390	42.0	6.68
530364307	PREDICTED: farnesyl pyrophosphate synthase isoform X2 [Homo sapiens]	18.13	3	4	5 2			5 1.		1.429	5 20.5		18.13	15	21		40.5	5.17
209969703	protein RCC2 (Homo sapiens)	13.60	1	3	7 2			3 14.		1.231	3 28.5		13.60	13	27		56.0	8.78
4506201	proteasome subunit beta type-5 isoform 1 [Homo sapiens]	8.37	4	2	2	6 0.990		2 2.		1.095	2 6.6		8.37	6	6	263	28.5	6.92
7662314 578827386	zinc finger protein 432 [Homo sapiens] PREDICTED: endonuclease 8-like 1 isoform X6 [Homo sapiens]	3.68	4	1	3 1-	4 0.990 6 0.989		2 2.		1.142 1.058	2 19.4	58.80 20.74	3.68	3	14		74.8 48.8	8.75 10.11
40806221	thymocyte nuclear protein 1 (soform 1 (Homo sapiens)	21.78	5	2 .	5 1			3 11.		0.991	3 89		21.78	12	16		46.6 25.7	9.25
530395269	PREDICTED: hemopexin isoform X1 [Homo sapiens]	78.14	4	33 3	-					1.293 53			78.14	97	1862		51.6	7.02
38201710	probable ATP-dependent RNA helicase DDX17 isoform 1 [Homo sapiens]	14.13	5	3 1				3 4.		0.939	3 3.4	720.24	14.13	32	32		80.2	8.27
45580723	haptoglobin-related protein precursor (Homo sapiens)	62.64	7	6 2			1			1.105 1			62.64	78	2216		39.0	7.09
9845511	ras-related C3 botulinum toxin substrate 1 isoform Rac1 [Homo sapiens]	42.19	8	3	8 5			5 8.		1.035	3 4.0		42.19	24	59		21.4	8.50
5901926	cleavage and polyadenylation specificity factor subunit 5 [Homo sapiens]	7.49	1	2	2	6 0.989		2 2.		1.218	2 2.8		7.49	6	6	227	26.2	8.82
4557759 526479824	myeloperoxidase precursor (Homo saplens)	61.48	3	44 51	0 93		27	9 7.		1.156 27 0.995	7 14.0		61.48 16.88	142	939		83.8 17.2	8.97 8.68
122939159	dynactin subunit 3 isoform 4 [Homo saplens] protein-arginine delminase type-2 [Homo saplens]	16.88 21.50	5	11 1	3 1.	6 0.989		5 4.		0.995 1.347 1	5 21.2	108.33 2226.00	21.50	8 20	12	665	75.5	5.59
209529703	signal-regulatory protein beta-1 isoform 3 precursor (Homo sapiens)	12.06	13	3	4 2	7 0.989		3 3.		1.122	3 3.1	420.86	12.06	12	27		43.3	7.83
17402893	phosphoserine aminotransferase isoform 1 [Homo sapiens]	10.27	2	3	5 1			3 1.		1.117	3 9.1	190.62	10.27	13	13		40.4	7.66
530371139	PREDICTED: N-myc-interactor isoform X1 [Homo sapiens]	24.10	1	6	6 2			В 4.	.3	1.155	8 17.5	785.08	24.10	17	29	307	35.0	5.34
4885377	histone H1.3 [Homo saplens]	35.29	4	3 1				3 4.		1.156	3 5.0		35.29	38	250		22.3	11.02
578838605	PREDICTED: cohesin subunit SA-2 isoform X7 [Homo sapiens]	2.42	3	1 :	-	4 0.989		1		1.664	1	61.12	2.42	3	4	1199	138.4	5.41
5803181 4505529	stress-induced-phosphoprotein 1 isoform b [Homo sapiens]	40.52 51.24	3	7 1						1.114 2 1.240 10	0 6.8 8 27.0		40.52 51.24	49	79		62.6 23.6	6.80 5.11
4505529 262206315	alpha-1-acid glycoprotein 2 precursor [Homo sapiens] L-selectin precursor [Homo sapiens]	51.24 14.55	1	/ 1	4 64 6 2			9 9.		1.240 10 1.179	8 27.0 2 13.6		51.24 14.55	42	645		23.6 43.6	7.15
7706425	LSM8 homolog, U6 small nuclear RNA associated [Homo sapiens]	23.96	1	2	2	6 0.989		2 2.		1.179	2 13.0	267.01	23.96	10	Z1	365	10.4	4.48
578828789	PREDICTED: cholesteryl ester transfer protein isoform X1 [Homo sapiens]	6.77	3	1	2 1			3 0		1.545	3 34.3		6.77	2	10		29.1	6.52
4503011	carboxypeptidase N catalytic chain precursor [Homo sapiens]	20.96	1	6	7 3	8 0.989	1	1 6.	2	1.243 1	1 11.4	1572.63	20.96	21	38	458	52.3	7.34
32189394	ATP synthase subunit beta, mitochondrial precursor [Homo sapiens]	14.74	1	4	5 1	8 0.989		5 5.	.0	1.236	5 17.9	939.90	14.74	15	18	529	56.5	5.40
8051595	GA-binding protein subunit beta-1 isoform beta 2 [Homo sapiens]	9.14	8	1 .	4	5 0.988		1		1.228	1	38.89	9.14	5	5	383	41.3	4.84
530420952	PREDICTED: male-specific lethal 3 homolog isoform X2 [Homo sapiens]	1.69	5	1	1	2 0.988		1		1.990	1	38.90	1.69	2	2	355	40.6	8.85
530395059	PREDICTED: glycosyltransferase-like protein LARGE2 isoform X3 [Homo sapiens]	4.03	3	1 :	3	6 0.988		1		1.485	1	0.00	4.03	3	6	496	56.9	8.13
5031855	lymphocyte cytosolic protein 2 [Homo sapiens]	10.51	1	4 !	5 1·			5 4.		1.270	5 13.1		10.51 5.21	15	19		60.2 84.2	6.27
530378251 19923483	PREDICTED: rho GTPase-activating protein 24 isoform X1 [Homo sapiens] ras-related protein Rab-14 [Homo sapiens]	5.21 36.28	16	4	6 2 5 1			5 2. 4 4.		1.073	5 4.2 4 17.5		36.28	- 6	22		23.9	6.67
74272287	matrix metalloproteinase-9 preproprotein [Homo sapiens]	65.91	10	41 4	1 59					1.210 19			65.91	121	591		78.4	6.06
578826102	PREDICTED: tryptophantRNA ligase, cytoplasmic isoform X4 [Homo sapiens]	44.37	2	15 1	9 6		2	D 3.		1.195 2			44.37	50	67		53.1	6.23
226498192	protein atonal homolog 8 (Homo sapiens)	10.59	5	1 .	4 .	4 0.988		1				28.87	10.59	4	4	321	34.6	10.21
189083849	delta-aminolevulinic acid dehydratase [Homo sapiens]	25.15	2	6	6 2	8 0.988	1	11.		1.005 1	0 10.4	1147.04	25.15	18	28		36.3	6.79
28416940	ribosome maturation protein SBDS [Homo sapiens]	12.40	10	1 !	5 2	8 0.988		1		1.183	1	263.51	12.40	11	28	250	28.7	8.75
15011972	rho guanine nucleotide exchange factor 1 isoform 2 [Homo sapiens]	21.93	9	14 1	7 6	6 0.988	2	8.		1.156 2	0 25.3	1930.62	21.93	44	66		102.4	5.66
4557389 568815719	complement component C8 alpha chain precursor [Homo sapiens] clathrin heavy chain 1 isoform 2 [Homo sapiens]	38.70 22.75	1	16 11	8 8		2	5 8. D 8.		1.204 2 1.157 2	4 16.7 8 21.3	3243.49 3593.77	38.70 22.75	49	160	584 1679	65.1 191.9	6.47 5.69
19923327	neuroepithelial cell-transforming gene 1 protein isoform 2 (Homo sapiens)	22.75	3	22 3	1 16	0 0.988 2 0.988	3	8.		1.157 2	8 21.3	3593.77	22.75	82	160	16/9 542	61.8	8.88
22208975	high mobility group protein HMG-I/HMG-Y isoform b [Homo sapiens]	37.50	1	1	3 1	6 0.988		5 8.		1.149	5 13.0		37.50	6	16	96	10.7	10.32
5902134	coronin-1A [Homo sapiens]	63.12	13	28 3	1 49		15			1.215 14			63.12	93	491	461	51.0	6.68
23238188	testin isoform 2 [Homo sapiens]	6.80	3	1 :	2	4 0.987		1		1.037	1	191.47	6.80	4	4	412	46.9	7.59
530426780	PREDICTED: TNF receptor-associated factor 2 isoform X2 [Homo sapiens]	1.88	1	1	1	5 0.987		1		1.179	1	72.39	1.88	3	5	533	59.1	7.52
530436491	PREDICTED: uncharacterized protein LOC101930119 [Homo sapiens]	4.09	2	1	1 .	4 0.987		1		1.230	1	32.33	4.09	1	4	220	24.5	9.17
547234776 315221152	RRP12-like protein isoform 3 [Homo sapiens]  60S ribosomal protein L11 isoform 2 [Homo sapiens]	3.01 26.55	3	1 .	4 31: 7 4			0 6.		1.514 7 1.309	5 37.5	1744.06 219.28	3.01 26.55	6	315 46		132.6 20.1	8.68 9.60
315221152 4504349	hemoglobin subunit beta [Homo sapiens]	26.55 95.24	2	1 12 19				6 11		1.309	6 10.1		26.55 95.24	16	5142		20.1	7.28
530397196	PREDICTED: syntaxin-3 isoform X5 [Homo sapiens]	16.23	6	2	9 514. 5 7:			2 5.		1.103	2 16.4	162.72	95.24 16.23	11	78		30.6	5.36
578803212	PREDICTED: protein dpy-30 homolog isoform X3 [Homo sapiens]	32.50	2	1	3	9 0.987		2 19.		1.120	2 21.1	315.97	32.50	5	9	120	13.9	7.50
156071465	rho GTPase-activating protein 4 isoform 2 [Homo sapiens]	18.50	2	7 1	3 4			9 8.	.7	1.106	8 7.6	1133.31	18.50	30	45	946	105.0	6.34
578829954	PREDICTED: phosphoribosylformylglycinamidine synthase isoform X1 [Homo sapiens]	5.49	2	3	4 1	3 0.987		3 10.	.7	1.023	3 11.6	322.13	5.49	10	13		102.1	5.91
21618349	dual specificity mitogen-activated protein kinase kinase 3 isoform B [Homo sapiens]	21.04	4	2	6 1			3 0.		1.181	3 11.5		21.04	10	15		39.3	7.43
578825543	PREDICTED: centrosomal protein of 128 kDa isoform X2 [Homo sapiens]	6.92	2	1 '	9 3			3 2.		1.045	3 2.6		6.92	13	38		123.1	6.60
25777615 578809447	26S proteasome non-ATPase regulatory subunit 7 [Homo sapiens]  PREDICTED: tetratricopeptide repeat protein 29 isoform X4 [Homo sapiens]	14.81	7	1	4 1	4 0.986 4 0.986		2 18.	4	1.758	2 2.6	530.03 38.07	14.81	8	14		37.0 56.9	6.77 5.78
67782358	complement factor B preproprotein (Homo sapiens)	61.65	1	43 45	5 64		16	6 10.	.1	1.244 15	7 18.7	17960.45	61.65	133	642		85.5	7.06
295986608	immunoglobulin lambda-like polypeptide 5 isoform 1 (Homo sapiens)	56.54	2	11 1:	3 236	6 0.986	71	7 8.	.9	1.272 69	6 26.8	79482.27	56.54	36	2366	214	23.0	8.84
5803013	endoplasmic reticulum resident protein 29 isoform 1 precursor [Homo sapiens]	39.46	2	5	9 4		1	D 11.		1.147 1	0 25.8	1339.17	39.46	19	49	261	29.0	7.31
578807879	PREDICTED: kalirin isoform X5 [Homo sapiens]	2.03	10	1	7 1	0.986		1		1.589	1	29.50	2.03	7	10		336.1	5.96
47157322	protein kinase C beta type isoform 1 [Homo sapiens]	11.33	14	4	9 2			4 6.		1.167	4 27.9	398.10	11.33	20	23		76.8	7.01
530379112 92091600	PREDICTED: ras GTPase-activating-like protein IQGAP2 isoform X5 [Homo sapiens] arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 isoform c [Hon	8.63 3.66	11	3 1	1 7	8 0.986 7 0.986		5 1. 5 1		1.229 1.142	5 31.2 5 19.3	1781.43 339.45	8.63 3.66	26	78		173.8 162.1	5.78 6.23
50345982	ATP synthase subunit alpha, mitochondrial isoform c [Homo sapiens]	15.11	3	4	8 1	0.700		2 2		1.142	2 15.9		3.00	15	17		162.1	8.24
17149836	peptidyl-prolyl cis-trans isomerase FKBP1A isoform a [Homo sapiens]	88.89	2	7	9 9		, ,	8 8.		1.216 2	R 17.9		88.89	25	97		11.9	8.16
530397287	PREDICTED: neuroblast differentiation-associated protein AHNAK isoform X5 [Homo sapiens]	13.73	9	8 2	2 7		-	7 6.		1.047	7 8.1	948.80	13.73	50	76		614.8	6.18
124248516	neutrophil defensin 1 precursor (Homo sapiens)	67.02	2	6	7 28	1 0.986	8	6 5.	.1	1.281 8	5 17.3	3332.30	67.02	19	281	94	10.2	6.99
4503107	cystatin-C precursor [Homo sapiens]	19.18	1	2	2	6 0.986		2 0.		1.174	2 8.5		19.18	6	6	146	15.8	8.75
22538393	A-kinase anchor protein 9 isoform 3 [Homo sapiens]	5.26	41	5 2						1.386 1			5.26	57	148		451.8	4.98
4507645	triosephosphate isomerase isoform 1 [Homo sapiens]	84.34	3	15 16						1.137 7	5 13.3		84.34	45	229		26.7	6.90
10835049 4757766	transforming protein RhoA precursor (Homo sapiens) rho GTPase-activating protein 1 (Homo sapiens)	65.80 28.93	3	10	9 9					1.335 2 1.143 1	9 27.3 8 13.7		65.80 28.93	27	93		21.8 50.4	6.10
4757766 5901922	rho GTPase-activating protein 1 [Homo sapiens] hsp90 co-chaperone Cdc37 [Homo sapiens]	28.93 12.96	45	4	1 5			9 7. 7 3.		1.143 1 1.172	8 13.7 7 9.8		28.93 12.96	31	58		50.4 44.4	6.29 5.25
117676370	tumor necrosis factor alpha-induced protein 8 isoform b [Homo sapiens]	26.06	5	2	4 4			7 3. 4 9.		1.172	7 9.8 3 1.9		26.06	13	47		21.9	8.75
578822609	PREDICTED: ninjurin-2 isoform X2 [Homo sapiens]	13.21	3	1 .	2	9 0.985		2 8.		1.651	2 46.7	55.54	13.21	5	9	106	11.7	10.15
16306550	selenium-binding protein 1 isoform 1 (Homo sapiens)	25.21	3	7	7 3			9.	.3	1.042 1	0 5.6		25.21	20	33		52.4	6.37
48255966	UTPglucose-1-phosphate uridylyltransferase isoform a [Homo sapiens]	54.33	3	21 24	4 14	6 0.985	4	B 8.	.2	1.187 4	7 16.2	5340.90	54.33	69	146		56.9	8.15
530411199	PREDICTED: protein phosphatase Slingshot homolog 2 isoform X2 [Homo sapiens]	2.45	2	1 .	4	6 0.985		1				29.24	2.45	4	6	1430	158.9	5.53
14210504	AP-1 complex subunit mu-1 isoform 2 [Homo sapiens]	9.69	4	1 .	4 :	8 0.985		1		1.075	1	144.36	9.69	6	8	423	48.6	7.30
551411917 269847552	DBF4-type zinc finger-containing protein 2 isoform 2 [Homo sapiens]	2.55 3.81	4	1 1	8 1	1 0.985 7 0.985		1		1.153 1.187	1	23.21 26.22	2.55	8	11	2352 788	264.9 89.6	6.11
269847552 530395344	ventricular zone-expressed PH domain-containing protein homolog 1 isoform 2 [Homo sapiens] PREDICTED: rho-related GTP-binding protein RhoG isoform X1 [Homo sapiens]	46.60	5	6	7 3	0.985		6 10.		1.187	6 11.2		3.81 46.60	5	30	191	21.3	8.12
5031985	nuclear transport factor 2 [Homo sapiens]	29.92	1	3	3 1	1 0.985		4 5.		1.037	4 7.1	616.23	29.92	8	11		14.5	5.38
514239920	complement component C8 beta chain isoform 3 [Homo sapiens]	57.28	5	16 2	0 11-		3	4 7.		1.280 2	8 15.6		57.28	54	114		60.1	7.77

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Accession 34147630	Description elongation factor Tu, mitochondrial precursor [Homo sapiens]	ΣCoverage 5.27	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/114 0.98		A8: 115/114 Variability [%	A8: 117	/116 AB: 117/116 Cour	A8: 117/116 Variability [%]		Coverage A(3,6,7) 5.27	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs 455	MW [kDa] 49.8	calc. pl
28195394	histone H2A type 2-B [Homo sapiens]	45.38		2 1	1 6	5 5	7 0.98		2 6	5.0	1.219	2 16.3		45.38	18	3 5	130	14.0	10.89
70995211	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor [Homo sapiens]	3.96		1 1	1 1		2 0.98		1		1.370	1	52.47	3.96	2	2 3	328	35.8	8.00
4503117	cystatin-B [Homo sapiens]	59.18		1 4	4 5	3	5 0.985	5 1	0 3	3.4	1.090	10 8.0		59.18	14	35	98	11.1	7.56
578815934	PREDICTED: triple QxxK/R motif-containing protein isoform X1 [Homo sapiens]	6.98		1 1	1 1		4 0.985	5	1		1.127	1	90.72	6.98	3	3 4	86	9.7	9.36
4503529	eukaryotic initiation factor 4A-I isoform 1 [Homo sapiens]	35.22		3 10	D 14				•	1.7	1.103	16 11.8		35.22	38	59		46.1	5.48
5174411	CD5 antigen-like precursor (Homo sapiens)	43.23		2 13	3 13	10				5.8	1.193	34 17.6		43.23	38	3 104		38.1	5.47
58331240 578818360	fetuin-B precursor (Homo sapiens)	15.45 7.24		3 4	4 5	1	15 0.984 16 0.984		4 5	5.8	1.327	3 11.0	495.98 42.56	15.45 7.24	13	3 15	382	42.0 233.5	
578818360 17978519	PREDICTED: ankyrin repeat domain-containing protein 26 isoform X3 [Homo sapiens]	7.24		9 1	1 17	3	8 0.984 8 0.984		1	10	1.369	2 12.5			25	36	2031	233.5	
17978519 4757760	vacuolar protein sorting-associated protein 26A isoform 1 [Homo sapiens] adjoonectin precursor [Homo sapiens]	6.15		1	1 2	2	9 0.984			1.0	1.242	3 64		7.65 6.15	4	1 8	244	38.1 26.4	
4506003	serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 1 [Homo sapiens]	25.45		6 3	3 7	3				2.3	1.059	5 3.6		25.45	21	35		37.5	
530382085	PREDICTED: ribosyldihydronicotinamide dehydrogenase [quinone] isoform X3 [Homo sapiens]	51.95		2	7 8	3 4				3.4	1.161	13 7.2		51.95	23	3 46		25.9	
224028248	non-POU domain-containing octamer-binding protein isoform 2 [Homo sapiens]	18.59		2	4 6	3	32 0.984		9 13	3.6	1.118	9 20.1	1197.18	18.59	15	5 32	382	43.8	8.63
5453760	NEDD8 precursor (Homo sapiens)	37.04		1 1	1 3	3 2	0.984	1	2 6	i.6	1.402	2 16.3	814.48	37.04	7	7 20	81	9.1	8.43
269914167	transmembrane emp24 domain-containing protein 6 precursor [Homo sapiens]	4.17		1 1	1 1		9 0.984		1		0.730	1	29.91	4.17	1	1 9	240	27.6	
33350932	cytoplasmic dynein 1 heavy chain 1 [Homo sapiens]	4.41		1 5	5 22				5 11		1.088	4 37.8		4.41	37	7 51		532.1	
578810877	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X14 [Hom	3.29		5 1	1 4	1 1				5.3	1.553	4 31.2			8	3 19		100.8	
530363148	PREDICTED: splicing factor, proline- and glutamine-rich isoform X5 [Homo sapiens]	20.93		2	7 10	2				7.6	1.082	8 6.1		20.93	24	1 28		72.2	
542133044 108796653	zinc finger protein 343 isoform 3 [Homo sapiens]	6.09 16.51	1	4 1	1 3		9 0.98			5.9	1.052 0.903	3 4.6 4 9.6		6.09	5	9	509 321	58.8 34.0	
555290081	phosphoglycolate phosphatase [Homo sapiens]  3'(2'),5'-bisphosphate nucleotidase 1 isoform 2 [Homo sapiens]	6.32		5 1	1 1		3 0.98		1	2.7	0.846	1	270.47	6.32	7	3	253	27.5	
18379349	synaptic vesicle membrane protein VAT-1 homolog (Homo sapiens)	62.09		2 15	5 18	15.			9 12	2.3	1.198	48 25.2		62.09	52	2 152		41.9	
189458812	1,4-alpha-glucan-branching enzyme [Homo sapiens]	36.18		1 13	3 18	3 13				5.6	1.247	27 11.3		36.18	48	3 135		80.4	6.32
124028517	transcription factor PU.1 isoform 2 [Homo sapiens]	13.70		2	2 4	1 1	0.98	3	2 3	3.4	1.213	2 34.2	199.60	13.70	8	3 10	270	31.1	6.80
530379128	PREDICTED: lysM and putative peptidoglycan-binding domain-containing protein 3 isoform X1 (	5.23	1	0 1	1 3	3	8 0.983			7.0	1.190	2 4.2		5.23	7	7 8	306	34.5	5.97
11641247	Golgi-associated plant pathogenesis-related protein 1 isoform a [Homo sapiens]	51.30		5 5	5 6	5 2	25 0.983			5.3	1.213	8 8.6		51.30	16	5 25	154	17.2	9.41
530379765	PREDICTED: eukaryotic peptide chain release factor subunit 1 isoform X2 [Homo sapiens]	8.42		3 2	2 4	1 1	0.98			2.0	1.135	2 17.		8.42	9	10		45.4	5.57
4826902 586798140	serpin B10 (Homo sapiens) bridging integrator 2 isoform 2 (Homo sapiens)	70.03 30.43	-	1 23	3 23 9 13					5.9	1.143 1.114	51 18.6 15 20.7		70.03 30.43	69	9 150 3 53		45.4 59.2	6.16 5.00
586798140 24308273	bridging integrator 2 isoform 2 [Homo sapiens] costars family protein ABRACL [Homo sapiens]	30.43	3	9	13	S 5				5.0	1.114	15 20.3 4 31.8		30.43 38.27	33	7 16		59.2 9.1	
24308273 578821763	PREDICTED: calpain-1 catalytic subunit isoform X1 [Homo sapiens]	38.27		1 10	2 3 9 20	10				1.5	1.112	4 31.8 31 25.5		38.27	50	7 18		9.1 81.8	6.29 5.67
578813403	PREDICTED: calgain-1 catalytic subunit isolorm X1 [nomo sapiens]  PREDICTED: glycinetRNA ligase isoform X1 [Homo sapiens]	18.18		2	4 7	7 1				5.4	1.039	4 14.2		18.18	16	5 18		69.9	
578809641	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 3 isoform X1 [Homo	5.50		3 1	1 6		7 0.982		1		1.501	1	44.56	5.50	6	5	873	100.8	
4505185	macrophage migration inhibitory factor (Homo sapiens)	87.83		3 5	5 5	14			3 9	9.4	1.183	16 6.4		87.83	15	5 140		12.5	
6912352	protein argonaute-1 (Homo sapiens)	3.97		1 1	1 4		6 0.982	2	1		1.191	1	58.38	3.97	6	5 6	857	97.2	9.16
384229049	thymidine phosphorylase isoform 1 proprotein [Homo sapiens]	48.34		2 13	3 16	7	0.982	2 2	3	7.6	1.170	23 17.4	3356.63	48.34	44	73	482	49.9	5.53
4758256	eukaryotic translation initiation factor 2 subunit 1 [Homo sapiens]	6.03		1 2	2 2	2	6 0.982			1.2	1.037	2 0.5		6.03	6	5 6	315	36.1	
629266054	probable G-protein coupled receptor 179 precursor [Homo sapiens]	2.92		1 1	1 7	2				2.9	1.100	4 30.2		2.92	9	9 25		257.2	
4503149	cathepsin G preproprotein (Homo sapiens)	59.61		3 15	5 17					5.6	1.174	78 14.0		59.61	50	282		28.8	
20070130	transcription factor BTF3 isoform B [Homo sapiens]	10.49		2 1	1 2		8 0.982				2.896	1	153.36	10.49	4	1 8	162	17.7	7.50
11342670 38201684	azurocidin preproprotein [Homo sapiens] ribonuclease pancreatic precursor [Homo sapiens]	53.39 14.74		1 9	9 9	25	6 0.982		3 E 2 21	3.4	1.152 1.245	60 19.2		53.39 14.74	27	253	251 156	26.9 17.6	
88703045	proline-rich protein 11 [Homo sapiens]	6.94		1	1 .	5 15				1.1	1.438	20 28.		6.94	3	152		40.1	
530402140	PREDICTED: S-formylglutathione hydrolase isoform X1 [Homo sapiens]	65.25		1 11	1 12					7.6	1.180	16 14.1		65.25	36	65		31.4	
115529463	serine/threonine-protein kinase D1 [Homo sapiens]	1.21		2 1	1 3	1 1	14 0.98			7.0	1.823	2 3.	62.68	1.21	5	5 14	912	101.6	
7706254	nucleolar protein 58 [Homo sapiens]	4.73		1 1	1 3	1	15 0.98		1		1.077	1	151.63	4.73	7	7 15		59.5	
4504351	hemoglobin subunit delta (Homo sapiens)	95.24		1 8	B 17	238	0.98	1 8	6 9	9.5	1.072	86 10.9	114443.61	95.24	50	2380	147	16.0	8.05
530405979	PREDICTED: pyruvate kinase PKM isoform X3 [Homo sapiens]	84.93	2	5 4	4 49					1.4	1.245	34 24.6		84.93	145	1109	531	57.9	7.84
162287326	tyrosine-protein kinase Lyn isoform B [Homo sapiens]	9.98	9	7 3	3 5	5 2		1		7.8	1.072	4 6.8		9.98	14	1 22	491	56.0	6.49
530365780	PREDICTED: rab GTPase-activating protein 1-like isoform X2 [Homo sapiens]	6.51	2	4 1	1 7	1 1	19 0.98	I .	2 2	2.2	1.074	2 4.		6.51	12	2 19		115.3	5.47
530383216	PREDICTED: ras-related GTP-binding protein D isoform X1 [Homo sapiens]	2.31		4 1	1 1		2 0.98		1		1.178	1	42.37	2.31	2	2	303	34.2	
4504345	hemoglobin subunit alpha [Homo sapiens]	96.48		2 17	7 18	456					1.088 14	24 10.6		96.48	54	4565		15.2	8.68
18543329 312596881	26S proteasome non-ATPase regulatory subunit 9 isoform 1 [Homo sapiens]	13.45 23.12		2 4	4 4	1 1:				2.8	1.094	5 5.6		13.45	12	2 15		24.7 44.8	6.95 8.18
4504255	26S protease regulatory subunit 8 isoform 2 [Homo sapiens] histone H2A.Z [Homo sapiens]	53.91		3 3	2 4	5 5			7 16		1.051	6 11.5		53.12	20	5 50		13.5	0.10
4504255	coagulation factor IX preproprotein [Homo sapiens]	9.33		7 3	3 0	1 1				3.2	1.051	4 153		9.33	10	) 14		51.7	
17999541	vacuolar protein sorting-associated protein 35 [Homo sapiens]	21.23		5 14	4 14					5.7		24 16.0		21.23	40	70		91.6	
530391036	PREDICTED: solute carrier family 2, facilitated glucose transporter member 8 isoform X1 [Home	2.87		4 1	1 2	2	2 0.980	)	1		1.024	1	27.81	2.87	2	2	314	34.3	
578831041	PREDICTED: cytokine receptor-like factor 3 isoform X1 [Homo sapiens]	15.50		2	4 4	1 1:	12 0.980	)	4 7	1.7	1.165	4 2.6	450.51	15.50	12	2 12	400	44.8	
24234756	interleukin enhancer-binding factor 3 isoform c [Homo sapiens]	18.84	1	0 10	D 11	3	88 0.980	1	1 7	1.2	1.154	11 15.1	1372.95	18.84	32	2 38	690	74.6	8.24
5032315	dystrophin Dp427p2 isoform [Homo sapiens]	5.56	4	7 1	1 25	6	3 0.980	)	1		1.525	1	246.04	5.56	38	3 63	3562	412.1	5.83
304555581	elongation factor 1-delta isoform 1 [Homo sapiens]	16.07	1	2 1	1 8	3			2 2	2.0	1.192	2 7.2		16.07	19	36		71.4	
20149583	nucleoside diphosphate-linked moiety X motif 6 isoform a [Homo sapiens]	5.70		2 1	1 2	2	4 0.980		1				42.11	5.70	4	1 4	316	35.7	
20357559	galectin-10 (Homo sapiens)	47.89		1 3	3 6	5 7			4 12		1.066	14 7.3		47.89	13	3 70		16.4	
24307939	T-complex protein 1 subunit epsilon [Homo sapiens]	31.98		1 9	9 12					1.0	1.099	10 10.9		31.98	31	44		59.6	
347543829 372266129	dihydropyrimidinase-related protein 2 isoform 3 [Homo sapiens] protein flightless-1 homolog isoform 3 [Homo sapiens]	17.54 9.56	1	5	7 8 6 12	2 4				5.3 3.3	1.121	8 19.3 8 26.4		17.54 9.56	21	23		58.1 138.4	
8922873	GTPase IMAP family member 4 [Homo sapiens]	23.71		3	3 8	3 1				2.1	1.150	3 18.3		23.71	19	3 19		37.5	
6005890	transcription elongation factor B polypeptide 2 isoform a [Homo sapiens]	5.93		3	1 1		4 0.979		1		1.200	1	101.12	5.93	3	3	118	13.1	4.88
578829028	PREDICTED: lysophosphatidylcholine acyltransferase 2 isoform X2 [Homo sapiens]	5.94		2 1	1 3	1	3 0.979		1		1.234	1	77.56	5.94	5	5 13	488	54.4	5.91
5902076	serine/arginine-rich splicing factor 1 isoform 1 [Homo sapiens]	10.08		1 1	1 3	3 1	1 0.979	,	1		0.988	1	180.60	10.08	9	9 11	248	27.7	10.36
395132436	60S ribosomal protein L18 isoform 2 [Homo sapiens]	6.92		2 1	1 1		3 0.979		1		0.979	1	128.81	6.92	3	3	159	18.1	11.84
530388218	PREDICTED: brefeldin A-inhibited guanine nucleotide-exchange protein 1 isoform X2 [Homo saj	6.08		4 1	1 12	6	1 0.979		1		1.157	1	36.18	6.08	18	3 61		208.0	5.85
4506623	60S ribosomal protein L27 [Homo sapiens]	11.03		1 1	1 2	2	4 0.978		1		1.652	1	71.97	11.03	4	1 4	136	15.8	
530418240	PREDICTED: regulation of nuclear pre-mRNA domain-containing protein 1B isoform X1 [Homo s	18.25		2 1	1 4		9 0.978		1		1.600	1	186.18	18.25	7	,	285	32.4	5.52
578829677 50659080	PREDICTED: SET and MYND domain-containing protein 4 isoform X3 [Homo sapiens] alpha-1-antichymotrypsin precursor [Homo sapiens]	4.29 46.57		3 1	1 3	1 18	7 0.978		1	7.0	1.218	1 53 12.2	72.92 6125.36	4.29 46.57	6	3 184	700 423	77.3 47.6	7.01 5.52
32171249	prostaglandin-H2 D-isomerase precursor [Homo sapiens]	23.68		3 21	1 21	1 10			-	1.8	1.145	4 12.8		23.68	0.3	7 1/2		21.0	0.00
119395750	keratin, type II cytoskeletal 1 [Homo sapiens]	23.08 45.19	2	5 16	6 25					1.6	1.145	23 10.0		23.08 45.19	71	1 144		66.0	
30089926	F-box only protein 11 isoform 1 [Homo sapiens]	1.07		5 1	1 1	1 1			3 12		1.154	3 15.0		1.07	71	3 10		94.0	
50428938	ATPase ASNA1 (Homo sapiens)	5.46		1 1	1 2	2	4 0.978		1		0.959	1	68.26	5.46	4	1 4	348	38.8	
578815059	PREDICTED: cathepsin B isoform X1 [Homo sapiens]	22.42		1 4	4 6	5 5	7 0.978	3 1	4 4	1.9	1.095	14 5.1	1288.30	22.42	17	7 57	339	37.8	
348041385	MOB kinase activator 1B isoform 3 [Homo sapiens]	40.82		5 4	4 4	1 1	2 0.978	3	4 3	3.4	1.173	4 5.6	322.39	40.82	12	2 12		16.6	
530381903	PREDICTED: high mobility group protein HMG-I/HMG-Y isoform X3 [Homo sapiens]	43.93		1 3	2 4	1 1				1.0	1.173	4 9.6		43.93	9	1		11.7	
199562283	retrotransposon-like protein 1 [Homo sapiens]	3.83		1 1	1 5	5 1				1.2	1.251	4 27.4		3.83	9	9 18		154.9	
56790932	echinoderm microtubule-associated protein-like 1 isoform a [Homo sapiens]	2.88		1 1	1 3	1				5.7	1.088	2 0.3		2.88	7	7 11		91.9	
169636415	complement component C6 precursor (Homo sapiens)	41.97		5 27	7 31					5.5	1.270	55 29.4		41.97	86	177		104.7	
5729770	tripeptidyl-peptidase 1 preproprotein [Homo sapiens]	13.32		1 3	3 5	5 2			, ,	5.1	1.249	7 31.2		13.32	13	3 25		61.2	
117414148 157738649	protein broad-minded (Homo sapiens) neurofilament medium polypeptide isoform 1 [Homo sapiens]	2.23 9.06		4	2 5 1 12	4.			1		1.704 0.971	1	287.62 942.33	2.23 9.06	13	3 42 1 63		144.7 102.4	
157738649	protein Niban [Homo sapiens]	15.30		1	. 12 R n	2 6			2	5.5	1.299	11 22.3		9.06 15.30	21	5 38		102.4	
283806699	zinc finger BED domain-containing protein 1 [Homo sapiens]	3.60		1	1 3	3	6 0.97		1		1.299	1	45.43	3.60	20	5	694	78.1	6.10
4504957	lysosome-associated membrane glycoprotein 2 isoform A precursor [Homo sapiens]	17.80		3	3 4	1			5 11	1.0	0.984	5 22.3		17.80	12	2 1	410	44.9	
530417951	PREDICTED: RNA-binding protein Raly isoform X3 [Homo sapiens]	17.24		4	2 5	1	18 0.97			0.3	1.121	3 9.0		17.24	11	18	290	30.3	9.63
578800895	PREDICTED: melanoma inhibitory activity protein 3 isoform X3 [Homo sapiens]	2.35		4	1 6	i	7 0.97	,	1		1.086	1	36.77	2.35	6	5	1872	209.3	4.81
238859593	UDP-glucose:glycoprotein glucosyltransferase 2 precursor [Homo sapiens]	6.20		1 1	1 12	2 1			1		1.155	1	23.58	6.20	12	13		174.6	
4505621	phosphatidylethanolamine-binding protein 1 preproprotein [Homo sapiens]	82.89		1 9	9 11	7	78 0.97	2	1 8	3.8	1.169	21 15.9	2354.59	82.89	33	3 78	187	21.0	7.53

Accession	Decertation	ΣCoverage Σ# Proteins	S# Hologo Dontides S# D	Se ne	50 AD. 225/25	A9. 11E/214.0-	A9, 115/114 Wardahilla, (C.)	AD: 117/22/	AD. 117/114 Count AD. 117/114 Count	by [9/] C	oro A(2 / =	Couprag- 4/2 / =	# Peptides A(3,6,7) # PSM A(3,6,7)	# AAs	MW [kDa]	colo -1
Accession 5453710	Description  LIM and SH3 domain protein 1 isoform a [Homo sapiens]	ΣCoverage Σ# Proteins 72.80	2# Unique Peptides Σ# Peptides 4 10 1	2.# PSM 2	ls A8: 115/114 63 0.977	AB: 115/114 Count	A8: 115/114 Variability [%] 0 10.8	AB: 117/116 1.154	A8: 117/116 Count A8: 117/116 Variabilit	ty [%] So 20.8	ore A(3,6,7) 1205.96	72.80 Coverage A(3,6,7)	# reptides A(3,6,7) # PSM A(3,6,7)	# AAs 261	MW [kDa] 29.7	calc. pl 7.05
6912238	peroxiredoxin-5, mitochondrial isoform a precursor [Homo sapiens]	61.21	4 10 1	2 1	75 0.977	5		1.157	51	17.6	6489.83	61.21	34 175	214	22.0	8.57
530377475	PREDICTED: nephronectin isoform X3 [Homo sapiens]	1.08	8 1	1	1 0.977		1	1.776	1		20.02	1.08	1 1	461	50.2	8.25
56699409 578835477	RNA-binding motif protein, X chromosome isoform 1 [Homo sapiens] PREDICTED: NSFL1 cofactor p47 isoform X4 [Homo sapiens]	17.14 23.17	4 4	8	42 0.977 19 0.977		8 5.1 4 3.9	1.272	8	12.6	1272.48 519.60	17.14 23.17	19 42	391 259	42.3 28.5	10.05 9.38
380837121	vesicle-trafficking protein SEC22b precursor [Homo sapiens]	30.70	1 4	6	32 0.977		5 3.5	1.203	5	15.0	600.24	30.70	15 32	215	24.7	8.51
4507511	metalloproteinase inhibitor 2 precursor [Homo sapiens]	20.91	1 3	4	14 0.977		3 1.3	1.218	3	20.7	257.01	20.91	11 14	220	24.4	7.49
22091452	apolipoprotein M isoform 1 [Homo sapiens]	57.98	3 7		48 0.977	1	4 9.5	1.145	14	41.8	1497.72	57.98	25 48	188	21.2	6.01
188595677	integrin beta-2 precursor (Homo sapiens)	17.56	2 9 1	3	42 0.976	1	2 3.7	1.144	12	11.0	1227.07	17.56	30 42	769	84.7	6.95
300934782 66933016	transportin-3 isoform 2 [Homo sapiens] inosine-5'-monophosphate dehydrogenase 2 [Homo sapiens]	4.31 17.51	3 1	4	8 0.976 13 0.976		4 6.6	1.295	1	4.7	157.26 475.16	4.31 17.51	8 8	859 514	97.3 55.8	5.44 6.90
578838944	PREDICTED: NF-kappa-B essential modulator isoform X6 (Homo sapiens)	6.72	6 1		12 0.976		1	1.469	1	4.7	32.01	6.72	7 12		53.1	6.62
4504041	guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 1 [Homo sapiens]	42.54	22 6 1	3	59 0.976	. 1	3 6.4	1.266	12	24.0	2305.68	42.54	34 59	355	40.4	5.54
21281677	WD repeat-containing protein 36 [Homo sapiens]	1.68	1 1	2	5 0.976		1	1.472	1		14.81	1.68	2 5	951	105.3	7.53
237649049	small nuclear ribonucleoprotein Sm D2 isoform 2 [Homo sapiens]	25.93	2 3	3	9 0.976		3 1.7	1.215	3	27.8	236.08	25.93	9 9	108	12.4	9.89
4503625 530411225	coagulation factor X preproprotein [Homo sapiens] PREDICTED: Golgi SNAP receptor complex member 1 isoform X3 [Homo sapiens]	18.24 23.24	3 7	9	9 0.976		0 5.5	1.095	10	12.1	711.98 140.37	18.24 23.24	22 34	488 185	54.7 21.2	5.94 9.61
258679498	carbonic anhydrase 1 isoform a [Homo sapiens]	83.52	3 12 1	4 7	52 0.976		0 9.3	1.085	140	9.0	20643.20	83.52	42 752	261	28.9	7.12
578798051	PREDICTED: uncharacterized protein LOC100293211 [Homo sapiens]	23.33	2 5		45 0.976			1.243	49	24.5	8614.25	23.33	21 445		29.5	8.59
530422109	PREDICTED: RNA-binding protein 41 isoform X2 [Homo sapiens]	7.36	7 2		19 0.976		1	1.101	1		57.52	7.36	5 19	394	44.9	9.60
4557469	AP-2 complex subunit beta isoform b [Homo sapiens]	14.94	3 6 1	3	40 0.976		7 2.5	1.167	7	5.9	1131.86	14.94	34 40	937	104.5	5.38
323510705 530412701	signal recognition particle 19 kDa protein isoform 6 [Homo sapiens] PREDICTED: band 3 anion transport protein isoform X2 [Homo sapiens]	24.75 9.57	3 1	1	2 0.976 25 0.976		9 2.6	1.555	1 9	26.6	50.26 988.10	24.75 9.57	2 2 16 25	101 846	11.5 94.1	9.04 6.16
83700231	cytotoxic T-lymphocyte protein 4 isoform CTLA-4delTM precursor [Homo sapiens]	7.47	2 1	2	3 0.976		7 2.0	1.152	1	20.0	30.69	7.47	3 3	174	19.1	8.47
544186046	protein disulfide-isomerase A6 isoform b (Homo sapiens)	23.16	8 7	9	36 0.975	1	0 6.9	1.151	10	6.2	1443.32	23.16	23 36	488	53.2	5.53
530408977	PREDICTED: sulfotransferase 1A1 isoform X1 [Homo sapiens]	39.66	7 9 1		54 0.975	1	8 4.7	1.454	18	18.0	1866.71	39.66	27 54	295	34.1	6.62
530425159	PREDICTED: neutrophil elastase isoform X1 [Homo sapiens]	55.06	1 8 1	1 3	17 0.975	8	6 8.7	1.258	77	20.3	11655.41	55.06	32 317	267	28.5	9.35
546230986 578822219	beta-glucuronidase isoform 2 precursor [Homo sapiens]  PREDICTED: nuclear factor related to kappa-B-binding protein isoform X5 [Homo sapiens]	7.52 2.40	6 1	3	9 0.975		1	1.150	1		45.17 41.99	7.52 2.40	7 9	505 1294	58.3 139.9	6.99 8.87
94721252	vesicle-associated membrane protein-associated protein A isoform 2 [Homo sapiens]	15.66	2 3	3	10 0.975		4 7.9	1.012	4	20.5	208.56	15.66	7 10	249	27.9	8.62
118442839	complement factor H-related protein 1 precursor [Homo sapiens]	38.18	3 2 1	-	72 0.975		3 6.3	1.094	3	1.8	1717.31	38.18	29 72		37.6	7.39
342349321	interleukin-18 isoform 2 proprotein [Homo sapiens]	9.52	2 1		10 0.975		2 3.9	1.273	2	8.8	56.24	9.52	6 10	189	21.9	4.78
50428935 15431295	microtubule-associated protein 1S [Homo sapiens]  60S ribosomal protein L13 isoform 1 [Homo sapiens]	4.34 14.69	1 3		12 0.975 13 0.974		3 0.6	1.214	3	29.2	222.22 356.10	4.34 14.69	11 12 6 13		112.1 24.2	7.30 11.65
578840723	PREDICTED: V-set and immunoglobulin domain-containing protein 1-like [Homo sapiens]	14.69 24.80	1 8		13 0.974		8 4.1	1.095	73	14.4	2855.67	14.69 24.80	6 13 25 264	211	24.2	8.54
299758394	dynamin-2 isoform 5 (Homo sapiens)		23 12 1		51 0.974		2 3.8	1.191	12	20.8	797.51	19.10	46 51	869	97.9	7.44
255958306	perilipin-3 isoform 3 [Homo sapiens]	39.10	3 11 1	_	59 0.974		4 7.1	1.146	14	15.2	1413.80	39.10	32 59	422	45.8	5.43
26051231 23111047	serine beta-lactamase-like protein LACTB, mitochondrial isoform a precursor [Homo sapiens]	4.02 7.18	4 1	3	14 0.974 9 0.974		1 3 1.0	1.222	1	11.7	28.34	4.02 7.18	3 14	547 404	60.7 46.8	8.53
23111047 21361659	sorting nexin-5 isoform a [Homo sapiens] importin-9 [Homo sapiens]	7.18 6.53	1 2	3	9 0.974		3 1.0	0.944 1.521	3	11.7	324.06 210.24	7.18 6.53	6 9 7 10		46.8 115.9	6.76 4.81
66346685	plasminogen activator inhibitor 1 RNA-binding protein isoform 4 [Homo sapiens]	13.18	4 3		13 0.974		4 5.6	1.217	4	8.1	251.47	13.18	10 13	387	42.4	8.44
4885583	rho-associated protein kinase 1 [Homo sapiens]	10.78	1 4 1		40 0.974		4 1.7	1.161	3	6.1	454.74	10.78	30 40	1354	158.1	5.90
530391093	PREDICTED: protein prenyltransferase alpha subunit repeat-containing protein 1 isoform X2 [H	9.73	17 2	4	36 0.974		3 12.4	5.364	2	425.9	209.56	9.73	9 36	401	46.3	6.99
530425592	PREDICTED: putative hydrolase RBBP9 isoform X1 [Homo sapiens]	10.16	2 1	1	3 0.974		1	1.283	1	50.7	91.25	10.16	3 3	128	14.7	5.72
578813594 4502171	PREDICTED: actin, cytoplasmic 1 isoform X1 [Homo sapiens] adenine phosphoribosyltransferase isoform a [Homo sapiens]	97.23 2 49.44	23 3 3		96 0.974 45 0.974		3 6.6 5 9.3	2.422 1.133	2	31.8	165999.28 1870.46	97.23 49.44	86 4096 21 45	253 180	28.2 19.6	5.34 6.02
51477708	heterogeneous nuclear ribonucleoprotein D0 isoform d [Homo sapiens]	24.74	6 6		42 0.974		1 8.4	1.177	11	31.4	823.10	24.74	23 42	287	30.7	8.41
530407875	PREDICTED: RNA-binding protein FUS isoform X3 [Homo sapiens]	14.64	6 3	3	15 0.974		4 7.0	1.053	4	3.4	772.78	14.64	9 15	321	33.2	9.17
404211881	obscurin isoform IC [Homo sapiens]		43 3 3		88 0.974		2 12.4	1.398	2	28.7	310.94	3.79	54 88	8923	972.4	5.99
537361067 78191798	armadillo repeat-containing protein 8 isoform 5 [Homo sapiens]	6.67	8 1 3 16 1	-	14 0.973 80 0.973		7 9	1.155	1	13.3	26.71 2269.15	6.67	11 14 51 80	600 638	67.1	6.73 8.22
78191798 320202986	plasma kallikrein preproprotein [Homo sapiens] alcohol dehydrogenase [NADP(+)] [Homo sapiens]	31.97 49.54	3 16 1 5 11 1	-	80 0.973 50 0.973		2 7.9 4 3.5	1.299	21	13.3	2269.15 1959.97	31.97 49.54	51 80 35 50	638 325	71.3	8.22 6.79
578831012	PREDICTED: hematological and neurological expressed 1 protein isoform X1 [Homo sapiens]	28.11	5 2		10 0.973		3 5.9	1.129	3	8.5	312.21	28.11	7 10		19.4	8.48
38158015	mastermind-like protein 3 [Homo sapiens]	1.50	1 1 .	2	3 0.973		1	1.156	1		25.71	1.50	2 3	1133	121.6	7.52
55956899	keratin, type I cytoskeletal 9 [Homo saplens]	30.34	2 6 1		37 0.973		6 10.6	1.095	6	3.6	1237.10	30.34	26 37	623	62.0	5.24
530394359 578814467	PREDICTED: mini-chromosome maintenance complex-binding protein isoform X1 [Homo sapler] PREDICTED: tyrosine-protein phosphatase non-receptor type 12 isoform X2 [Homo saplens]	1.36 4.41	3 1	1	7 0.973 7 0.973		3 8.4 2 5.4	1.114 0.984	3	1.4	88.75 157.54	1.36	2 12	587 748	66.5 84.4	5.95 5.60
44890052	stathmin isoform a [Homo sapiens]	45.64	5 6	9	29 0.973		8 6.2	1.174	8	4.2	928.66	45.64	23 29	149	17.3	5.97
530425819	PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]	21.11	2 4		15 0.973		4 7.7	1.226	4	15.8	392.40	21.11	15 15	289	32.1	5.85
7661862	protein phosphatase 1F [Homo sapiens]	16.52	1 2	5	25 0.973		6 5.1	1.114	6	11.1	704.77	16.52	9 25	454	49.8	5.10
112382370	folate receptor gamma precursor (Homo sapiens)	15.51	3 2	4	8 0.973		2 4.6	1.003	2	3.7	166.23	15.51	7 8	245	27.9	7.66
19920317 27886588	cytoskeleton-associated protein 4 [Homo sapiens] protein-tyrosine kinase 2-beta isoform b [Homo sapiens]	3.49 10.96	1 1	2	6 0.972 20 0.972		3 1.5	1.205	1	9.3	166.79 173.40	3.49 10.96	6 6 17 20	602 967	66.0 111.1	5.92 5.91
27886588 4502165	apolipoprotein F precursor [Homo sapiens]	7.36	3 3 1	2	8 0.972		2 3.0	1.155	3	32.5	270.53	7.36	17 20 4 8	326	35.4	5.64
530414265	PREDICTED: cytosolic non-specific dipeptidase isoform X2 [Homo sapiens]	17.05	2 5	6	21 0.972		7 3.7	1.131	7	21.4	587.93	17.05	15 21	475	52.8	5.97
578799625	PREDICTED: NAD kinase isoform X5 [Homo sapiens]	19.50	5 6	6	21 0.972		7 9.1	1.184	7	24.2	1118.77	19.50	18 21	359	39.6	5.80
217272894	116 kDa U5 small nuclear ribonucleoprotein component isoform b [Homo sapiens]	8.86	4 2	8	28 0.972		2 3.2	1.352	2	7.9	694.79	8.86	14 28	937	105.3	5.22
530368297	PREDICTED: quinone oxidoreductase PIG3 isoform X1 [Homo sapiens]  copine-1 isoform c [Homo sapiens]	10.70	2 2	3	7 0.972		2 7.6	1.162	2	9.6	152.95 1350.95	10.70	7 7	243 536	26.8 58.9	9.13 5.83
311893345 10835073	copine-1 isoform c [Homo sapiens] qlycylpeptide N-tetradecanoyltransferase 1 [Homo sapiens]	17.16	7 2	2	39 0.972 5 0.972		0 8.8 2 10.9	1.085	2	9.6	1350.95	17.16 5.04	22 39 5 5	536 496	58.9 56.8	5.83 7.80
530365431	PREDICTED: sorting nexin-27 isoform X4 (Homo sapiens)	8.45	5 1	3	6 0.972		1	1.049	1		108.21	8.45	5 6	355	41.8	6.79
19913408	DNA topoisomerase 2-beta [Homo sapiens]	4.63	2 1		25 0.972		1	1.589	1		138.52	4.63	13 25	1621	182.5	8.06
194688149	serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform isoform 3 [Homo saple	6.82	10 3		12 0.971		2 3.0	1.215	2	3.9	204.83	6.82	12 12	469	52.6	6.23
545479138 6466450	cell division cycle and apoptosis regulator protein 1 isoform b [Homo sapiens]  catechol O-methyltransferase isoform S-COMT [Homo sapiens]	5.55 6.79	2 1	8	40 0.971 3 0.971		1	9.580 0.998	1		61.08 238.11	5.55 6.79	15 40	1135 221	131.0 24.4	5.76 5.33
4885375	histone H1.2 [Homo sapiens]	58.69	2 1 38 6 1	9 2	3 0.971		2 2.9	1.078	12	5.0	12355.37	58.69	3 3 55 317		21.4	10.93
4503047	cysteine-rich protein 1 [Homo sapiens]	10.39	1 1	1	1 0.971		1	1.105	1		26.74	10.39	1 1	77	8.5	8.75
4503143	cathepsin D preproprotein [Homo sapiens]	25.73	1 5	9	46 0.971	1	0 6.3	1.141	10	15.6	1329.52	25.73	24 46	412	44.5	6.54
178557739	complement C4-B preproprotein [Homo sapiens]	73.45	21 4 10			2	9 8.9 3 2.4	1.317	28	35.1	60080.02	73.45	306 1646	1744	192.6	7.27
54112121 6006001	splicing factor 3B subunit 3 (Homo sapiens) glutathione peroxidase 3 precursor (Homo sapiens)	4.44 22.12	1 3		13 0.971 34 0.971	1		1.605	12	8.4 5.4	365.26 775.80	4.44 22.12	11 13	1217 226	135.5 25.5	5.26 8.13
21464101	14-3-3 protein gamma (Homo sapiens)	57.89	1 8 1		89 0.971	1	9 9.2	1.117	19	13.0	4895.96	57.89	47 189	247	28.3	4.89
530389397	PREDICTED: protein LYRIC isoform X2 [Homo sapiens]	5.10	4 1	3	6 0.971		1	0.966	1		168.37	5.10	5 6	549	60.1	9.48
50592994	thioredoxin isoform 1 [Homo sapiens]	55.24	3 5	-	84 0.971	2		1.172	25	20.6	2657.35	55.24	15 84	105	11.7	4.92
4502643 169636428	T-complex protein 1 subunit zeta isoform a [Homo sapiens] calicin [Homo sapiens]	28.06	7 11 1		85 0.971 10 0.970	2	9 7.3	1.246	29	10.1	3160.48 57.22	28.06	33 85 7 10	531 588	58.0 66.5	6.68 8.18
169636428 23110942	calicin [Homo sapiens] proteasome subunit alpha type-5 isoform 1 [Homo sapiens]	2.89 32.37	2 4	-	10 0.970 33 0.970		9 6.2	1.924	9	23.1	57.22 1231.60	2.89 32.37	7 10		66.5 26.4	8.18 4.79
578815984	PREDICTED: arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 isoforr	3.44	7 1		10 0.970		1	1.151	1		48.09	3.44	8 10	1076	119.4	7.74
22027538	programmed cell death 6-interacting protein isoform 1 [Homo sapiens]	33.99	3 16 2	1	93 0.970		7 7.4	1.152	24	16.5	3078.16	33.99	52 93		96.0	6.52
578811290	PREDICTED: PDZ and LIM domain protein 7 isoform X5 [Homo sapiens]	9.57	6 1	2	7 0.970		2 1.9	1.207	2	1.8	230.81	9.57	4 7	188	21.1	9.66
578832229 578802655	PREDICTED: lethal(3)malignant brain tumor-like protein 4 isoform X6 [Homo sapiens]  PREDICTED: SET and MYND domain-containing protein 5 isoform X2 [Homo sapiens]	1.14 7.97	4 1	1	4 0.970 7 0.970		2 0.1	1.210	2	1.9	29.04 32.32	1.14 7.97	1 4	527 389	60.1 44.4	7.39 5.00
578802655 578803564	PREDICTED: SET and MYND domain-containing protein 5 isoform X2 [Homo sapiens]  PREDICTED: nuclear body protein SP140 isoform X11 [Homo sapiens]	7.97	4 1	7	7 0.970		1	1.189 0.879	1		32.32 45.34	7.97	6 7 9 10	389 845	44.4 95.4	5.00
578811443	PREDICTED: dynein heavy chain 8, axonemal isoform X1 [Homo sapiens]	4.67	27 1 2		31 0.970		1	1.967	1		680.50	4.67	43 131		538.3	6.13
221316634	LIM domain only protein 7 isoform 2 [Homo sapiens]	1.16	15 1	2	4 0.969		1	1.151	1		30.23	1.16	4 4	1385	158.1	6.29
156627579	tetranectin precursor (Homo sapiens)	48.02	2 6	8	33 0.969		9 8.6	1.296	9	31.0	1238.24	48.02	20 33	202	22.5	5.67
578817662 14149680	PREDICTED: 72 kDa inositol polyphosphate 5-phosphatase isoform X2 [Homo sapiens] extended synaptotagmin-1 isoform 2 [Homo sapiens]	4.59 4.98	3 1	5	5 0.969 15 0.969		2 2.4	1.106 1.121	1	0.5	51.07 308.60	4.59 4.98	3 5 14 15	610 1104	66.2 122.8	8.90 5.83
.4147000	-yprotogram r toorom z (nomo suptCtb)	4.70	- 2	-	0.905		2.4	1.121	-	0.0	500.00	4.70	15	1104	122.0	0.03

Accession 578831699	Description  PREDICTED: UPF0378 protein KIAA0100 isoform X2 [Homo sapiens]	ΣCoverage 5.93	Σ# Proteins Σ# Unique Peptide	s Σ# Peptides	Σ# PSMs	AB: 115/114 0.969	A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116	A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7) 45.58		# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa] 237.2	calc. pl
4503771	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [Homo sapiens]	16.62	3	2	5 40	0.969	,	3 85	1.44	3 3	15.6	111.25		13	3 40	379	44.4	5.08
379698844	coiled-coil domain-containing protein 51 isoform 2 [Homo sapiens]	7.62	2	2	3	0.969		2 1.5			43.6				5 5	302	33.6	6.96
118402586	lactoylglutathione lyase [Homo sapiens]	46.74	1	9	9 3		1	2 9.6			13.9			25	5 37	184	20.8	5.31
530407070	PREDICTED: tyrosine-protein kinase Fes/Fps isoform X6 [Homo sapiens]	8.11	4	2	8 45			7 2.4			18.7			16	6 45		85.4	6.90
11056044 4757804	inorganic pyrophosphatase [Homo sapiens] copper transport protein ATOX1 [Homo sapiens]	24.57 32.35	1	5	6 23			6 6.6 5 5.6			2.8			16	6 22 R 14		32.6 7.4	5.86 7.24
27754778	ficolin-3 isoform 2 precursor [Homo sapiens]	25.35	2	6	6 3	0.968		2 5.6			2 20.4			18	B 14	288	31.7	6.84
40789306	protein ZNF365 isoform C [Homo sapiens]	3.46	2	1 :	2 :	3 0.968		1	1.11		1	29.53		3	3 3	462	52.5	6.77
38788372	intron-binding protein aquarius [Homo sapiens]	3.70	1	1 .	6 4	0.968		1	1.13			19.98		9	9 9	1485	171.2	6.37
19913416	AP-2 complex subunit alpha-1 isoform 2 [Homo sapiens]	13.40	2	3 1:	2 21	0.968		3 4.3			3.1			23	3 28		105.3	7.66
64762445	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 isoform b [Homo sapiens]	6.16	5	1	3 !	0.968		1	1.110			149.59			5 5	471	54.4	7.56
154355000 662033927	far upstream element-binding protein 2 (Homo sapiens) astrocytic phosphoprotein PEA-15 isoform c (Homo sapiens)	7.31 9.26	2	1	5 15	5 0.968 3 0.968		1	0.91			70.12 175.23			9 15	711	73.1 12.5	7.30 5.17
93277088	mediator of RNA polymerase II transcription subunit 12-like protein [Homo sapiens]	2.70	2	1 .	7 2			1	1.02			71.39		12	2 21		240.0	7.77
24234688	stress-70 protein, mitochondrial precursor [Homo sapiens]	8.39	1	1 .	6 2	0.967		1	1.05	7 1		113.40	8.39	12	2 22	679	73.6	6.16
530412652	PREDICTED: HEAT repeat-containing protein 6 isoform X2 [Homo sapiens]	1.18	2	1 :	2 1	0.967		2 0.7	1.02	5 2	2 3.4	95.14	1.18		5 8	1013	110.2	7.23
148612803	keratin, type II cytoskeletal 74 (Homo sapiens)	13.42	9	1 1	1 3:			1	1.43			243.06		21	1 33		57.8	7.71
530361304 148727247	PREDICTED: ribosomal protein S6 kinase alpha-1 isoform X2 [Homo sapiens] ubiquitin carboxyl-terminal hydrolase 5 isoform 2 [Homo sapiens]	4.04	17	2	3 1	0.967		2 4.4			2 18.1 2 17.0	137.53 160.93			6 6 B 14	643	72.7 93.2	8.25 5.08
578826513	PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8-	19.69	2	1	3 165			3 1.0			3 1.0			8	B 165		14.1	8.84
56237029	integrin alpha-5 precursor [Homo sapiens]	1.05	1	1	1 4	0.967		1	1.73			19.36	1.05	1	1 9	1049	114.5	5.77
8922601	ADP-ribosylation factor-like protein 8B [Homo sapiens]	4.84	1	1	1 :	0.966		1	1.01			164.11		3	3	186	21.5	8.43
4506209	26S protease regulatory subunit 7 isoform 1 (Homo sapiens)	11.55	2	4	5 1	0.966		4 8.1			1 14.7	384.49		13	3 15		48.6	5.95
18141299 11386157	zinc finger and BTB domain-containing protein 26 (Homo sapiens) cytidine deaminase (Homo sapiens)	2.27 86.99	1	1	1 :	3 0.966 3 0.966		3 10.6 4 8.5			29.0	61.58 1414.08		1	1 3 B 48	441	49.9 16.2	7.08 6.92
530413109	PREDICTED: hepatocyte growth factor-regulated tyrosine kinase substrate isoform X1 [Homo s	7.42	2	1	8 19	9 0.966	'	2 4.6			29.0			14	40	768	85.2	6.06
7706757	V-type proton ATPase subunit D [Homo sapiens]	12.15	1	1	3	7 0.966		1	1.22		10.0	74.98	12.15		7	247	28.2	9.36
28558975	mediator of RNA polymerase II transcription subunit 17 [Homo sapiens]	4.45	1	1 :	3 !	0.966		1				33.48	4.45	3	3 5	651	72.8	7.44
38202255	threoninetRNA ligase, cytoplasmic isoform 1 [Homo sapiens]	6.22	4	4	6 2			4 4.7			1 15.2			13	3 21		83.4	6.67
110227598	phospholipase B-like 1 precursor [Homo sapiens] syntaxin-7 [Homo sapiens]	34.36 22.61	1	11 1	3 95 5 1	0.966	2	4 8.3 5 4.3			12.9			37	7 95	5 553	63.2 29.8	9.06 5.55
170932494 34734066	syntaxin-7 [Homo saplens]  fibulin-1 isoform D precursor [Homo saplens]	22.61 17.78	4	9	5 1: 9 3:			-			10.8			12	2 17		29.8 77.2	5.55 5.26
47132587	protein kinase C delta-binding protein (Homo sapiens)	14.56	1	1	5 4	9 0.965		1	1.06		10.0	27.91		6	6 9	261	27.7	6.43
223972612	protein cramped-like (Homo sapiens)	2.44	1	1 .	4 !	0.965		1	1.36	В 1		29.07	2.44	4	4 5	1269	134.6	7.87
530393330	PREDICTED: zinc finger SWIM domain-containing protein 8 isoform X8 [Homo sapiens]	1.00	10	1 :	2 10	0.703		3 5.9			9.8			4	4 10		193.4	6.99
40353764	bisphosphoglycerate mutase (Homo sapiens)	34.36	1	6	6 2			8 10.0			15.8			17	7 23		30.0	6.54
162329583 5454096	cleavage and polyadenylation specificity factor subunit 6 [Homo sapiens] serine/threonine-protein kinase 4 [Homo sapiens]	8.35 20.53	4	1 .	4 25 8 34			1 4 5.5	1.05		23.6	281.64 502.15		10	0 25		59.2 55.6	7.15 5.07
5453607	T-complex protein 1 subunit eta isoform a [Homo sapiens]	22.84	4	8	9 4						2 22.5			20	3 47		59.3	7.65
4557701	keratin, type I cytoskeletal 17 [Homo sapiens]	41.44	14	6 1	9 69			6 5.0			13.1			48	B 69		48.1	5.02
7706563	ras-related protein Rab-8B [Homo sapiens]	30.92	22	2	6 39	0.964		4 8.7		B 4	6.7	1726.82	30.92	18	B 39		23.6	9.07
578814724	PREDICTED: maltase-glucoamylase, intestinal isoform X1 (Homo sapiens)	4.07	3	3	6 1:			3 17.6			80.3			12	2 12		311.8	5.41
578808151 530412093	PREDICTED: alpha-L-iduronidase isoform X2 [Homo sapiens]  PREDICTED: interferon-induced 35 kDa protein isoform X1 [Homo sapiens]	1.73	3	1	0 4	0.964		0 3.3	2.06 1.13		21.5	20.12 972.89		1	7 43	521	57.8	8.82 6.09
530365262	PREDICTED: Interreton-induced 35 Kda protein isotorm X1 (nomo sapiens)  PREDICTED: protein S100-A7 isoform X1 (Homo sapiens)	26.57 66.34	2	5 1	9 162		1	9 8.2			9 6.5	5485.19		21	6 162		31.5 11.5	6.77
530403277	PREDICTED: apoptotic chromatin condensation inducer in the nucleus isoform X4 [Homo sapler	6.86	19	1 !	5 15			1	1.04			72.97		9	9 15		67.5	7.59
392513662	interleukin enhancer-binding factor 2 isoform 2 [Homo sapiens]	18.47	2	2	3 1	0.964		4 1.5			21.4	399.61		8	B 15	352	38.9	4.94
311771547	RBM14-RBM4 protein isoform 2 [Homo sapiens]	18.64	5	1 :	2 1	3 0.964		2 0.8			2 16.3				5 8	118	12.9	8.21
578808923	PREDICTED: protein transport protein Sec31A isoform X23 [Homo sapiens]	7.58	12	2	6 1	0.964		2 12.8			14.7			9	9 11	897	99.1	6.80
4506017 4557395	serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform [Homo sapiens] carbonic anhydrase 2 isoform 1 [Homo sapiens]	44.66 67.31	5	11 1:	2 100	0.963		9 8.1 2 8.8			17.0	1117.08 4440.98		20	D 30 4 106		35.6 29.2	5.54 7.40
530366071	PREDICTED: BRO1 domain-containing protein BROX isoform X5 [Homo sapiens]	10.67	6	1	7 2			2 0.0	1.21		0.1	72.50		16	6 23		40.3	7.17
262263314	cystatin-F precursor [Homo sapiens]	4.83	1	1	1 !	0.963		2 7.3			64.0			3	3 5	145	16.4	8.48
11067747	cell division cycle 5-like protein [Homo sapiens]	5.86	12	1 (	6 3			1	1.43			83.02		10	D 34		92.2	8.18
300244560 118601081	cysteine-rich secretory protein 3 isoform 1 precursor [Homo sapiens]	39.15 21.82	2	6 1	8 3			1 6.5			15.0			21	1 37		29.0 85.1	7.80 4.91
578819487	heterogeneous nuclear ribonucleoprotein U-like protein 2 [Homo sapiens] PREDICTED: mannose-binding protein C isoform X3 [Homo sapiens]	18.15	8	10 1	4 41 5 1			2 2.5			2 31.5			35	1 11		26.1	5.49
118582255	ATP-binding cassette sub-family C member 8 isoform 2 [Homo sapiens]	2.72	3	1 1	6 3			3 0.1			6.3				9 30		176.9	7.81
14277700	40S ribosomal protein S12 [Homo sapiens]	6.06	1	1	1 :	3 0.962		1	1.19	2 1		121.99	6.06	3	3	132	14.5	7.21
4502955	collagen alpha-5(IV) chain isoform 1 precursor [Homo sapiens]	1.78	4	1 :	3 1	0.962		1	1.54			41.58		3	3 8	1685	160.9	7.62
4557892	phosphatidylcholine-sterol acyltransferase precursor [Homo sapiens]	7.27	1	2	3 1	0.962		2 9.8			2 29.6			1	7 8	440	49.5	6.11
530375762 13676857	PREDICTED: carboxypeptidase N subunit 2 isoform X1 [Homo sapiens] heat shock-related 70 kDa protein 2 [Homo sapiens]	31.19 22.54	1	1 1				8 5.0	1.23		3 23.6	1905.22 6169.50		33	7 207		60.5 70.0	5.99 5.74
4502951	collagen alpha-1(III) chain preproprotein [Homo sapiens]	7.30	1	5 .	8 2			6 7.5			7.9			19	9 20		138.5	6.57
578825257	PREDICTED: DNA ligase 4 isoform X4 [Homo sapiens]	5.71	8	1	4	7 0.961		2 7.6			1.1			4	4	911	103.9	7.96
212549536	regulator of G-protein signaling protein-like [Homo sapiens]	7.53	5	1 1	1 3	0.961		1	1.24	4 1		40.44		20	34		125.6	9.01
22538442	cathepsin Z preproprotein (Homo sapiens)	25.08	1	3	6 1			4 8.9			5.5			12	2 15		33.8	7.11
4507467 189217897	transforming growth factor-beta-induced protein ig-h3 precursor [Homo sapiens] syntaxin-binding protein 5 isoform a [Homo sapiens]	40.12 1.26	1	16 2	1 139	0.961		5 9.3	1.25		19.2	4376.12 60.84		53	3 139	683	74.6 123.4	7.71
4503515	eukaryotic translation initiation factor 3 subunit H [Homo sapiens]	11.65	3	2 .	4 10	0.960	)	2 7.4			2 3.1	88.92			7 10	352	39.9	6.54
57013276	tubulin alpha-1B chain [Homo saplens]	48.34	11	4 1	6 14			7 5.8			1 18.7	4669.63		47	7 144		50.1	5.06
32130518	apolipoprotein C-II precursor (Homo sapiens)	34.65	1	2	2 10	0.960		3 4.6	1.15	9 3	37.7				6 10	101	11.3	4.72
530387555	PREDICTED: proline synthase co-transcribed bacterial homolog protein isoform X1 [Homo saple	22.78	2	2	3 36	0.960	)	4 3.6			12.2			8	B 36	158	17.6	10.13
47078295	adenosine deaminase [Homo sapiens]	11.29	3	2	4 10	0.959	1	2 0.8			2.6			10	0 10	363	40.7	5.95
7706441 11415026	vacuolar protein sorting-associated protein 29 isoform 1 [Homo sapiens]  60S ribosomal protein L18a [Homo sapiens]	41.76 7.39	5	4 1	6 10	0.959		4 3.9	0.98		29.5	417.98 178.72		15	5 16	182	20.5 20.7	6.79 10.71
201860300	AH receptor-interacting protein [Homo sapiens]	3.94	1	1 .	2	0.959		1	1.01			87.91		3	3 5	330	37.6	6.29
148727341	serine-threonine kinase receptor-associated protein [Homo sapiens]	9.43	2	2	3 (	0.959		2 7.8	1.25	9 2	21.8	185.43	9.43		6 6	350	38.4	5.12
21361144	26S protease regulatory subunit 6A [Homo sapiens]	23.23	1	4	8 6			9 13.7			12.2			18	B 62		49.2	5.24
30102948	hyaluronan and proteoglycan link protein 3 precursor [Homo sapiens]	3.89	1	1 :	2	3 0.958		1	1.90			25.20		2	2 3	360	40.9	6.52
34485727	nck-associated protein 1-like isoform 1 [Homo sapiens]	13.13	2	2 1	1 2:			4 5.4			55.9			17	7 23		128.1	6.86 8.51
4507789 4502419	ubiquitin-conjugating enzyme E2 L3 isoform 1 [Homo sapiens] flavin reductase (NADPH) [Homo sapiens]	63.64 59.71	3	5 1	6 44 8 15			2 7.1 0 12.5			2 18.0			17	7 44 4 157		17.9 22.1	7.65
4758988	ras-related protein Rab-1A isoform 1 [Homo sapiens]	29.76	22	1	6 4			1 12.5	1.10		0.4	1676.65		15	B 45		22.1	6.21
307574657	uncharacterized protein C8orf34 isoform 1 (Homo sapiens)	1.49	3	1	1 :	0.957		1	1.18	7 1		29.64			2	538	59.4	6.07
557948049	GTPase-activating Rap/Ran-GAP domain-like protein 3 isoform b [Homo sapiens]	1.72	5	1 :	2	7 0.957		1	1.17			25.06		- 2	2	991	110.2	7.46
47551347	serine protease 57 precursor [Homo sapiens]	7.42	1	1	1 :	0.957		1	0.79			169.98		3	3 3	283	30.3	9.32
530400175 94538320	PREDICTED: amphoterin-induced protein 2 isoform X1 [Homo sapiens] hydroxyacylolutathione hydrolase, mitochondrial isoform 2 [Homo sapiens]	2.68 15.38	1	1 :	2 2			3 9.2			3 4.7 3 5.3			-	2 25		57.9 28.8	8.40 7.33
94538320 156231067	hydroxyacylglutathione hydrolase, mitochondrial isoform 2 [Homo sapiens]  TBC1 domain family member 8 [Homo sapiens]	15.38	4	1	3 10	0.957		1 4.4	1.11		5.3	190.66 29.23			3	260	28.8 130.8	7.33 5.52
530411822	PREDICTED: 5-azacytidine-induced protein 1 isoform X2 [Homo sapiens]	4.63	20	1	7 3			1	1.17			76.27		10	D 32		121.8	8.69
291575165	monocyte differentiation antigen CD14 precursor [Homo sapiens]	29.07	1	7	7 2			9 5.0	1.04	9 9	27.9			21	1 2		40.1	6.23
4758340	phenylalaninetRNA ligase alpha subunit [Homo sapiens]	3.35	1	1 :	2	0.957		1	1.47			83.89			6 7	508	57.5	7.80
122937345	unconventional myosin-Vb [Homo sapiens]	6.39	1	2 1				3 15.0			3 17.1	970.43		24	4 144	1848	213.5	7.20
14165466 530396842	polypyrimidine tract-binding protein 1 isoform c (Homo sapiens)	22.22 13.03	30	9 1			1	0 8.6			15.8			31	1 51		57.2 60.6	9.17 5.76
530396842 156627571	PREDICTED: serine/threonine-protein kinase PAK 1 isoform X2 [Homo sapiens] sorbitol dehydrogenase [Homo sapiens]	13.03 7.84	4	1	7 2!	0.956		2 3.8	1.01		10.4	545.40 268.55		18	B 25		60.6 38.3	5.76 7.97
						2.700	-										22.0	

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116	A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)		# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pl
378744212 29826323	GTP-binding protein Rit1 isoform 3 [Homo saplens] alpha-adducin isoform c [Homo saplens]	4.37 12.68	3		1 1	1 1	0.956	5	3 0.7	1.52		3 12.2	65.03 246.83	4.37 12.68	3	20	183	21.6	9.09
41393614	aipna-adducin isoform c [Homo sapiens] ras-related protein Rab-5C isoform a [Homo sapiens]	12.68 25.00	12		3 /	1 1			2 6.5			2 5.1		12.68 25.00	16	20	216	23.5	6.46 8.41
115430223	galectin-3 isoform 1 [Homo sapiens]	22.00	2			. 4			2 4.6			2 18.8		22.00	15	41	250	26.1	8.56
530420291	PREDICTED: gamma-parvin isoform X2 [Homo sapiens]	7.85	1		2 2	2	6 0.956		2 5.3			2 3.8		7.85	6	6	331	37.5	5.49
150170699	kinesin-like protein KIF26A [Homo sapiens]	2.50	1		2 6	. 1	9 0.956	5	2 1.5	1.15	6	1	111.05	2.50	11	19	1882	194.5	8.81
183603931	serine/threonine-protein phosphatase 6 catalytic subunit isoform c [Homo sapiens]	16.96	4		1 4	1 1	9 0.956	5	1	1.49	2	1	129.48	16.96	8	19	283	32.5	6.04
5901956	follistatin-related protein 1 precursor [Homo sapiens]	11.69	1		1 3	3	7 0.956		1	1.03		1	104.32	11.69	6	7	308	35.0	5.52
344179106	ragulator complex protein LAMTOR3 isoform 2 [Homo sapiens]	28.21	2		1 2	2	4 0.955		1	0.98		1	85.93	28.21	3	4	117	12.9	8.13
256222415	filamin-B isoform 4 [Homo sapiens]	4.93	9		2 14				3 2.7			3 1.0		4.93	34	75	2578	275.5	5.78
296179399	outer dense fiber protein 2-like isoform d (Homo sapiens)	15.74	24		1 12				1	2.57		1 18.4	148.06	15.74	24	52	591	68.6	6.55
62241042 21269877	bifunctional glutamate/prolinetRNA ligase [Homo sapiens]	7.08	1		4 11	3			6 3.5					7.08	24	34	1512	170.5	7.33
21269877 5454088	cysteinetRNA ligase, cytoplasmic isoform a [Homo sapiens] acidic leucine-rich nuclear phosphoprotein 32 family member B [Homo sapiens]	7.99 40.24			2 5	5 1			2 3.7			2 1.9 1 7.0		7.99 40.24	11	11 78	726 251	82.8 28.8	7.02 4.06
66529407	tensin-1 [Homo sapiens]	2.02	13				4 0.955		2 10.1	1.02		1 7.0	19.68	2.02	32	/0	1735	185.6	7.75
38202257	neutral alpha-glucosidase AB isoform 2 precursor (Homo sapiens)	16.74	5		3 11	. 3			9 8.7			9 27.1	846.14	16.74	29	32	944	106.8	6.14
62243068	insulin-like growth factor-binding protein 3 isoform b precursor [Homo sapiens]	14.09	55		3 4	. 2			3 8.1			3 12.6		14.09	12	24	291	31.7	8.69
51873055	fibulin-2 isoform b precursor [Homo sapiens]	6.50	3		1 2	2	7 0.955		1	1.17		1	128.42	6.50	5	7	1184	126.5	4.82
578832396	PREDICTED: trafficking protein particle complex subunit 8 isoform X4 [Homo sapiens]	2.84	5		1 4		9 0.954		1				44.95	2.84	4	9	1338	150.1	6.83
195972866	keratin, type I cytoskeletal 10 [Homo sapiens]	34.93	21	14	1 19	9	2 0.954		7 15.0			7 6.6		34.93	50	92	584	58.8	5.21
7661880	arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 [Homo sapiens]	15.00	2	!	5 9	4	1 0.95		6 6.7			6 13.4		15.00	21	41	740	81.5	7.66
17149853	FK506-binding protein-like [Homo sapiens]	4.30	16		1 2	2 1	0 0.954		1	1.38		1	44.31	4.30	4	10	349	38.2	5.50
31543385	choline-phosphate cytidylyltransferase A [Homo sapiens]	5.18	4		2 2	2	4 0.95		2 1.0			2 9.4		5.18	4	4	367	41.7	7.25
578799003 22165400	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X	3.35	7		2 9	2	6 0.95		3 2.2	1.18		3 11.9		3.35	18	26	4057	433.5	6.55
22165400 56788356	acyl-coenzyme A thioesterase 11 isoform 2 [Homo sapiens]	5.72 3.58	2		1 4		6 0.953 4 0.953		1	0.98		1	28.99 35.37	5.72 3.58	4	6	594 837	67.1 96.8	7.64 5.67
4557485	tuftelin-interacting protein 11 [Homo sapiens] ceruloplasmin precursor [Homo sapiens]	74.37	1		2 63	1 112			2 8.2			2 25.8		74.37	104	1125	1065	96.8 122.1	5.67
4885399	structural maintenance of chromosomes protein 3 (Homo sapiens)	12.24	7		2 16				2 6.7			2 25.6		12.24	30	103		141.5	7.18
383872480	ubiquitin-conjugating enzyme E2 variant 1 isoform a [Homo sapiens]	51.18	12		3 10	) 5			4 8.8			4 17.7		51.18	28	50	170	19.3	8.54
374253794	B-cell receptor-associated protein 31 isoform b [Homo sapiens]	8.54	9		1 3	3 1			1	1.20		17.7	123.55	8.54	8	11	246	28.0	8.44
46094009	melanoma inhibitory activity protein 2 precursor [Homo sapiens]	2.60	1		1 2	2	7 0.95	3	2 15.0	1.88	1 :	2 48.0		2.60	4	7	654	74.0	4.34
578806133	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Homo sapiens]	17.92	6		1 5	5 1			4 9.6	1.06	9	4 11.0	284.84	17.92	12	17	625	70.6	7.61
6912286	caspase-14 precursor [Homo sapiens]	14.88	1		2 3	3	9 0.95		2 8.9			2 8.0		14.88	9	9	242	27.7	5.58
109148542	alaninetRNA ligase, cytoplasmic [Homo sapiens]	10.74	2		3 8	3 1			3 2.8			3 27.2		10.74	14	17	968	106.7	5.53
70780355	ankyrin-1 isoform 2 [Homo sapiens]	4.65	6		2 7	2			2 5.3			2 5.6		4.65	15	25	1719	188.9	6.62
301171467	ATP-dependent RNA helicase DDX3X isoform 2 [Homo sapiens]	11.50	6		1 6	5 2			3 0.1			3 4.9		11.50	11	25	661	73.1	7.18
222144309	prenylated Rab acceptor protein 1 [Homo sapiens]	7.03	10	'	1 2	2 2			1	2.03	3	1	89.74	7.03	6	27	185	20.6	7.34
8393638 23097308	junctional adhesion molecule A precursor [Homo sapiens] nesprin-1 isoform 2 [Homo sapiens]	4.01 5.85	1		1 1		2 0.952 8 0.952		2 3.4 7 5.9			7 17.7	54.92 518.98	4.01 5.85	1	158	299 8749	32.6 1004.6	7.90 5.52
289547524	rab11 family-interacting protein 1 isoform 3 [Homo sapiens]	7.40	22		2 00	3 2			3 12.6			3 1.5		7.40	17	22	1283	137.1	5.52
41327771	probable ATP-dependent RNA helicase DDX23 [Homo sapiens]	8.29	1		1 7	1 1			2 1.5			2 8.3		7.40 8.29	17	17	820	95.5	9.55
530421644	PREDICTED: mediator of RNA polymerase II transcription subunit 14 isoform X2 [Homo sapien:	2.06	4		1 4	1 1			3 4.1			3 5.7		2.06	4	10	1410	156.3	8.69
98986457	host cell factor 1 [Homo sapiens]	2.06	5		3 5	. 2			3 2.4			3 1.1		2.06	13	21	2035	208.6	7.46
7657313	U6 snRNA-associated Sm-like protein LSm1 [Homo sapiens]	5.26	1		1 1		2 0.95		1	1.25		1	36.87	5.26	2	2	133	15.2	5.22
308737003	origin recognition complex subunit 3 isoform 3 [Homo sapiens]	5.99	5		1 2	2	6 0.95	1	1	2.00		1	29.41	5.99	2	6	568	65.9	7.62
578832501	PREDICTED: methyl-CpG-binding domain protein 1 isoform X28 [Homo saplens]	9.34	38		1 6	1	0 0.95	1	1	0.87	0 '	1	131.85	9.34	10	10	610	67.5	9.54
5031981	26S proteasome non-ATPase regulatory subunit 14 [Homo sapiens]	23.23	1		3 4	1 1	6 0.95		5 6.4			5 8.5		23.23	10	16	310	34.6	6.52
31657142	integrin alpha-1 precursor (Homo sapiens)	5.26	1		1 8	3 1	8 0.950		2 3.3			2 4.0		5.26	8	18	1179	130.8	6.29
578818505	PREDICTED: zinc finger protein 248 isoform X2 [Homo sapiens]	9.50	1		1 7	7	7 0.950		1	1.26		1	28.97	9.50	7	7	579	67.0	8.25
7706511	methionine-R-sulfoxide reductase B1 [Homo sapiens]	7.76	1		1 1	1	2 0.950		1	0.97		1	53.25	7.76	2	2	116	12.8	8.37
530414003 14150155	PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2 isoform X4 [Ho	4.73	3		1 1		6 0.950 3 0.950		2 5.7			2 2.6	100.26 37.70	4.73 4.55	3	6	169 176	18.5 20.7	5.54 6.34
530376083	vacuolar protein-sorting-associated protein 25 [Homo sapiens] PREDICTED: SH3 domain and tetratricopeptide repeat-containing protein 1 isoform X1 [Homo s	4.55 2.38	1		1	5 2			1	1.19		1	51.48	4.55 2.38	3	23	176	139.2	6.28
126032350	DNA-dependent protein kinase catalytic subunit isoform 2 [Homo sapiens]	9.67	16	11	35	5 13			3 10.9			2 18.1	996.99	9.67	70	133	4097	465.2	7.17
116875844	phosphopantothenatecysteine ligase isoform a [Homo sapiens]	7.07	3		1 2	2	4 0.94		1	1.25		1	112.68	7.07	4	4	311	34.0	6.71
4826665	copper chaperone for superoxide dismutase [Homo sapiens]	5.47	1		2 2	2	4 0.949	,	1	0.91	4	1	63.97	5.47	4	4	274	29.0	5.58
217416379	heterogeneous nuclear ribonucleoprotein L-like isoform 2 [Homo sapiens]	8.38	5		3 4	1 1			3 9.7			2 9.3		8.38	10	10	537	59.6	7.72
578837445	PREDICTED: unconventional myosin-XVIIIb isoform X4 [Homo sapiens]	3.55	3		1 9	1	8 0.949		1	1.21		1	31.10	3.55	9	18	2449	272.3	6.90
103472136	G-protein coupled receptor-associated sorting protein 1 [Homo sapiens]	1.15	1		1 2	2	2 0.948		1	1.07		1	27.73	1.15	2	2	1395	156.8	4.68
578809225	PREDICTED: ubiquitin-like modifier-activating enzyme 6 isoform X1 [Homo sapiens]	9.93	2		2 7	1 1			2 2.1			2 11.2		9.93	13	13	977	110.2	6.24
42794779	unconventional myosin-XVIIIa isoform b [Homo sapiens]	8.58	2	!	5 16				6 7.1			5 15.7		8.58	29	41	2039	231.1	6.20
148277022	selenoprotein P isoform 2 (Homo sapiens)	16.30	2		3 6	3			8 5.6			B 17.0		16.30	12	33	411	46.2	8.03
578807020	PREDICTED: programmed cell death protein 10 isoform X4 (Homo sapiens)	4.72	1		1 1		3 0.94		1	1.17		1	53.92	4.72	3	3	212	24.7	8.19
371877525 145309304	arachidonate 5-lipoxygenase isoform 2 [Homo sapiens] cadherin EGF LAG seven-pass G-type receptor 3 precursor [Homo sapiens]	5.30	3		2 3	3 1	4 0.94 1 0.94		3 3.2	1.16		3 2.3	492.12	5.30	7	14	642 3312	74.6 358.0	5.63 6.68
145309304 21070997	cadherin EGF LAG seven-pass G-type receptor 3 precursor [Homo sapiens] stromal interaction molecule 1 isoform 2 precursor [Homo sapiens]	7.01	1		1 9	1 2			1	0.98		1	21.21 194.62	3.26 7.01	9	11	3312 685	358.0 77.4	6.68
7657647	tropomodulin-2 isoform a [Homo sapiens]	8.55	1		1 3	1 1			1	1.05		1	134.59	7.01 8.55	10	20	351	39.6	5.07
530394454	PREDICTED: calcium/calmodulin-dependent protein kinase type II subunit gamma isoform X9 [	15.88	62		3 7	7 1			3 5.4			3 22.6		15.88	12	18	529	59.6	7.58
530407769	PREDICTED: serine/threonine-protein kinase SMG1 isoform X4 [Homo sapiens]	0.75	10		1 4	1 1			1	2.68		1	52.16	0.75	7	15		404.7	6.39
530382704	PREDICTED: serine/threonine-protein kinase RIO1 isoform X2 [Homo sapiens]	6.25	2		1 3	3	8 0.946	5	1	12.19	8	1	25.68	6.25	4	8	464	53.8	8.91
4507171	SPARC precursor [Homo sapiens]	8.58	1		1 2	2	5 0.946		1	0.88		1	238.70	8.58	5	5	303	34.6	4.84
194353959	phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit gamma isoform 3 [Ho	4.64	10		1 8	8 8			1	1.11		1	868.93	4.64	12	84	1445	165.6	6.93
40254808	perforin-1 precursor (Homo sapiens)	3.78	1		1 2	2 1			1	5.37		1	18.79	3.78	4	14	555	61.3	7.83
4506597	60S ribosomal protein L12 [Homo sapiens]	18.79	1		2 3	3	7 0.945		2 5.5			2 38.2		18.79	6	7	165	17.8	9.42
4826772	insulin-like growth factor-binding protein complex acid labile subunit isoform 2 precursor [Home	21.32	2		7 10	3			0 10.1			29.7	860.72	21.32	25	37	605	66.0	6.79
41349456 156631005	prolyl endopeptidase [Homo sapiens]  26S proteasome non-ATPase regulatory subunit 8 [Homo sapiens]	6.62	2		5 5	5 2			6 3.3			5 11.2		6.62	10	20	710	80.6	5.86 9.70
156631005 578815599	26S proteasome non-ATPase regulatory subunit 8 [Homo sapiens] PREDICTED: RNA-binding Raly-like protein isoform X6 [Homo sapiens]	15.43 14.35	1		4	1 2	0 0.944		2 3.5	0.87		1 8.7	91.19 422.12	15.43 14.35	6	10 27	350 237	39.6 26.4	9.70
7705753	complement C1q subcomponent subunit A precursor [Homo sapiens]	14.35	1		1 4	1 2	6 0.94		2 3.5			2 8.7 1 11.6		14.35	12	2/	237	26.4	9.11
4506667	60S acidic ribosomal protein PO (Homo sapiens)	11.99	1		3 4	1 1	0 0.94		3 5.9			3 7.6		11.99	9	10	317	34.3	5.97
611435005	lysine-specific demethylase 6A isoform 5 [Homo sapiens]	4.54	9		1 3				1	1.35		1	65.34	4.54	5	12	1322	145.1	7.44
320461537	adenosine kinase isoform c [Homo sapiens]	24.77	5	:	3 7	4	8 0.943	3	5 8.6	1.15	9 !	5 20.1	911.77	24.77	16	48	327	36.6	6.79
578800054	PREDICTED: far upstream element-binding protein 1 isoform X3 [Homo sapiens]	5.29	4		1 4	1 1	1 0.943	3	1	1.24	2	1	104.03	5.29	8	11	643	67.4	7.61
10835240	high mobility group nucleosome-binding domain-containing protein 4 [Homo sapiens]	25.56	1		1 5	5 4			3 1.7			3 17.7		25.56	14	43	90	9.5	10.48
5174613	nucleosome assembly protein 1-like 4 [Homo sapiens]	4.80	1		1 2	2 1	0 0.94		1	1.09		1	117.86	4.80	4	10	375	42.8	4.69
58331274	septin-5 isoform 2 (Homo sapiens)	22.25	2		3 6	i 2	5 0.942		3 12.5			2 40.7	175.05	22.25	11	25	346	39.3	7.20
578821286	PREDICTED: teneurin-4 isoform X1 [Homo saplens]	2.43	2		1 9	3	6 0.942		3 0.1			9.5	19.99	2.43	9	36	2794	310.5	6.49
115298659	spectrin alpha chain, erythrocytic 1 [Homo sapiens]	6.66	1		3 19	8	0.942		6 10.6			6 11.9		6.66	36	80	2419	279.8	5.05
239049591	glycogen (starch) synthase, muscle isoform 2 [Homo sapiens]	8.62	2		5 4	1	0 0.942		3 10.2			3.5		8.62	10	10	673	76.4	6.54
14916485	caspase-6 Isoform beta (Homo sapiens)  ATP-binding cassette sub-family F member 1 Isoform b (Homo sapiens)	12.25	3		1 2		5 0.94°		1	2.20		1	62.82 174.51	12.25 12.02	4	5 18	204 807	22.6 91.6	7.15 7.68
10947135 578815063		12.02	8		10	, 1	8 0.94° 4 0.94°		1	1.20	-	1	174.51 23.17	12.02	13	18	807 1406	91.6 149.5	7.68
578815063 578825065	PREDICTED: tyrosine-protein kinase SgK223 isoform X1 [Homo sapiens] PREDICTED: sciellin isoform X8 [Homo sapiens]	1.42 5.49	1		1 3	1 1	4 0.94°		1	1.23		1	23.17 182.16	1.42	3	4	1406	149.5	7.20 9.31
4507711	tetratricopeptide repeat protein 1 [Homo sapiens]	6.85	1		1 3		8 0.940		2 0.8		-		53.30	6.85	3	14	292	33.5	4.84
530410798	PREDICTED: nuclear receptor corepressor 1 isoform X7 [Homo sapiens]	4.06	13		1 10	) 2	1 0.940		1	2.95	7	1	37.58	4.06	14	21	2514	277.8	7.12
217416369	GTP-binding protein SAR1a (Homo sapiens)	5.56	2		1 1		2 0.940		1	1.61		1	104.76	5.56	2	2	198	22.4	6.68
22202629	apoptosis-inducing factor 1, mitochondrial isoform 2 precursor (Homo sapiens)	4.27	5		1 3	3 1	0 0.940	)	2 8.0	2.17	2	2 26.7	106.23	4.27	7	10	609	66.3	8.94
189181724	proteoglycan 4 isoform D precursor [Homo sapiens]	5.28	6		1 7	1 1	5 0.939		1	1.11	9	1	151.81	5.28	10	15	1270	136.5	9.54

	530414204 422398885 38327558 205360947 38505161 530373793 578808568 530375309 530382657 15431332 13129048 289547631	PREDICTE: asparagineIBMA (jages, cytoplasmic isoform X1 [Homo sapiens]  cytoplasmic dynnic i Intermediate chair 2 Abortne 1 [Homo sapiens]  interferor-induced guanylate-binding protein 2 [Homo sapiens]  protein-methiomes guanylate-binding protein 2 [Homo sapiens]  tutor domain-containing protein 1 [Homo sapiens]  tutor domain-containing protein 1 [Homo sapiens]  PREDICTED: midling resistance-associated protein 5 isoform X1 [Homo sapiens]  PREDICTED: NEDD4-binding protein 2 isoform X2 [Homo sapiens]  PREDICTED: Applicamenta-like protein 3 isoform X1 [Homo sapiens]  PREDICTED: John contended: like protein 3 isoform X1 [Homo sapiens]  PREDICTED: John contended [Homo sapiens]  PREDICTED: John contended [Homo sapiens]  REDICTED: John contended [Homo sapiens]	1.46 5.13.64 5.11.00 9.18 5.7.06 5.7.03 8.11.36 4.13.64	2# Unique Peptides 2 3 1 3 2	2# Peptides  1	3 24 19 48	0.939 0.939 0.938 0.938	A8: 115/114 Count	1 2 2 1	8.0	1.499 1.255 2 1.626	1 2 26.0 1	46.87 309.88 112.39	7 1.46 3 13.64 9 11.00	# Peptides A(3,6,7) # PSM 7 3 13 13	3 24	547 638 591	62.8 71.4 67.2	6.25 5.20 5.71
Service of the service from the Theorem 19.00   10   10   10   10   10   10   10	42239885 38327558 205360947 38505161 530373793 578808568 530375309 530382657 15431332 13129048 289547631	cytoplasmic dynien i retermediate chain Z koform I (Homo sapiens) interferon-induced aganyties beinding protein 2 (Homo sapiens) protein-enthronine sutlosdes oddisse MEAL sloftorm I (Homo sapiens) (Ludor domain-containing protein 1 (Homo sapiens) (Ludor domain-containing protein 1 (Homo sapiens) (PREDICTED: mutiditugi resistance-associated protein 5 isoform XI (Homo sapiens) (PREDICTED: NEDUS-landing protein 2 isoform XI (Homo sapiens) (PREDICTED: Dischneibuse) (Sapiens) (PREDICTED: Dischneibuse) (Sapiens) (PREDICTED: Johneibuse) (Sapiens) (PREDICTED: Johneibuse) (Sapiens) (Sapie	11.00 9.18 7.06 7.03 1.36	2 3 1 3 3 2	2 6 1 6 2 9	24 19 48 31	0.939 0.938 0.938		1	3.0	1.255 2 1.626	1	309.88 112.39	3 13.64 9 11.00	13 13	24 19	638 591	71.4 67.2	5.20 5.71
## Particular plant and pl	38327558 205360947 38505161 530373793 578808568 530375309 530382657 15431332 13129048 289547631	Interferon-induced guarylate-briding protein 2 (brinos sapiens) protein-methinomic guardiscie dostiae MoLA I tolorforn 1 (brinos sapiens) ludor domain-containing protein 1 (brinos sapiens) PREDICTID: multiprogresistance-associated protein 5 losform XI (brinos sapiens) PREDICTID: NEDDA-binding protein 2 losform X2 (brinos sapiens) PREDICTID: Applicamental: bila protein 3 losform X3 (brinos sapiens) PREDICTID: Josformosci-Like protein 3 losform X3 (brinos sapiens) PREDICTID: Josformosci-Like protein 3 losform X3 (brinos sapiens) PREDICTID: Josford salf (brinos sapiens)	11.00 9.18 7.06 7.03 1.36	3 2	1 6 2 9 1 9	19 48 31	0.938		1		1.626	1	112.39	11.00	13	19	591	67.2	5.71
Series of the series and many designed professors of the series of the s	38505161 530373793 578808568 530375309 530382657 15431332 13129048 289547631	protein-methionine sulfoxide outdisse MICAL I soform 1 (Homo sapiens) Induct domain-containing protein 1 (Homo sapiens) PREDICTED: multidrug resistance-associated protein 5 isoform XI (Homo sapiens) PREDICTED: NEDO4-ibriding protein 2 isoform X2 (Homo sapiens) PREDICTED: polymore-tile ike protein 3 isoform XI (Homo sapiens) PREDICTED: polymore-tile ike protein 3 isoform XI (Homo sapiens) PREDICTED: zinc finger and SCAM domain-containing protein 16 isoform X2 (Homo sapiens) scapases—1 isoform data (Homo sapiens)	7.06 : 7.03 8: 1.36 i	3 2	2 9	48 31						4 20.8	665.23		15	40	10/7	227.0	
March   Marc	530373793 578808568 530375309 530382657 15431332 13129048 289547631	tudor domain-containing protein I (Nemo sapiems)  PREDICTED. military nesistance-associated protein 5 isoform XI (Homo sapiens)  PREDICTED. NEDDA-binding protein 2 isoform X2 (Homo sapiens)  PREDICTED. photheractic like protein 5 isoform X1 (Homo sapiens)  PREDICTED. photheractic like protein 5 isoform X1 (Homo sapiens)  PREDICTED. zinc finger and SCAM domain-containing protein 16 isoform X2 (Homo sapiens)  capapase-1 isoform data (Homo sapiens)	7.03 83 1.36 8	2	1 9	31	0.938												6.40
Margin   Miles   Mil	578808568 530375309 530382657 15431332 13129048 289547631	PREDICTED: NEDD4-binding protein 2 isoform X2 [Homo sapiens] PREDICTED: polyhomeotic-like protein 3 isoform X3 [Homo sapiens] PREDICTED: zinc finger and SCAN domain-containing protein 16 isoform X2 [Homo sapiens] caspase-1 soform delta [Homo sapiens]	1.36	2					5	2.7	1.188	5 18.1	87.39	7.06	17	31	1189	132.8	6.46
Property of the property of	530375309 530382657 15431332 13129048 289547631	PREDICTED: polyhomeotic-like protein 3 isoform X3 [Homo sapiens]  PREDICTED: zinc finger and SCAN domain-containing protein 16 isoform X2 [Homo sapiens]  caspase-1 isoform delta [Homo sapiens]			1 8	15			1			1			12	15			8.66
March   Marc	530382657 15431332 13129048 289547631	PREDICTED: zinc finger and SCAN domain-containing protein 16 isoform X2 [Homo sapiens] caspase-1 isoform delta [Homo sapiens]	0.56	8	1 4	39		4	5 1			5 8.9			8	39			5.25
Service of the content of the conten	15431332 13129048 289547631	caspase-1 isoform delta [Homo sapiens]		6	1 1	3			1			1			3	3			7.27
Series of the se	13129048 289547631			2	1 2	3			1			1			2	3			6.71
Series of the property of the	289547631			5	3 4	12			1			4 3.4			9	12			
Marie   Mari				1	1 1	1						1 25.0			1 20	1			
Service of the form early 1 of 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		(OC elbasses I analytic I 23 (Users seeless)			5 10	40		10	,			25.8			28	40			
March   Marc				2	1 6	23			1			7 75			10	23			5.00
Martin   M				R .	5 7										15				8.82
Appendix	530382158		8.51	7	2 3	12	0.936		2	5.9	1.101	2 6.5	327.08	8.51	9	12	376	42.4	5.86
Section   Sect	42544123	splicing factor 1 isoform 3 [Homo sapiens]	4.93 1	1	1 2	6	0.936				1.222	1	79.20	4.93	6	6	548	59.7	9.50
March   Marc	13129018	gamma-glutamylcyclotransferase isoform 1 [Homo sapiens]	15.96	2	1 3	7	0.936				1.011	1	200.71	1 15.96	7	7	188	21.0	5.14
Michael   Mich	115387104	4-trimethylaminobutyraldehyde dehydrogenase [Homo sapiens]	9.65	1	1 5	31	0.935				1.166	1	271.57	7 9.65	13	31	518	56.3	6.57
Page   19   19   19   19   19   19   19   1	530393716	PREDICTED: S-adenosylmethionine synthase isoform type-1 isoform X2 [Homo sapiens]		3	1 3	7			1			1			6	7			6.33
Property of the Company of the Com				5	1 23	38			1			1			23	38			6.51
Property				1	1 2	4			1			1			4	4			5.07
Property				9	1 16							1			30				
Column   C				3	2 4/	1015			5			3 5.5			139	1015			6.84
Martin can by American plane agreed on the Plane agreed   1 m				1	1 1	3			1			1			3	3			7.23
March conclusions were not as colors and plant agreed   17   1   1   1   1   1   1   1   1				3	1 7	14			1			1			7				6.21
Second Content and Property a				4	1 1	3						1			3	.4			5.88
Main Company of Main Company	4826952			2	3 7	29			3 1			3 19.6			16	29			5.48
Margin   M	578804127	PREDICTED: protein unc-80 homolog isoform X3 [Homo sapiens]	3.43	4	1 12	47	0.933				1.177	1	76.78	3.43	16	47	3319	369.7	6.95
Applied   Marked By passed products on Telephone Whether Statem   14		hormonally up-regulated neu tumor-associated kinase [Homo sapiens]		1	1 1	2			1			1			2	2			9.13
Second   S		dual specificity protein phosphatase 19 isoform 2 [Homo sapiens]		2	1 1	14									2				8.07
			23.93	1 :	8 11	82		1:							29				4.61
March   Marc				2	5 9	29									23	29			7.65
Property		lysosome-associated membrane glycoprotein 1 precursor [Homo sapiens]		1 :	3 3	10									6	10			8.75
West   Miles				1	2 3	6			2			2 80.4			6	6			9.63
Section   Sect				1	1 1	4						2 92.0			2	- 4			7.21
Second   Commonwell   Commonw				1	2 10										15				5.34
Property				8	2 3										9				6.07
Marie Standard Stan	7705300		58.82	4	2 2	9	0.931		3	2.8	1.253	3 5.4	444.69	58.82	6	9	85	9.1	9.31
March   Marc	578816449	PREDICTED: sodium/potassium/calcium exchanger 2 isoform X3 [Homo sapiens]	3.42	2	1 3	18	0.931				1.110	1	46.14	1 3.42	4	18	644	71.6	6.27
Properties   Properties regular pergengengengengengengengengengengengengeng			4.07	2	1 3	13	0.931			3	3.207	1	29.77	7 4.07	5	13	369	44.1	7.61
Part   Company				1	1 2	2						1			2	2			7.30
March   Marc				3	2 2	4						1			4	4			6.15
1999				1 !	5 12				5			4 16.3			26				5.49
PRINCIPLO CONCESSION IN 18 1999 September 1 1 1 1				1	1 7							1			15				5.66
Process   Proc				3	1 3							1			5				
Program   Prog				1	1 62				1			2 22 1							
Margin   M				1	1 41	3/6						2 32.1			122	3/6			7.99
Section   Sect				2	1 1	2						1			2	2			11.53
Section   Sect				2	1 14	43						1			26	43			6.55
Section   Continues of the Continues of Prices Seguency   Co				3	2 4	9			2			2 60.9			9	9			7.53
Septical   Performance   Septical   Performance   Septical   Sep	4507131		24.42	1 :	2 2	9	0.928		3	3.4	1.237	3 10.5	307.89	24.42	6	9	86	9.7	4.67
Security		calmodulin-like protein 5 [Homo sapiens]		1 :	2 4	13									9	13			4.44
Selection   Sele				3	1 2	7			2 1			2 17.4			4	7			10.55
Applications   Paylog between places   Part   Part to form   Places supering   9.22   8   3   27   0.76   7   6.6   1.27   5   1.07   31.75   9.22   9   9.0   9		deoxycytidine kinase (Homo sapiens)		1	1 1	2			1			1			2	2			5.21
Part				4	2 7	18									13	18			5.64
Additional Continues and primal presents inform planes aspering   54.82   6   5   6   26   0.792   7   4.3   1.12   6   2.18   100,000   54.87   10   20   22   24.9   54.55   5.0   20   24.04   54.55   5.0   24.04   54.0		poly(U)-binding-splicing factor PUF60 isoform h [Homo sapiens]		8	3 3										9				5.33
24.04.00   1.05.					2 /	45									16				
Selection   Sele				2	1 2	26						5 21.8			16	26			6.90
Statistical		PREDICTED: sodium channel protein type 4 subunit alpha isoform X1 [Homo sapiens]		1	1 3	12						1			3	12			5.10
Seminorative   Semi			5.12	2	1 2	4	0.923				0.970	1	112 48	5 12	4	4	391	44.3	7.97
SECTION   SECT				1	1 1	10			2			2 1.6			2	10			6.79
Section   Sect	83582815		37.08	2	2 2	7	0.923		2 1	1.0	1.041	2 2.4	195.00	37.08	6	7	89	9.9	8.48
PREDICTID microtoxide-scale ross-leving factor 1 bottom XI (Heron sapiers)   5.46				6	1 3	9			1			1			5	9			9.74
SPECIFICE   Protein Hock hamolog 2 lauform Xe   Homo saplems   4.49				3	1 3				1			1			7				7.09
PREDICTID: Insolid 1.4.5Prignophate receptor type 1 bodom NO   1400   5.45   24   138   2695   30-5   6.1				6	3 51							1			81				5.31
1,424444   zisc finger and BB domain-containing protein a Spring and BB domain-containing protein and BB domain-containing protein a Spring and BB domain-containing protein and BB domain-containin				b .	1 4							1			8				5.53
PREFUTCAL   Insurance   Insu				3	1 15	138			1			30.5			24	138			6.11
Section Propriet Profite Rights Call Principles (Part Profite Rights Call Principles (Part Profite Rights Call Principles (Part Profite Rights Call Principles Rights Call Rights				2	1 2	5						1			2	5			6.92 8.70
PREDICTE unthreacherized protein Clourit Bisoform X2 [None septers]   6.12   1   7   72   0.920   4   3.4   6.618   2   8.4   199.42   6.12   10   22   898   10.6   6.2   11.7   11.7   11.7   12.5   13.5				9	1 3	11						1			10				4.58
Second Procession   Seco				1	1 7	77			1			2 88.4			10				6.27
1479-642   regulator of rhomosome condensation isoform. (Homo sapiens) 3.09 3 1 2 8 0.200 1 0.028 1 0.				2	1 1	3			1			1			3	3			5.94
3794444   APP-super pyrophosphatase (Homo sapiens)   15.07   1   2   3   7   0.919   2   2.18   0.988   2   51.3   20.06   15.07   6   7   21   24.3   34   31356984   1356984   14.0   14.0   15.07   1   1   1   1   1   1   1   1   1			3.09	3	1 2	8			1			1	65.12		6	8	421	44.9	7.52
13359688   CLLF-like MAVIL transmentance durain containing protein 2 loadrom 2 [Homo saplems]   9.23   2   1   1   3   0.919   1   0.047   1   0.75   1.044   1   2.019   1   0.047   1	37594464	ADP-sugar pyrophosphatase [Homo sapiens]	15.07	1 :	2 3	7	0.919		2 2	3.8	0.968	2 51.3		5 15.07	6	7			4.94
1897-13-66   extracelular sulfatines Gulf 1 precursor (Homo sapiens)   4.82   4   12   871   10.0   9.0   12.223371   10.0   1		CKLF-like MARVEL transmembrane domain-containing protein 2 isoform 2 [Homo sapiens]		2	1 1	3			1			1	76.31		3	3	195	21.4	9.95
1876/08615   non-receptor lyroine-protein histones PKZ (Platron sapients)   2.36   3   3   1136   12.5   1315   1316   1315				4	1 4	12			1			1			4	12			9.09
35133860   Serinic/Precinie-proteine) proteins proteins 2A 56 Alba regulatory suburt alpha isoform isoform 2 [H 3 0.3] 2   2   429   50.2   5.5				1	1 3	8			2 1			2 50.6			5	8			5.76
S0308-187   PREDICTED zinc finger CW-type PWWP domain protein 1 ladorm XT [Homo sapiens]		non-receptor tyrosine-protein kinase TYK2 (Homo sapiens)		1	1 3	3						1			3	3			7.15
691242   DOC-Interacting protein 13-alpha [Normo sapiens]   5.36   1   1   3   8   0.915   2   1.6   3.822   2   45.18   344.71   5.36   5   8   709   79.6   5.4   5.2   5.4   7.5   7.		serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform isoform 2 [H		2	1 1	2						1			2	2			5.78
2248331   apoptic protease activating factor 1 knofrm of libron sapiens    12.86   5   4   14   26   0.015   4   8   3   12.76   3   8   417.96   12.86   26   26   26   27.005   137.0   6.9   139.0   14.88   6.25   2   2   28.0   137.0   1.7   1.7   1.9		PKELDICIEU: zinc finger CW-type PWWP domain protein 1 isoform X7 [Homo sapiens]		4	1 4	29						1			8	29			7.74
91984773 MAD/Pit-hydrate ejmenses precursor (Homo sapiens) 6.25 1 1 1 2 0.015 1 1.190 1 44.88 6.25 2 2 288 31.7 7.4 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2		appointed a protection of the			1 3	8									5	8			5.41 6.44
2489399 protein ME72BMB isoform 1 [Homo saplems] 17.65 1 1 1 2 0.914 1 0.853 1 1 44.27 17.65 2 2 1 119 13.4 5.8 5.8 5.8 5.8 5.8 5.8 5.8 5.8 5.8 5.8				1	14	26						3 8.8			20	26			7.66
5788377033 PREDICTED: calcineurin-birding protein cabin-1 bortom X11 [Nomo sapiens] 4.04 9 1 1 13 2 0.914 2 7.8 83.0 9 1 1 19 2 0.912 2 7.8 83.0 9 1 1 19 1 19 1 19 1 19 1 19 1 19 1 1				1	1 1	2						1			2	2			5.80
1399298   Immunoglobulin lambdis-like polypeptide 1 isoform a precursor [Homo sapiers]   16.43   1   2   3   835   0.913   19   13.9   1.411   17   66.8   8818.09   16.43   7   835   213   22.9   10.0				9	1 11	37			2						20	32			6.58
20995597   UMP-OMP kinase losform b [Homo saplens]   4.47   2   1   1   2   0.912   2   2.4   1.102   2   11.7   33.53   4.47   1   2   179   20.2   7.6		immunoglobulin lambda-like polypeptide 1 isoform a precursor [Homo sapiens]		1 :	2 3			19			1.411 13	7 66.8			7				10.07
164382713 cadherin-5 preproprotein (Homo sapiens) 0.64 1 1 1 1 5 0.912 5 7.4 2.504 5 32.5 91.86 0.64 3 15 784 87.5 5.4 6857820 phosphaticlylinositol 5-phosphate 4-kinase type-2 alpha (Homo sapiens) 3.45 1 1 1 4 0.912 1 1.594 1 16.80 3.45 2 4 406 46.2 6.5	209915597	UMP-CMP kinase isoform b [Homo sapiens]	4.47	2	1 1	2					1.102	2 11.7	33.53		1	2	179	20.2	7.64
6657820 phosphatidylinositol 5-phosphate 4-kinase type-2 alpha (Homo supiens) 3.45 1 1 1 4 0.912 1 1.594 1 116.80 3.45 2 4 4.06 46.2 6.5				1	1 1	15									3	15			5.43
193083114 poly/(C)-binding protein 2 isoform g (Homo sapiens) 33.96 35 4 8 24 0.911 4 2.0 1.233 4 31.6 572.16 33.96 21 24 318 33.5 8.2			3.45	1	1 1	4	0.912		1		1.594	1	116.80	3.45	2	4	406	46.2	6.99
		poly(rC)-binding protein 2 isoform g [Homo sapiens]		5	4 8	24			1			4 31.6			21	24			8.24
				1	1 1	3						1			3	3			8.44
				2	1 5	16						1			11				6.58
126723547 protein NYNRIN [Homo saplens] 2.27 1 1 4 11 0.909 1 1.149 1 14.73 2.27 4 11 1898 208.2 8.0	126723547	protein NYNKIN [Homo saplens]	2.27	1 .	1 4	11	0.909				1.149	1	14.73	5 2.27	4	11	1898	208.2	8.02

										,							, ,		
Accession	Description	ΣCoverage	Σ# Proteins Σ# Uniqu	ue Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]			A8: 117/116 Variability [%]	Score A(3,6,7)		# Peptides A(3,6,7)	# PSM A(3,6,7)		MW [kDa]	calc. pl
531990811 151301228	ubiquitin-conjugating enzyme E2 A isoform 4 [Homo sapiens] pre-mRNA-processing factor 40 homolog A [Homo sapiens]	10.08	3	1	2	- 3	0.908		1	1.35		1	33.37 148.50	10.08	3	3	119 930	13.6	4.75 7.99
578805786	PREDICTED: bis(5'-adenosyl)-triphosphatase isoform X4 [Homo sapiens]	6.12	2	1	1	3	3 0.906		1	1.26		1	110.77	6.12	3	3	147	16.8	7.08
239735492	transcriptional activator Myb isoform 6 [Homo sapiens]	8.86	3	1	8	86	0.906		2 0.	1.41	7	2 12.6	83.33	8.86	16	86	745	83.6	7.24
530366140	PREDICTED: protein lin-9 homolog isoform X1 [Homo sapiens]	1.63	1	1	1	- 2	2 0.905		1	2.74		1	24.78	1.63	2	2	615	70.0	9.67
578824446	PREDICTED: mitochondrial inner membrane protease ATP23 homolog isoform X2 [Homo sapier	6.49	2	1	2		0.905		1	1.25		1	33.34	6.49	2	5	185	21.3	7.56
4505215 530360517	interstitial collagenase isoform 1 preproprotein [Homo sapiens]  PREDICTED: serine/threonine-protein kinase mTOR isoform X1 [Homo sapiens]	10.87	2	2	5	13	0.902		2 15.6	1.09		2 37.5	125.48 42.42	10.87	8	13	469 2549	54.0 288.7	6.96 7.17
296531459	band 4.1-like protein 5 isoform 2 [Homo sapiens]	6.55	6	1	4	34			1	1.27		1	27.71	6.55	4	34	687	77.5	6.79
93352551	CWF19-like protein 1 [Homo sapiens]	9.67	1	1	5	11	0.901		2 10.5	1.23	4 3	2 28.7	273.21	9.67	7	11	538	60.6	7.24
530367362	PREDICTED: EGF-containing fibulin-like extracellular matrix protein 1 isoform X2 [Homo sapien:	7.55	2	3	4	11			3 4.3			3 1.6		7.55	11	11	543	59.3	7.74
5031815	lysinetRNA ligase isoform 2 (Homo sapiens)	8.88	2	2	5	27			2 13.5			2 3.5		8.88	12	27	597	68.0	6.35
23238231 530382432	high mobility group nucleosome-binding domain-containing protein 3 isoform HMGN3b (Homo s PREDICTED: dystonin isoform X8 [Homo sapiens]	19.48	7	1	- 1	16			3 6.0	1.16 9.09		3 9.4	362.67 188.43	19.48	3	16 115	77 7709	8.4 875.1	10.26 5.35
4758226	transcription factor E2F2 [Homo sapiens]	2.29	1	1	1	110	0.899		1	1.23		1	25.07	2.29	1	2	437	47.5	4.87
96304457	low molecular weight phosphotyrosine protein phosphatase isoform d (Homo sapiens)	16.07	2	1	1	- 3	0.899		1	1.39		1	263.79	16.07	3	3	112	12.2	7.74
530423350	PREDICTED: importin-5 isoform X2 [Homo sapiens]	6.91	1	1	6	12			1	1.34		1	183.76	6.91	9	12		125.5	4.92
33188456	ubiquitin-conjugating enzyme E2 D2 isoform 2 (Homo sapiens)	29.66	7	2	2	- 6	0.897	:	2 21.			1	141.77	29.66	4	6	118	13.6	8.29
5453994 6912638	double-strand-break repair protein rad21 homolog [Homo sapiens] ras suppressor protein 1 isoform 1 [Homo sapiens]	4.91 26.71	1	2	3	10	0.897		2 22.2			2 18.0 4 23.2		4.91 26.71	9	10	631 277	71.6 31.5	4.65 8.65
528524494	dynein light chain roadblock-type 1 isoform b [Homo sapiens]	19.05	7	1	1	10	3 0.896		1 10.5	1.20		4 23.2	163.34	19.05	3	3	63	7.3	7.25
54792150	zinc finger protein 473 (Homo sapiens)	4.94	1	1	5	12			1	0.88		1	26.20	4.94	5	12	871	100.1	8.27
17105394	60S ribosomal protein L23a [Homo sapiens]	12.18	1	1	2	3	0.895		1	1.12		1	43.80	12.18	3	3	156	17.7	10.45
149944590	SRR1-like protein [Homo sapiens]	5.31	1	1	2	2	0.895		1	1.18		1	28.01	5.31	2	2	339	38.5	5.41
17158039	histone deacetylase 9 isoform 1 (Homo sapiens)	3.07	4	1	5	ç	0.895		1	14.78		1	29.14	3.07	7	9	1011	111.2	6.89
530418521 4507947	PREDICTED: zinc finger SWIM domain-containing protein 1 isoform X2 [Homo sapiens] tyrosinetRNA ligase, cytoplasmic [Homo sapiens]	1.03	1	1	1	1	0.894		2 9.:	1.14		2 6.9	29.47 140.71	1.03 8.90	1	1	485 528	55.0 59.1	7.42 7.05
56847620	transcription factor BTF3 homolog 4 isoform 1 [Homo sapiens]	24.68	1	1	2	10			1	2.20		1	58.08	24.68	4	10	158	17.3	6.35
557129022	ubiquitin carboxyl-terminal hydrolase 7 isoform 3 [Homo sapiens]	13.06	3	1	11	30	0.890		1	1.20		1	209.54	13.06	19	30	1003	116.9	5.90
9506363	SAM and SH3 domain-containing protein 3 [Homo sapiens]	4.21	2	1	1		0.889		2 9.1			2 17.5		4.21	3	5	380	41.6	5.27
396578115	IQ and AAA domain-containing protein 1 isoform 2 [Homo sapiens]	6.91	3	1	6	18			1	2.10		1	28.82	6.91	6	18	781	90.4	9.33
565324221 19913446	calcium-binding protein 39-like (Homo sapiens)	15.73 4.15	1	1	7	44	0.888			1.45		1	241.01 56.66	15.73 4.15	15	44	337 193	39.1 22.4	8.40 4.97
19913446 578804386	neuron-specific calcium-binding protein hippocalcin [Homo sapiens]  PREDICTED: septin-2 isoform X10 [Homo sapiens]	4.15 26.80	6	1	1 5	3	3 0.886 9 0.885		1	1.10		1	56.66 161.72	4.15 26.80	3	3	193 194	22.4	4.97 6.55
530389882	PREDICTED: kinesin-like protein KIF24 isoform X2 [Homo sapiens]	1.19	4	1	2		0.885		1	1.36		1	43.21	1.19	2	3	1007	110.4	7.53
194306543	oxidation resistance protein 1 isoform 2 [Homo sapiens]	2.50	11	1	2	4	0.883		1	0.94	1 '	1	109.60	2.50	4	4	839	93.7	5.19
578823270	PREDICTED: oxysterol-binding protein-related protein 8 isoform X6 (Homo sapiens)	6.38	5	1	6	22	0.000		1	0.81		1	130.93	6.38	10	22	847	96.9	7.55
124256474 530384769	diacylglycerol kinase gamma isoform 2 (Homo sapiens)  PREDICTED: Integrin beta-8 isoform X2 (Homo sapiens)	3.52 5.36	3	1	3	17	3 0.883 7 0.882		1	1.42		1	21.02 67.90	3.52 5.36	3	3	766 634	86.2 71.2	6.65 7.68
530384769	PREDICTED: integrin beta-8 isoform X2 [Homo sapiens]  PREDICTED: sperm-associated antiqen 1 isoform X2 [Homo sapiens]	5.36	21	1	5	19	0.002		2 1.4			2 1.6		5.36	10	17	634 884	71.2 98.8	6.87
14150098	transmembrane protein 79 [Homo sapiens]	2.03	1	1	1	- 13	1 0.880		1.	1.04	,	2 1.0	40.66	2.03	2	4	394	43.5	4.93
578803150	PREDICTED: exportin-1 isoform X5 [Homo sapiens]	6.97	5	3	6	15	0.879		3 21.6	1.62	2 :	3 1.0	203.56	6.97	14	15	904	104.1	5.78
118572606	hemicentin-1 precursor [Homo sapiens]	1.22	1	1	7	16			1	1.51		1	34.40	1.22	7	16	5635	613.0	6.49
530403141	PREDICTED: mirror-image polydactyly gene 1 protein isoform X2 [Homo sapiens]	3.29	3	- 1	2	14			4 5.3			4 13.7		3.29	6	14	365	42.6	6.05
530396574 56550081	PREDICTED: C2 domain-containing protein 3 isoform X5 [Homo sapiens] mitotic checkpoint protein BUB3 isoform b [Homo sapiens]	1.79 9.20	6	1	4	27	7 0.878 I 0.877		7 3.2			3 0.8 2 20.8		1.79 9.20	8	27	1676 326	186.3 36.9	8.40 6.84
153791662	coiled-coil domain-containing protein 71 [Homo sapiens]	9.42	1	1	5		7 0.876		2 24	1.42		20.0	22.57	9.42	5	7	467	49.6	11.80
525313660	24-hydroxycholesterol 7-alpha-hydroxylase isoform 3 [Homo sapiens]	3.70	5	1	2	11	0.875		1	1.97		1	141.91	3.70	5	11	297	34.5	8.37
545478755	protein arginine N-methyltransferase 5 isoform f [Homo sapiens]	11.16	6	1	4		0.875		1	1.63		1	210.98	11.16	6	6	466	53.5	6.14
530361637	PREDICTED: splicing factor 3A subunit 3 isoform X1 [Homo saplens]	5.13	2	1	2	- 6	0.874		1	1.10		1	62.09	5.13	4	6	448	52.4	5.27
530411988 565324225	PREDICTED: granulins isoform X1 [Homo sapiens] tyrosine-protein kinase BTK isoform 3 [Homo sapiens]	20.91 9.38	1	7	9	53	0.874		B 8.4	1.18		8 15.0	1500.57 35.41	20.91 9.38	21	53	593 693	63.5 79.9	6.83 7.46
4504297	histone H3.1 [Homo sapiens]	58.82	3	1	11	112			3 7.3			1	1749.57	9.38 58.82	7	112	136	15.4	11.12
530386628	PREDICTED: myosin regulatory light chain 10 isoform X1 [Homo sapiens]	25.85	1	1	3	- 1	7 0.865		1	1.13		1	133.93	25.85	7	7	147	16.9	4.70
242117893	apoptosis regulator BAX isoform sigma [Homo sapiens]	7.26	4	1	1	3	0.863		1	1.33		1	115.17	7.26	3	3	179	19.7	5.40
4506699	40S ribosomal protein S21 [Homo sapiens]	10.84	1	1	1	3	0.861		1	1.33		1	48.68	10.84	3	3	83	9.1	8.50
4759264	COP9 signalosome complex subunit 2 isoform 1 [Homo sapiens] ras-related GTP-binding protein A [Homo sapiens]	13.09 15.34	2	1	5		0.860 0.859		1 17.0	1.62		2 9.8	350.20 663.87	13.09 15.34	7	48	443	51.6 36.5	5.53
5729999 187608516	arf-GAP with colled-coil, ANK repeat and PH domain-containing protein 2 [Homo sapiens]	15.34	26	2	7	48	0.859		2 17.0		7	2 9.8 2 12.4		15.34	16	48	313 778	36.5 88.0	7.72 6.80
261244906	neurabin-1 isoform 5 [Homo sapiens]	7.34	8	1	5	16	0.858		1	1.12		1	27.79	7.34	5	16	1090	122.3	5.15
157671917	colled-coil domain-containing protein 178 isoform 2 [Homo sapiens]	6.88	2	1	7	23			1	1.16	8	1	28.49	6.88	7	23	829	97.5	6.25
157694524	plexin-D1 precursor [Homo sapiens]	2.18	1	1	5	18	0.855		1	1.21		1	44.21	2.18	5	18	1925	211.9	7.20
301601630 4505501	LIM and senescent cell antigen-like-containing domain protein 1 isoform b [Homo sapiens]	6.77 8.79	12	1	2	4	0.853 0.852		2 36.3	1.33		2 89.7	137.90 189.19	6.77 8.79	4	4	325 273	37.2 30.9	8.05
10864011	oxidized low-density lipoprotein receptor 1 isoform 1 [Homo sapiens] sulfide:quinone oxidoreductase. mitochondrial [Homo sapiens]	7.78	3	2	2	- 4	1 0.852		2 36.	2.64		2 89.7	189.19	8.79 7.78	4	4	273 450	49.9	7.28 9.11
530367595	PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X5 [Homo sapier	3.93	11	1	6	18	0.851		1	1.71		1	48.34	3.93	10	18	1247	134.0	7.50
4885099	carbonic anhydrase 3 [Homo sapiens]	13.85	1	1	2		0.850		1	1.12		1	47.70	13.85	4	4	260	29.5	7.34
33457348	UPF0556 protein C19orf10 precursor [Homo sapiens]	11.56	1	2	2	8	0.847		3 23.5			3 13.8		11.56	5	8	173	18.8	6.68
221136806	putative zinc finger CCHC domain-containing protein 18 (Homo sapiens)	3.47	1	1	2	10			2 2.:			2 5.0		3.47	2	10	403	45.1	7.39
24638446 15826852	histone H2A type 2-C [Homo sapiens]  Golqi resident protein GCP60 [Homo sapiens]	60.47 4.55	4	1	7	90	0.840		6 16.3	2.51 1.43		4 10.3	2331.87 272.25	60.47 4.55	21	90	129 528	14.0	10.90 5.06
15826852 46488915	astrotactin-2 isoform a precursor [Homo sapiens]	1.86	6	1	3	2	7 0.838		1	3.80		1	35.13	4.55 1.86	3	3	1288	142.5	5.06
526118265	Golgin subfamily A member 5 (Homo sapiens)	4.38	1	1	5	52			1	1.35		1	98.43	4.38	9	52		82.9	5.83
7706244	protein CutA isoform 2 precursor (Homo sapiens)	8.97	3	1	1	4	1 0.836		2 2.3			2 20.6		8.97	2	4	156	16.8	5.21
530408197	PREDICTED: alpha-hemoglobin-stabilizing protein isoform X2 [Homo sapiens]	12.75	1	1	1	- 2	0.836		1	1.28		1	52.86	12.75	2	2	102	11.8	5.00
578802647	PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo sapiens]	8.09	3	1	2	37			5 21.6			5 5.8		8.09	6	37	272	29.6	8.38
10863889 10835085	U4/U6.U5 tri-snRNP-associated protein 1 [Homo sapiens] metallothionein-1H [Homo sapiens]	6.00	1	- 1	5	54	0.831 0.828		1	0.99		1	296.55 115.11	6.00 13.11	12	54	800 61	90.2	6.13 8.06
7669542	paired box protein Pax-8 isoform PAX8E [Homo sapiens]	6.97	4	1	2		3 0.825		1	1.06		1	25.20	6.97	2	3	287	31.0	8.54
530414991	PREDICTED: transmembrane protein 161A isoform X1 [Homo sapiens]	2.26	3	1	2	17	7 0.814		3 7.4	3.99	8 2	2 52.1		2.26	4	17	354	39.2	8.38
578836047	PREDICTED: probable ATP-dependent RNA helicase DDX27 isoform X1 [Homo sapiens]	6.41	2	2	5	9	0.812		2 10.2	1.09	4 2	2 2.1	28.34	6.41	5	9	421	48.8	10.11
578816585	PREDICTED: DENN domain-containing protein 4C isoform X4 [Homo sapiens]	1.85	5	1	3	60	0.808		3 6.0	1.26	8	3 3.6		1.85	7	60	1456	162.1	6.57
530402083	PREDICTED: A-kinase anchor protein 11 isoform X4 [Homo sapiens]	2.51	5	1	7	36	0.804		1				80.38	2.51	11	36	1796	198.4	5.64
156938287 578824412	SH2 domain-containing protein 5 isoform 1 [Homo sapiens]	4.73 3.12	1	1	2		0.804 0.799		1	1.05		1	31.73 34.30	4.73 3.12	6	25	423 2340	46.8 250.5	8.51 8.51
578824412 83267866	PREDICTED: neuron navigator 3 isoform X3 [Homo sapiens] dynein light chain 1, cytoplasmic [Homo sapiens]	3.12 24.72	1	1	1	25	0.799		1	0.76		1	34.30 36.58	3.12 24.72	8	25	2340 89	250.5 10.4	7.40
8923579	ragulator complex protein LAMTOR1 [Homo sapiens]	19.25	1	1	1		2 0.792		1	0.62		1	38.30	19.25	2	2	161	17.7	5.15
578811583	PREDICTED: N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase isoform X7 [Hom	6.43	3	1	2	20	0.785		1	0.93	6	1	92.17	6.43	3	20	311	35.7	8.40
23503317	colled-coil domain-containing protein 96 [Homo sapiens]	4.14	1	1	3	8	0.781		1	1.18		1	31.13	4.14	5	8	555	62.7	4.94
530407863	PREDICTED: calcium-regulated heat stable protein 1 isoform X1 [Homo sapiens]	16.07	2	2	2		0.778		2 19.3	1.34		2 7.2	78.20	16.07	5	5	168	18.1	8.85
530406506 386642875	PREDICTED: spatacsin isoform X2 (Homo sapiens)	5.60 3.26	5	1	11	46	0.769			1.09		1	60.73 32.04	5.60 3.26	20	46	2357 430	269.0 47.3	5.96 6.06
386642875 4503519	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase isoform 3 [Homo : eukaryotic translation initiation factor 3 subunit F [Homo sapiens]	3.26 10.08	1	1	2		2 0.765		1	1.24 2.36		1	32.04 70.25	3.26 10.08	2	2	430 357	47.3 37.5	6.06 5.45
475808427	POTE ankyrin domain family member I [Homo sapiens]	15.35	24	1	20	2067			3 3.4			3 2.0		15.35	47	2067	1075	121.2	6.21
153791352	POTE ankyrin domain family member F [Homo sapiens]	22.60	22	1	21	1284	0.740	10	0 8.9	1.28	5 10	0 21.3	33815.97	22.60	50	1284	1075	121.4	6.20
63055057	beta-actin-like protein 2 [Homo sapiens]	43.35	2	1	17				1	1.39		1	35106.48	43.35	50	1425		42.0	5.59
578804287 222144324	PREDICTED: integrin alpha-6 isoform X2 [Homo sapiens]	5.77 72.09	4	1	6	51 144			2 8.9	0.62		1	37.47 5176.50	5.77 72.09	12	51		117.7	6.86 4.84
222144324	myosin regulatory light chain 12B [Homo sapiens]	12.09	6	- 1	12	144	· U.652		2 8.4	0.89	,		5176.50	12.09	36	144	1/2	19.8	4.84

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	7# DS14-	A8: 115/114	A8: 115/114 Count	A8: 115/114 Variability [%]	AR: 117/114	AR: 117/116 Count	A8: 117/116 Variability [%]	Score 4/3 £ 7\	Coverage A(3 4 7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pl
578820587	PREDICTED: paired box protein Pax-6 isoform X8 [Homo sapiens]	3.94	Z# Proteins	Z# Ornque Peptides	Z# replides	Z# PSWS	AB: 115/114 0.616		No. 113/114 Variability [76]	AB: 117/116 1.243		Mo. 117/110 Valiability [76]	22.51	3.94	# replices A(3,0,7)	# F3M A(3,0,7)	355	39.2	9.23
300360487	protein canopy homolog 2 isoform 2 precursor [Homo sapiens]	19.05		, 1		3				1.243			84.44	19.05	3	3	355	9.1	7.30
578807667	PREDICTED: major facilitator superfamily domain-containing protein 1 isoform X1 [Homo sapiel	6.11		1 1		3			1	1.050			31.80		3	3	475	51.7	7.36
530391566	PREDICTED: terminal uridylyltransferase 7 isoform X4 [Homo sapiens]	6.59	8	7 1	11	22	0.494			1.068	1		36.90	6.59	11	22	1381	157.7	6.47
94536743	protein DDX26B [Homo sapiens]	8.71		1 1	. 8	17	0.479	,	1				21.17	8.71	10	17		96.6	8.73
530378724	PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sapiens]	4.08	4	7 3	3 24	198	0.478	3	5 20.3	1.052		10.8	1021.39	4.08	46	198	4609	526.8	6.01
13430848	nuclear receptor subfamily 1 group D member 1 [Homo sapiens]	3.75		1 1	3	4	0.477	,	ı	4.626	1		24.84	3.75	3	4	614	66.8	8.50
530384633	PREDICTED: uncharacterized protein KIAA0895 isoform X3 [Homo sapiens]	5.82		1 1	. 2	134	0.471		1	1.099	1		152.73	5.82	4	134	275	32.1	7.84
218505779	protocadherin-15 isoform CD1-6 precursor [Homo sapiens]	0.90		3 1	2	6	0.433	3	1	1.309	1		42.47	0.90	4	6	1886	208.2	5.11
297206791	fibrous sheath-interacting protein 2 [Homo sapiens]	4.26	30	1	32								109.07	4.26	45	73		789.4	6.68
	kinesin-like protein KIF21B isoform 4 [Homo sapiens]	6.40	54	9 2									916.71	6.40	31	116		179.6	
359718912	probable E3 ubiquitin-protein ligase HECTD4 [Homo sapiens]	2.73		1 1	13								54.90	2.73	23	48	4284	469.7	6.15
5453908	phosphatidylinositol transfer protein alpha isoform [Homo sapiens]	6.67		1 1	1 2								192.87	6.67	5	5	270	31.8	6.55
255652953	zinc finger CCCH domain-containing protein 18 isoform 2 [Homo sapiens]	0.84		2 1	1	2							27.93	0.84	2	2	953	106.3	8.32
62955803	nucleoporin NUP188 homolog (Homo sapiens)	2.12			4								66.71	2.12	10			195.9	
	ATP-dependent RNA helicase DHX29 [Homo sapiens]	3.29	35		1 6								150.86	3.29	14	20		155.1	8.09
20070266	GTP-binding protein REM 1 [Homo sapiens]	5.37	1	5 2		7							88.87	5.37	5	7	298	32.9	
222537743	phosphatidylinositol phosphatase PTPRQ precursor [Homo sapiens]	1.70		7 1									347.73	1.70	10	167		257.1	5.73 7.81
47578107 126116589	nipped-B-like protein isoform B [Homo sapiens] fibrocystin-L precursor [Homo sapiens]	5.90 0.78		1	20								494.34 124.78	5.90 0.78	33	74		304.2 465.4	
50428940	mediator of RNA polymerase II transcription subunit 25 [Homo sapiens]	0.78		1		17							124.78 31.57	0.78	9	1/	4243 747	465.4 78.1	8.34
229892308	shuqoshin-like 2 isoform 2 [Homo sapiens]	3.65			6	11							39.27	3.65	10	11		143.9	
4758302	enhancer of rudimentary homolog (Homo sapiens)	5.77		1 1		3							78.86	5.77	3	3	104	12.3	
242332527	uncharacterized protein C5orf42 [Homo sapiens]	2.38				_							55.85	2.38	13	19	3197	361.5	6.99
27734719	thiamine transporter 1 [Homo sapiens]	3.62	1	2 1	. 2								74.91	3.62	4	5	497	55.4	
28827813	NACHT, LRR and PYD domains-containing protein 14 [Homo sapiens]	3.75		2 1	. 5	27	,						30.82	3.75	9	27		124.7	6.61
	phosphatidylinositol transfer protein beta isoform isoform 2 [Homo sapiens]	13.60		3 1	5	16							189.66	13.60	12		272	31.6	
530380645	PREDICTED: BTB/POZ domain-containing protein KCTD16 isoform X1 [Homo saplens]	6.54		1 1	4	6							46.61	6.54	6	6	428	49.1	
21359947	popeye domain-containing protein 3 (Homo sapiens)	2.75		1 1	1	3	1						43.99	2.75	3	3	291	33.8	7.96
578807537	PREDICTED: serine/threonine-protein phosphatase 2A regulatory subunit B" subunit alpha isofo	3.48		3 1	3	8	1						26.49	3.48	4	8	1150	130.2	5.21
	G protein-coupled receptor kinase 6 isoform C [Homo sapiens]	4.64		3 1	3	10	)						75.28	4.64	5	10	560	64.3	8.44
7019435	interleukin-17C precursor [Homo sapiens]	3.05		1 1	1	2	2						23.75	3.05	2	2	197	21.8	8.12
578814066	PREDICTED: filamin-C isoform X1 [Homo sapiens]	3.99		3 1	12	78	В						1949.40	3.99	30	78	2632	281.4	6.04
530369681	PREDICTED: striated muscle preferentially expressed protein kinase isoform X2 [Homo sapiens]	3.43	2	3 1	14	26							38.42	3.43	18	26	3206	347.6	8.50
578836045	PREDICTED: ubiquinol-cytochrome-c reductase complex assembly factor 1 isoform X1 [Homo s	2.27	10			9	,						158.37	2.27	3	9	220	25.0	
530363589	PREDICTED: zinc finger MYM-type protein 4 isoform X1 [Homo sapiens]	6.25	11		1 8								42.14	6.25	11	61	1551	173.0	
578817778	PREDICTED: serine/threonine-protein kinase WNK2 isoform X10 [Homo sapiens]	1.03	11		3		8						81.77	1.03	6	8	2227	234.8	
530390571	PREDICTED: nucleoredoxin-like protein 2 isoform X2 [Homo sapiens]	4.32		1 1			)						48.17	4.32	4	10	139	15.5	
578819920	PREDICTED: polycomb group RING finger protein 5 isoform X5 [Homo sapiens]	5.26	2		1 2		1						90.99	5.26	5	7	190	22.0	
530384400	PREDICTED: nucleotide-binding oligomerization domain-containing protein 1 isoform X9 [Homo	5.96	51	5 1	7	52							242.18	5.96	11	32	705	79.4	
530424332	PREDICTED: epithelial splicing regulatory protein 2 isoform X2 [Homo sapiens]	4.05		2 1	4	_							78.34	4.05	8	8	716	77.2	
530387276	PREDICTED: WD repeat-containing protein 60 isoform X1 [Homo sapiens]	3.42		1		10							34.28	3.42	1	16 10	878 631	98.7 71.9	
578822940	PREDICTED: protein asunder homolog isoform X4 [Homo sapiens]	5.23		1	4								30.29	5.23	6				6.62 5.69
530363232 88703062	PREDICTED: synaptonemal complex protein 1 isoform X4 [Homo sapiens]  40S ribosomal protein S4, Y isoform 2 [Homo sapiens]	6.30 2.28		1 1		21							53.86 47.10	6.30 2.28	15	21	921 263	107.6 29.3	
323510690	4US ribosomai protein S4, Y isoform 2 [Homo sapiens] serine/threonine-protein kinase Nek2 isoform 2 [Homo sapiens]	7.29			1	2							47.10 37.68	7.29	1	2	263 384	29.3	10.08 8.41
578806449	PREDICTED: protein SEC13 homolog isoform X6 [Homo sapiens]	5.19			4	. 2							29.21	5.19	4	3	308	34.0	
53831995	splicing factor 3A subunit 1 isoform 2 [Homo sapiens]	5.19		) 1	5								29.21	5.19	5	10	728	81.6	
	PREDICTED: exocyst complex component 2 isoform X1 [Homo sapiens]	5.52		1 1									51.17	5.52	9	44		104.0	
295789158	sodium-dependent phosphate transport protein 2B isoform b [Homo sapiens]	4.06		2 1	4								22.14	4.06	4	5	689	75.5	
41581463	formin-binding protein 1-like isoform 2 [Homo sapiens]	11.52		1	7	39							26.00	11.52	7	39	547	63.5	6.19
222352143	TBC1 domain family member 2A isoform 2 [Homo sapiens]	3.49		3 1	3								29.00	3.49	3	4	917	104.0	
9966851	cysteinyl leukotriene receptor 2 [Homo sapiens]	4.34		1	2	- 11							21.69		2	11		39.6	
189409140	telomeric repeat-binding factor 1 isoform 2 [Homo sapiens]	7.40		1 1	4	7	-						51.50	7.40	4	7	419	48.2	
22027514	cell division cycle-associated protein 7 isoform 2 [Homo sapiens]	7.55		5 0	4	31							66.20	7.55	7	31	371	42.5	
530416714	PREDICTED: prostate tumor-overexpressed gene 1 protein isoform X1 [Homo sapiens]	6.50		1 1	3	8	1						22.29	6.50	4	8	431	47.8	9.88
530372667	PREDICTED: plexin-B1 isoform X3 [Homo sapiens]	2.23		3 1	4	13							47.39	2.23	4	13	1211	135.1	6.33
530373023	PREDICTED: CUB domain-containing protein 1 isoform X1 [Homo sapiens]	2.99		2 1	4	6							32.20	2.99	4	6	770	86.0	7.64
55770876	neurogenic locus notch homolog protein 4 preproprotein [Homo sapiens]	0.75		1 1	3	4	ı						24.41	0.75	3	4	2003	209.5	5.73
222352168	protein ANKUB1 [Homo sapiens]	0.92		1 1	1	1							20.17	0.92	1	1	544	61.2	9.20
578832581	PREDICTED: zinc finger protein 532 isoform X14 [Homo sapiens]	2.45	14	1 1	4	6							40.63	2.45	4	6	1060	114.0	8.54

## Appendix B iTRAQ Set 2

578806381 93204867 612407822 557878699	Description dual oxidase 2 precursor [Homo saplens] PREDICTED: kinesin-like protein KIF15 isoform X2 [Homo saplens] probable G-protein coupled receptor 158 precursor [Homo saplens]	ΣCoverage 0.52 1.40	35	1	1 2	4	1.755		A8: 115/114 Variability [%]	1.196	1	()	84.85	0.52	,	4 4	# AAs 1548	MW [kDa] 175.3	calc. pl 3 7.85
578806381 93204867 612407822 557878699	PREDICTED: kinesin-like protein KIF15 isoform X2 [Homo sapiens]	1.40																	
612407822 557878699			31	1	1 2	3	1,711		1	2.833			46.01	1.40		3 3	1285	147.9	
557878699		1.32	32		1 2	3	1.511		1	1.597			39.60	1.32		3 3	1215		
557878699	carcinoembryonic antigen-related cell adhesion molecule 6 preprop	2.91	1		1 1	2	1.447		1	1.125			64.62	2.91		2 2	344		
578813594	ubiquitin-fold modifier 1 isoform 2 [Homo sapiens]	42.17	3	1	1 1	3	1.415	1	1	1.088	1		200.01	42.17		3 3	83	8.9	9 9.31
	PREDICTED: actin, cytoplasmic 1 isoform X1 [Homo sapiens]	95.26	1	1	1 23	2814	1.414	1	1	1.324	1		133155.76	95.26	6	7 2814	253	28.2	2 5.34
17865802	vacuolar protein sorting-associated protein 4B [Homo sapiens]	5.18	1	1	1 1	2	1.349		1				100.74	5.18		2 2	444		
530416619	PREDICTED: sodium/potassium-transporting ATPase subunit alpha	0.63	1	1	1 1	2	1.334		1	1.392	1		29.40	0.63		2 2	1261		
27501446	density-regulated protein [Homo sapiens]	9.09	1	1	1 1	3	1.331		1	1.212	1		213.48	9.09		3 3	198	22.	
14790190	msx2-interacting protein [Homo sapiens]	0.14	1	1	1 1	3	1.271		2 61.3	2.977		160.3	19.72	0.14		2 3	3664	402.0	0 7.64
	serine/threonine-protein phosphatase 4 regulatory subunit 2 [Hom	4.08	1	1	1 1	1	1.269	1	1	1.443	1		44.84	4.08		1 1	417	46.9	9 4.54
	latexin [Homo sapiens]	4.50	1	1	1 1	2	1.259		1	0.901	1		39.36	4.50		2 2	222		
	PREDICTED: collagen alpha-1(XXVII) chain isoform X3 [Homo sapi	0.74	4	1	1 1	8	1.259		5.2	1.270	4	31.2		0.74		2 8	1087		
	synaptotagmin-like protein 1 isoform 2 [Homo sapiens]	4.55	9		2 2	4	1.245		2 40.3	1.152		25.8		4.55		4 4	550		
	small nuclear ribonucleoprotein F [Homo sapiens]	15.12	1	1	1 1	3	1.230		1	1.133	1		218.00	15.12		3 3	86		
	PREDICTED: protein dopey-2 isoform X1 [Homo sapiens]	0.44	51	1	1 2	4	1.220		1	0.645	1		44.37	0.44		4 4	2298		
	tubulin beta-4A chain isoform 3 [Homo sapiens]	53.15	6		1 16	139	1.189		1	1.178			5325.57	53.15	4	4 139			
530422607 4885099	PREDICTED: rho guanine nucleotide exchange factor 6 isoform X5	2.25 3.46	4		1	1	1.172		1	1.096			26.38 87.97	2.25		1 1	622 260		
	carbonic anhydrase 3 [Homo sapiens] PREDICTED: transcription factor 7 isoform X10 [Homo sapiens]	2.33	72		1	3	1.169			2.079			27.87	2.33		3 3	258		
	small integral membrane protein 24 precursor [Homo sapiens]	15.38	12			2	1.162			1.247			109.38	15.38		2 2	130		
		1.52	- 1		1	3	1.159		3 16.0			4.4		1.52		3	1515		
	glycogen debranching enzyme isoform 2 [Homo sapiens] lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [f	2.80	3		2 2	- /	1.159		3 16.0	0.962 1.388		4.4	46.78	2.80		4 /	322		
	eukarvotic translation initiation factor 6 isoform a [Homo sapiens]	23.67	1		2 2	2 0	1.154		3 6.0	1.046		5.6		23.67		2 2	245		
	PREDICTED: mini-chromosome maintenance complex-binding prot	1.36	2		1 1	1	1.151		1	1.099		5.0	31.94	1.36		1 1	587		
	alpha-endosulfine isoform 8 [Homo sapiens]	19.05	5			6	1.145		65	0.947		5.6		19.05		3 6	105		
	protein-tyrosine kinase 2-beta isoform b [Homo sapiens]	1.45	3	-	1	3	1.144		0.0	0.947	-	5.0	129.86	1,45		3 3	967		
	PREDICTED: uveal autoantigen with colled-coil domains and ankyri	0.72	5		1	1	1.144		1	1.454			22.10	0.72		1 1	1392		
	transcription elongation factor A protein-like 3 [Homo sapiens]	10.50	1		1	3	1.140		1	1.136			204.75	10.50		3 3	200		
	ras-related protein Rab-35 isoform 1 [Homo sapiens]	18.41	21	-	1 4	22	1.135		1	1.402			1079.99	18.41	1	1 22			
	CUGBP Elav-like family member 2 isoform 4 [Homo sapiens]	10.66	17		2 2	4	1.133		2 13.1	1.427		26.8		10.66		4 4	488		
	minor histocompatibility protein HA-1 isoform 1 precursor [Homo s	2.02	5		2 2	8	1.133		3 3.2	0.950	-	4.6		2.02		6 8	1136		
	PREDICTED: tyrosine-protein kinase SgK223 isoform X1 [Homo sar	0.57	1	1	1 1	1	1.133		1	1.595			28.32	0.57		1 1	1406		
	protein NDRG1 isoform 3 [Homo sapiens]	4.47	3	1	1 1	3	1.128		1	1.001	1		169.55	4.47		3 3	313		
	nuclear receptor corepressor 1 isoform 3 [Homo sapiens]	0.21	11	-	1 1	2	1.125		1	0.863			16.70	0.21		2 2	2337		
	PREDICTED: tripeptidyl-peptidase 2 isoform X4 [Homo sapiens]	1.89	5		2 2	17	1.124		7 39.3	1.054		12.4		1.89		6 17			
	PREDICTED: centrosomal protein of 290 kDa isoform X3 [Homo sa	0.30	5	1	1 1	2	1.122		1	1.483	1		27.75	0.30		2 2	2353	275.6	6 6.10
5031711	eukaryotic translation initiation factor 1b [Homo sapiens]	26.55	2		2 2	6	1.122		2 7.0	1.191		3.3	407.90	26.55		6 6	113		
	ras-related protein Rab-5B isoform 2 [Homo sapiens]	27.01	5		2 4	15	1.122		2 8.8	1.021		29.3	621.10	27.01	1	2 15	174	19.	1 7.30
	AP-3 complex subunit delta-1 isoform 2 [Homo sapiens]	1.13	3	1	1 1	3	1.120		1	1.110	1		161.17	1.13		3 3	1153		
14110414	heterogeneous nuclear ribonucleoprotein D0 isoform c [Homo sapir	29.41	9	1	1 9	40	1.119		2 17.1	1.129	:	0.7	1708.57	29.41	2	0 40			8 8.16
6912242	DCC-interacting protein 13-alpha [Homo sapiens]	3.53	1	1	1 1	2	1.117	1	1				79.86	3.53		2 2	709	79.6	
7662502	malignant T-cell-amplified sequence 1 isoform 1 [Homo sapiens]	19.34	2		2 2	6	1.116		2 22.1	0.881		32.8	307.93	19.34		6 6	181	20.5	5 8.82
578826489	PREDICTED: uncharacterized protein LOC102723683 [Homo sapier	2.55	1	1	1 1	1	1.116		1	1.003	1		27.21	2.55		1 1	353	38.0	
282847388	uncharacterized protein C10orf62 [Homo sapiens]	3.14	1	1	1 1	1	1.115	5	1	1.365	1		25.08	3.14		1 1	223	25.	1 7.59
578835493	PREDICTED: glycogen phosphorylase, brain form isoform X1 [Hom	7.47	1	1	1 6	48	1.115	1	1	1.056	1		1923.36	7.47	1	6 48	843	96.6	6.86
	eukaryotic translation initiation factor 4 gamma 1 isoform 4 [Homo	0.78	7	1	1 1	3	1.115		1	1.087	1		97.94	0.78		3 3	1404		
	PREDICTED: prefoldin subunit 3 isoform X1 [Homo sapiens]	6.25	2	1	1 1	1	1.114		1	1.087	1		27.08	6.25		1 1	192		
10863895	thymosin beta-10 [Homo sapiens]	31.82	1	1	1 3	23	1.114		1	1.192	1		554.03	31.82		6 23			
	PREDICTED: FK506-binding protein 15 isoform X2 [Homo sapiens]	2.52	3		2 2	4	1.114		1	1.032	1		159.34	2.52		4 4	1151		
4557663	immunoglobulin-binding protein 1 [Homo sapiens]	6.49	1	1	1 1	3	1.113		1	1.058	1		294.56	6.49		3 3	339		
530367723	PREDICTED: HEAT repeat-containing protein 5B isoform X1 [Homo	0.37	4	1	1 1	2	1.113		1	1.392	1		20.91	0.37		2 2	1881		
530427505	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X	6.07	8	-	1 4	8	1.112		6.6	1.124	-	25.3	197.66	6.07		8 8	676 358		
166706885	dematin isoform 3 [Homo sapiens]	5.59 7.95	6		1	2	1.110		1	1.088			92.88	5.59		2 2	358 151		
	26S proteasome non-ATPase regulatory subunit 10 isoform 2 [Hor		2		1	3	1.109		2 10.5	1.113		31.0	111.53	7.95		3 3			
	vacuolar fusion protein MON1 homolog B isoform 3 [Homo sapiens angiomotin-like protein 2 isoform 3 [Homo sapiens]	1.50	1		1	2	1.109		2 10.5	2.746 1.003		21.0	29.56 28.22	1.50 2.32		1 2	401		
	PREDICTED: kinesin-like protein KIF21A isoform X9 [Homo sapiens]	1.00	17			- 1	1.109			1.660			26.67	1.00		1 1	1607		
		1.13	17			- 1	1.106			1.629			24.51	1.13		1	529		
	YTH domain-containing family protein 2 isoform 2 [Homo sapiens] apolipoprotein F precursor [Homo sapiens]	4.29	2			1	1.106		1	1.629			163.22	4.29		1 1	326		
	PREDICTED: dihydropyrimidine dehydrogenase [NADP(+)] isoform	1.46	1		1	2	1.100		1	1.108			140.26	1.46		3 3	889		
	SLIT and NTRK-like protein 1 precursor [Homo sapiens]	1.44	1			2	1.100			1.031			33.34	1.44		2 2	696		
	protein SPT2 homolog [Homo sapiens]	1.44	23		1	14	1.100		5 17.4	1.031		39.0		1.44		5 14	685		
	COMM domain-containing protein 10 [Homo sapiens]	5.94	1		1 1	14	1.099		17.4	1.205		39.0	269.18	5.94		3 3	202		
	PREDICTED: eukaryotic translation initiation factor 3 subunit L isofi	2.79	A		1	3	1.099		1	1.197			174.81	2.79		3 3	466		
	PREDICTED: editalyotic translation initiation ractor 3 subdime ison	1.72	7		1	3	1.098		1	1.097			60.02	1.72		3 3	583		
	PREDICTED: U1 small nuclear ribonucleoprotein 70 kDa isoform X2	2.57	2	1	i	3	1.098		1	0.987			147.29	2.57		3 3	428		
	PREDICTED: actin-related protein 2/3 complex subunit 5-like prote	16.99	1	1	1 3	13	1.097		1	1.172	1		448.78	16.99		8 13			
	PREDICTED: E3 SUMO-protein ligase RanBP2 isoform X5 [Homo sa	0.45	32	1	1 2	8	1.096		1	1.175	1		103.57	0.45		6 8	3136		
10880134	beta-arrestin-1 isoform B [Homo sapiens]	6.10	8	1	1 2	13	1.095		2 13.0	0.953	1	47.0	374.87	6.10		6 13	410	46.3	3 6.34
	AMP deaminase 2 isoform 3 [Homo sapiens]	0.79	5	1	1 1	2	1.094		1	1.097	1		31.76	0.79		2 2	760		
10863901	MAP kinase-activated protein kinase 2 isoform 1 [Homo sapiens]	3.24	3	1	1 1	3	1.094	1	1	1.415	1		91.59	3.24		3 3	370	42.2	2 8.25
530397816	PREDICTED: probable ATP-dependent RNA helicase DDX6 isoform	7.87	2		2 2	5	1.092	2	2 8.3	1.065	:	87.1	215.88	7.87		5 5	483	54.4	4 8.66
	PREDICTED: RUN domain-containing protein 3B isoform X3 [Homo	1.79	1	1	1 1	1	1.091		1	1.413			30.87	1.79		1 1	336		
55743118	rab3 GTPase-activating protein catalytic subunit isoform 2 [Homo s	0.82	2	1	1 1	2	1.091		1	1.069	1		38.94	0.82		2 2	981	110.5	5 5.55
578822867	PREDICTED: lymphoid-restricted membrane protein isoform X10 [F	2.91	2	1	1 1	4	1.091		2 10.9	1.068		5.1	74.92	2.91		2 4	446	50.4	4 6.25
	PREDICTED: colled-coll domain-containing protein KIAA1407 isofor	1.95	3		2 2	3	1.091		2 10.3	1.512		50.9	30.55	1.95		3 3	615	72.4	
	PREDICTED: phosphoribosylformylglycinamidine synthase isoform	1.27	2	1	1 1	1	1.090		1	1.076	1		35.50	1.27		1 1	947		
	protein FAM114A2 [Homo sapiens]	2.18	2	1	1 1	3	1.090		1	1.004	1		220.81	2.18		3 3	505		
	U6 snRNA-associated Sm-like protein LSm7 [Homo sapiens]	32.04	1	1	2 2	8	1.088		5.9	1.295	1	12.4		32.04		6 8	103		
	zyxin [Homo sapiens]	9.44	3	1	3 3	15	1.088		3.5	1.126	Ę	19.4		9.44		9 15	572		
	replication protein A 32 kDa subunit isoform 2 [Homo sapiens]	12.64	3	1	1 1	3	1.088		1	1.397	1		185.33	12.64		3 3	174		
530364259	PREDICTED: torsin-1A-interacting protein 2 isoform X3 [Homo sapi	6.81	1	1	1 1	3	1.087		1	0.886	1		134.21	6.81		3 3	470		
	serine/arginine-rich splicing factor 2 [Homo sapiens]	11.76	2	1	2 2	8	1.087		3.1	1.827	1	153.2		11.76		5 8	221		
	PREDICTED: tRNA pseudouridine(38/39) synthase isoform X2 [Hor	3.98	3	1	1 1	- 1	1.087		1	1.409	1		24.38	3.98		1 1	176		
	DNA ligase 1 isoform 3 [Homo sapiens]	0.94	5	1	1 1	- 1	1.086		1	1.338	1		28.67	0.94		1 1	851	93.9	9 6.01
	kelch-like protein 35 [Homo sapiens]	1.20	1	1	1 1	3	1.086		1	1.125	1		58.25	1.20		3 3	583		
	PREDICTED: serine/threonine-protein kinase OSR1 isoform X1 [Hor	1.74	2	1	1 1	2	1.086		1	1.097	1		39.40	1.74		2 2	460		
	PREDICTED: S-formylglutathione hydrolase isoform X1 [Homo sapi	39.01	1	1	7 7	28	1.085		0 4.9	1.115	10	7.8		39.01	1	9 28			
	inositol monophosphatase 2 [Homo sapiens]	7.99	1	1	1 1	3	1.085		1	0.980	1		264.24	7.99		3 3	288		
	serine/threonine-protein phosphatase 5 isoform 2 [Homo sapiens]	2.31	2	1	1 1	1	1.085		1	1.184	1		20.04	2.31		1 1	477		
	cytochrome b-245 heavy chain [Homo sapiens]	2.98	1	1	1 1	2	1.084			1.276			102.68	2.98		2 2	570		
94721252	vesicle-associated membrane protein-associated protein A isoform	5.62	2		1	3	1.084			1.005	1		73.89	5.62		3 3	249		
530393504	PREDICTED: annexin A7 isoform X2 [Homo sapiens]	3.76	4		1	3	1.083	1		1.128			361.15	3.76		3	426	46.0	0 7.18

												•							
Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs			A8: 115/114 Variability [%]		A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)		7) # Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs		
388240801	lamin-B2 [Homo sapiens]	7.90	1	4	4 4	15	1.0		5 1.	2 1.088	5	8.5	838.25	7.90	12	2 15	620	0 69.9	
53831995 578806449	splicing factor 3A subunit 1 isoform 2 [Homo saplens] PREDICTED: protein SEC13 homolog isoform X6 [Homo saplens]	1.24 4.87	2		1 1	1	1.0		1	1.217	1		30.64 31.60	1.24 4.87			728		
530407875	PREDICTED: protein Sects nomonog soform X6 (nomo sapiens) PREDICTED: RNA-binding protein FUS isoform X3 (Homo sapiens)	10.28			2 2	1	1.0		3 0.		1	14.3		10.28			300		
	small nuclear ribonucleoprotein E [Homo sapiens]	27.17	1		1 1	3	1.0		1	0.764	1	14.3	232.16	27.17		3 3	92		
	nuclear autoantigen Sp-100 isoform 2 [Homo sapiens]	3.30	6	1	1 5	30	1.0		1				359.62	3.30	10	2 30	879		
578819255	PREDICTED: AP-3 complex subunit mu-1 isoform X1 [Homo sapien	5.98	8		2 2	10	1.0	1	1	1.422	1		237.75	5.98		5 10	418	8 46.9	9 6.93
254028213	IQ domain-containing protein F6 [Homo sapiens]	6.54	2	1	1 1	1	1.0	1	1	1.263	1		40.23	6.54		1 1	107	7 13.1	1 11.71
	PREDICTED: GTPase IMAP family member 4 isoform X2 [Homo sap		10	1	1 1	1	1.0		1	1.342	1		0.00	2.63		1 1	190		
	dnaJ homolog subfamily C member 8 [Homo sapiens]	7.51	1		2 2	. 8	1.0		3 8.		3	22.7		7.51		5 8	3 253		
	DNA topoisomerase 1 [Homo sapiens]	3.92	6		3 3	12			4 3.		4	8.3		3.92	· ·	9 12			
	peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 isoform 2 [H		2		1 1	3	1.0		1	1.132	1		181.18	9.02		3 3	133		
24431933 115495445	reticulon-4 isoform B [Homo sapiens]	12.33	3		2 2	11	1.0		4 5. 2 5.		3	16.1	429.67 33.95	12.33 0.75		5 11	373		
119703753	ankyrin repeat domain-containing protein 30A [Homo sapiens] keratin, type II cytoskeletal 6B [Homo sapiens]	25.00	14		1 1	. 00	1.0		2 2.		2	6.8		25.00	4*	1 2	9 564		
	DNA repair endonuclease XPF [Homo sapiens]	1.86	10		1 10	09	1.0		2	1.558	1	0.0	28.19	1.86	42	1 1	916		
	putative oxidoreductase GLYR1 [Homo sapiens]	3.62	5		2 2	7	1.0		3 0.			5.6		3.62		5 7	7 553		
	PREDICTED: serologically defined colon cancer antigen 8 isoform X	1.48	9		1 1	4	1.0		2 1.		2	7.1		1.48		3 4	1 406		
	paired box protein Pax-8 isoform PAX8E [Homo sapiens]	2.09	4	1	1 1	2	1.0	9	1	0.786	1		31.20	2.09		2 2	287	7 31.0	0 8.54
6857820	phosphatidylinositol 5-phosphate 4-kinase type-2 alpha [Homo sap	3.45	1	1	1 1	6	1.0	8	2 7.	B 1.142	2	0.9	319.10	3.45	3	3 6	406	6 46.2	2 6.99
7657381	pre-mRNA-processing factor 19 [Homo sapiens]	4.56	1	1	1 1	3	1.0	8	1	2.036	1		163.64	4.56	3	3 3	504	4 55.1	1 6.61
6912356	echinoderm microtubule-associated protein-like 2 isoform 2 [Homo	3.39	5	1	2 2	6	1.0		2 10.	1 0.972	2	16.9		3.39		6 é	649		
	collagen alpha-1(VII) chain precursor [Homo sapiens]	0.37	1	1	1 1	1	1.0		1				38.71	0.37	1	1 1	2944		
4501893	alpha-actinin-2 isoform 1 [Homo sapiens]	18.57	41	1	1 16	127			1	1.642	1		5178.23	18.57	41	1 127			
	PREDICTED: pericentrin isoform X6 [Homo sapiens]	0.25	7	1	1 1	1	1.0		1				21.43	0.25		1 1	3139		
59859885 530387776	40S ribosomal protein SA [Homo sapiens]	25.76 1.88	1		4 4	10	1.0		4 4.	3 1.188 1.274	4	24.3	503.63 130.64	25.76 1.88	10	10	295		
530387776 194018522	PREDICTED: acid ceramidase isoform X1 [Homo saplens] eukaryotic peptide chain release factor GTP-binding subunit ERF3A		3		1 1	3	1.0		2 7.		1	14.9		1.88 3.21		3	3 373		
530425819	PREDICTED: adipocyte plasma membrane-associated protein isofor	3.21	2		1 1	3	1.0		1	1.116	1	14.9	93.31	3.21		3	3 289		
156564401	vesicle-fusing ATPase [Homo sapiens]	2.82	2		2 2	8	1.0		3 19.		3	5.6		2.82		5 5	3 744		
145386517	phostensin [Homo sapiens]	3.75	1	1	1 1	9	1.0		3 1.		3	9.8		3.75		3 9	613		
55770888	early endosome antigen 1 [Homo sapiens]	0.99	2	1	1 1	3	1.0	5	1	0.816	1		144.21	0.99	1	3 3	1411	1 162.4	4 5.66
17986001	major histocompatibility complex, class I, B precursor [Homo saple	9.39	11		2 2	6	1.0		2 9.		2	26.0		9.39		6 6	362		
	CAP-Gly domain-containing linker protein 1 isoform b [Homo sapier		8	1	1 1	3	1.0		1	2.513	1		47.88	0.43	3	3 3	1392		
122937345	unconventional myosin-Vb [Homo saplens]	0.43	1	:	2 2	16			2 27.		2	2.1		0.43	4	4 16	1040		
4503507	eukaryotic translation initiation factor 2 subunit 3 [Homo sapiens]	7.20	17	1 3	3 4	- 11			3 0.		3	5.7		7.20	11	1 11			1 8.40
254540132 46909584	myeloma-overexpressed gene 2 protein isoform 2 [Homo sapiens]	35.09	1	1	1 1	3	1.0		1	1.113	1	30.9	114.93	35.09		3 3	57		
	cAMP-dependent protein kinase catalytic subunit alpha isoform 2 [I	13.70	18		5 5	17			6 6.		6			13.70	14	4 17			
	PREDICTED: lysophosphatidylcholine acyltransferase 2 isoform X2 PREDICTED: protein LZIC isoform X5 [Homo sapiens]	2.46 15.79	2		1 1	5	1.0		2 23.		2	18.4	204.28 466.47	2.46 15.79	-	3 5	488		
	26S proteasome non-ATPase regulatory subunit 3 [Homo sapiens]	5.24	1		2 2	9	1.0		2 4.		3	68.5		5.24		5 5	5 534		
4506715	40S ribosomal protein S28 [Homo sapiens]	17.39	i		1 1	3	1.0		1	1.133	1	00.5	199.62	17.39		3 3	3 69		
	glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapid		3	1	1 25	1693			1	1.176	1		89140.91	92.83	74	4 1693			
47458820	signal transducer and activator of transcription 3 isoform 3 [Homo	2.49	6	1	1 1	5	1.0	3	2 5.	9 0.957	2	6.2	271.50	2.49	1	3 5	722		1 7.12
291190772	platelet glycoprotein Ib alpha chain precursor [Homo sapiens]	1.53	1	1	1 1	3	1.0	3	1	1.098	1		74.89	1.53	3	3 3	652	2 71.5	
	tumor necrosis factor alpha-induced protein 8 isoform b [Homo sap		5	1	2 2	9	1.0		3 0.		3	11.3		14.89		5	188		
112382370	folate receptor gamma precursor [Homo sapiens]	3.27	1	1	1 1	3	1.0		1	1.036	1		146.16	3.27	3	3 3	3 245		
15826852	Golgi resident protein GCP60 [Homo sapiens]	4.55	1	1	1 1	3	1.0		1	1.209	1		236.80	4.55		3 3	528		
530396980 530413911	PREDICTED: lysosomal Pro-X carboxypeptidase isoform X1 [Homo PREDICTED: DNA endonuclease RBBP8 isoform X2 [Homo sapiens]	7.67 1.28	3		2 2	11	1.0		4 5.	7 1.236	4	32.8	435.62 28.83	7.67 1.28		5 11	391		
	PREDICTED: DNA endonuclease Robbe isolorm X2 [nomo sapiens] PREDICTED: selenide, water dikinase 1 isoform X1 [Homo sapiens]	6.92	4		2 2		1.0		2 5.	2 1.136	2	83		6.92			390		
601984520	polyubiquitin-C [Homo sapiens]	80.15	7		9 9	100			16 11.		36	8.2		80.15	26	5 100			
578804376	PREDICTED: bifunctional purine biosynthesis protein PURH isoform		2		3 3	12			5 4.		5	12.3		7.32		8 12			
16418381	vacuolar protein sorting-associated protein 26B [Homo sapiens]	5.36	1	1	1 1	3	1.0	9	1	1.072	1		191.86	5.36	1	3 3	3 336	6 39.1	1 7.36
530380512	PREDICTED: histidinetRNA ligase, cytoplasmic isoform X1 [Homo		9		2 5	13			2 5.		2	20.1	400.68	11.14	13	3 13			
34734066	fibulin-1 isoform D precursor [Homo sapiens]	10.53	3	1	1 7	21	1.0		2 1.		2	8.9		10.53	19	9 21			
	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D i	4.87	2		3 3	8	1.0		3 7.		3	4.9		4.87	3	8	677		
	vascular non-inflammatory molecule 2 isoform 3 precursor [Homo :	4.35	4	1	1 1	3	1.0		1	1.222	1		132.68	4.35	1	3	3 299		
194018472	plasma serine protease inhibitor preproprotein [Homo sapiens]	4.68	1	-	2 2	4	1.0		2 5.		2	60.0		4.68	4	4 4	1 406		
4826932	peptidyl-prolyl cis-trans isomerase D [Homo sapiens]	7.84 6.32	6		1 2	7	1.0		1	1.060			148.62	7.84		5 7	370		
	RNA-binding protein 8A [Homo sapiens] nucleoside diphosphate kinase A isoform b [Homo sapiens]	6.32 56.58	1		1 1	120			2 0.	1.234 8 1.096	1	4.0	192.61 4500.07	6.32 56.58	2	3 5 120	174		
	PREDICTED: ubiA prenyltransferase domain-containing protein 1 is	4.74	2		1 1	120	1.0		2 0.		2	33.6		4.74	26	120	3 211		
	COMM domain-containing protein 2 [Homo sapiens]	12.06	1		1 1	6	1.0		2 2.		2	10.0		12.06		3 6	199		
578817031	PREDICTED: kinesin-like protein KIF12 isoform X8 [Homo sapiens]	1.10	1	1	1 1	2	1.0		1	1.873	1	10.0	37.77	1.10		2	635		
14790115	caspase-3 preproprotein [Homo sapiens]	6.86	- 1		2 2	6	1.0	6	2 0.	1 0.990	2	21.0	190.58	6.86		5 6	277	7 31.6	6 6.54
5174655	reticulon-3 isoform a [Homo sapiens]	7.20	5	1	1 2	7	1.0		2 10.	1 1.095	2	1.1	280.10	7.20	4	4 7	7 236		
28416940	ribosome maturation protein SBDS [Homo sapiens]	4.00	1	1	1 1	3	1.0		1	1.150	1		67.17	4.00	3	3 3	250		
	PREDICTED: aspartyl/asparaginyl beta-hydroxylase isoform X18 [H		18	1	1 1	1	1.0		1	1.825	1		24.92	1.24		1 1	563		
4885385	histone H3.3 [Homo saplens]	54.41	2		1 8	62	1.0		3 0.		2	46.9		54.41	23	3 62			
	PREDICTED: ubiquitin-like modifier-activating enzyme 6 isoform X1	2.87	9	3	3 3	7	1.0		2 10.		2	6.3		2.87		7 7	977		
	UPF0687 protein C20orf27 isoform 2 [Homo sapiens]		2		3	14	1.0		5 3.	1.147	5	11.7	706.85 42.64	24.71 5.71		14	1 174		
	PREDICTED: protein sprouty homolog 2 isoform X2 [Homo sapiens U5 small nuclear ribonucleoprotein 200 kDa helicase [Homo sapien	1.59			2 2		1.0		3 12	0.882	2	19		1.59			3 2136		
	PREDICTED: thioredoxin-like protein 1 isoform X2 [Homo sapiens]	27.06	3		4 4	12			4 11.		3	1.5		27.06	10	2 12			
	PREDICTED: protein LYRIC isoform X2 [Homo sapiens]	3.10	4		2 2	5	1.0		2 9.		2	9.5		3.10		4 5	549		
38202257	neutral alpha-glucosidase AB isoform 2 precursor [Homo sapiens]	7.31	5		4 4	12			4 11.		4	7.5		7.31	10	2 12			
323510690	serine/threonine-protein kinase Nek2 isoform 2 [Homo sapiens]	1.82	4	1	1 1	3	1.0		1	1.245	1		74.40	1.82		2 3	384		
41327764	aflatoxin B1 aldehyde reductase member 2 [Homo sapiens]	11.70	1	3	3 3	9	1.0		3 5.		3	2.2		11.70	9	9 9	359		
	26S protease regulatory subunit 4 [Homo sapiens]	10.68	1	3	3 3	12	1.0		5 2.		5	4.7		10.68	Ç	9 12	2 440		
661903023	hepatocyte growth factor activator isoform 1 preproprotein [Homo	2.11	2		1 2	5	1.0		1	1.198	1		90.91	2.11		5 5	662		
	cytoplasmic protein NCK1 isoform 2 [Homo sapiens]	3.19	2	1	1 1	3	1.0		1	1.047	1		98.72	3.19		3 3	313		
5901922 530396842	hsp90 co-chaperone Cdc37 [Homo saplens] PREDICTED: serine/threonine-protein kinase PAK 1 isoform X2 [Ho	11.11	1	4	4 5	16	1.0		4 6.		4	12.3		11.11	13	16	378		
		3.49 0.75	3		1 2	5	1.0		1	2.878	1		116.04 30.14	3.49 0.75			5 545		
270132935 414144872	ras-responsive element-binding protein 1 isoform 3 [Homo saplens coatomer subunit zeta-1 isoform 3 [Homo saplens]	0.75 6.25	3		1 1	1	1.0		1	1.252	1		30.14 123.45	0.75 6.25		1	1476		
	PREDICTED: inaD-like protein isoform X11 [Homo sapiens]	0.46	8		1 1	3	1.0		3 1.		3	19.3		0.46		3	1296		
	40S ribosomal protein S8 [Homo saplens]	5.29	3		1 1	3	1.0		1	1.177	1	17.3	183.64	5.29		3	208		
	COP9 signalosome complex subunit 4 isoform 2 [Homo sapiens]	11.93	57		2 3	7	1.0		2 4.		2	0.1	191.17	11.93		7	7 352		
578827388	PREDICTED: endonuclease 8-like 1 isoform X7 [Homo saplens]	1.28	5	1	1 1	1	1.0	1	1	1.075	1		22.12	1.28		1 1	390	0 43.7	7 9.92
	pleckstrin homology domain-containing family G member 6 isoform	0.79	3	1	1 1	4	1.0		2 1.		2	65.9	34.02	0.79		2 4	758		
222080070							1.0	0											
31377806	polymeric immunoglobulin receptor precursor [Homo sapiens]	2.49	2	1	1 1	3			1	1.007	1		139.70	2.49	-	3	764		
31377806 109689695		2.49 0.72 16.95	1	1	1 1	1	1.0	0	1 6.	1.787	1	5.7	28.64	0.72 16.95		1 1	764 1 1104 2 118	4 127.6	6 7.24

MINISTED					
Series of the se	) # AAs MW [kD	# AAs	MW [kDa]		calc. pl
Seed of the seed o	3 96	96		10.4	4.48
MINISTER   MARCON AMERICAN CONTROL   1	5 749			84.4	6.99
A STANDAR SAR A PROMER SAR A STANDAR SAR A S	52 710			76.6	4.70
Name of March and March and March 1989 179 189 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1	3 565			63.5	9.45
STATEMENT PROPERTY PROPERTY MAY 19 1	13 631	631	7	73.9	6.05
Second Second Column   1965	6 210	210	2	22.3	6.40
Martin   M	3 82	82		9.4	4.83
Ministry	18 248	248	2	27.6	5.73
Marcell and marker of presented   1.00   1	29 879	879	9	98.7	5.57
March   Marc	6 336	336	3	38.2	7.65
Section 1. Section mane 4. 15. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	30 147	147	1	16.7	6.24
Margin Antening designed in the Property of the Control of the C	3 395	395	4	41.6	5.12
March   Marc	6 199	199	7	22.1	8.10
Section 4. Ministry of the control o	246 246	246	7	28.1	4.83
March   Marc	29 846	846	g	94.1	6.16
Section 1. Monthly preparation specified systems and extension places of the control of the cont	1 816			87.2	8.59
March   Marc	124 171	171	1	19.8	4.81
March   Marc	32 200	200		22.5	8.38
Mile	3 169			19.8	7.24
Mile				109.0	8.18
Margin   Margin and encourage part of Processing   1989   1   3   5   100   5   27   130   1   1   13   15   100   1   1   13   13   1   100   1   1   1   1   1   1   1	4 117			12.6	9.28
Marchest 2 improves on preventions of preventions	9 123			13.9	5.52
Memory   M	2 624			70.8	6.86
Second content permission of general permi	10 152			16.9	6.13
March   Marc	73 93			10.4	4.93
Application of the property in the property	3 653			72.9	6.47
Second Column   Process	3 631			69.9	6.46
March   Section   Processing Pr	1 323			36.4	6.65
March   Marc	3 08	98		10.3	10.23
Margin   M	14 740	740		81.5	7.66
Section   Ministry   Section   Sec				270.1	5.67
1975-200   Part   Par				105.6	5.47
March   Marc	74 136			15.4	11.27
Management and Marked Statem   Management and Marked Statem   Management and Marked Statem   Management and M				49.0	7.52
Section of prints to prints of prints (prints)   10	1 437 43 806				7.52 5.78
1985    Proceedings of the processor o	43 806 3 194			88.9 22.6	5.78 10.65
Properties of the processor of planes responsed   6.63   9   11   1   75   1.60   20   12   100   20   12   20   30   30   40   41   41   41   41   41   41   4	3 214			22.9	5.44
Model	75 240			26.8	4.73
MINISTER	3 274				6.02
Second Column   Proceedings   Proceedings   Process				30.7	
Ministry   1985   Ministry	12 382 91 227			43.0	5.08
### STATES   1.50   1.5				22.7 17.7	4.63
Section   Processing of section of the Park   198   5   1   1   3   1000   1   1000   1   1000   1   1000   1   1	5 152				10.99
1979-18-10				38.3	5.53
Properties   Propose personal   4-67   1   10   10   10   10   10   10   10	3 108			11.0	4.84
Second color   Seco	2 147			17.1	5.10
Processing   Process   P	140 396			45.3	5.38
PRINCIPLE MAY CONTRIGUE Amendment propries from partners   204   1   7   7   2   1.09   11   1.00   11   1.00				47.2	5.03
PRESENCE Description selected   0.24   9   1   2   1.09   1   2   2   2   2   2   2   2   2   2	165 781			87.2	7.81
EMBOS   Sulfs, with containments   Emportant (Prices agent)   Contained   Flores agent)   Contained	24 503			51.2	11.47
Mail				221.5	9.42
Company   Comp				42.0	5.39
Section   PREDICTE former containing period   Company				59.6	9.16
SPINSEATY   Profession recognis invases informed [New coppinal]   1.25   3   1   1   7   1.088   2   5.2   1.448   2   8.7   64.548   1.25   3   3   3   3   3   3   3   3   3	5 128			14.8	9.19
SPAIRAGETT   SPA				253.3	8.46
Marked   M				64.3	8.44
2017/19/18   Accord anomals group   protein   Februs or speem]   0.64   1   1   1   1   1   1   1   1   1				28.5	9.38
25779622   265 protectioner non-NT beer regulating yearset 2 forform 1 [plens   1,11   3   7   7   20   1,048   8   4,7   1,059   8   1,14   1,055,55   1,11   1,	363 427			47.9	6.65
Section   Sect				140.8	6.92
Section   Factor capping protein subset algebra   1960 segond   18.74   3   8   11   196   1,048   40   8   8   11.38   38   13.1   95.71   58.74   33   33.00000000000000000000000000000				100.1	5.20
PRIDECTID Asimytes throse scoranys 1 storm XI [Perro sage]				58.9	5.85
1,000,000,000,000,000,000,000,000,000,0	195 286			32.9	5.69
1980/986   muclease-sensitive element-binding protein   Homo sepiems   4.95   8   3   19   10   10   4   4.90   0.95   4   1.71   30   0.145   50   1888   6   1886/985   1888   1888   6   1886/985   1888	1 187			20.7	7.93
1886/08.11   dynaminist   20 kDa protein, microbordial lodorm 2 (Homo sage)   1,62   1   1   2   7   1,047   1   1,124   1   1,157   1,62   4   4   5,046   1,046   1,047	8 324			35.9	9.88
1844289   Complement factor H-related proteins   1920 to Complement   2020 t	119 248			28.5	4.69
SPECIFIED DNA-quartities real-principles (36) per legions (31)   SPECIFIED DNA-quartities real-principles (34) per legions (35)   SPECIFIED DNA-quartities real-principles (34)   SPECIFIED DNA-quartities real-principles (34)   SPECIFIED DNA-quartities (				107.5	7.99
1776 19    endophilin-X broform 2   Brono sapients    5.00   5   2   2   5   1.046   2   2.4   1.585   2   33.6   30.0234   66.26   20				37.6	7.39
166.2514 de cestociats-timulating factor 1 [Norm suplems] 46.26 4 7 7 6 7 6 7 1.046 22 7.4 1.151 22 2.42 30.02.4 46.26 20 70.705411 mutualistic machine processor [Norm suplems] 15.63 1 1 1 1 5 1.046 2 2 2.1 1.006 2 2 1.9 21.65 1 5.83 3 3 1.705411				35.5	8.12
Processing   1.5	5 320			36.3	5.15
Separation   Sep				23.8	5.68
4506583 replication protein A 70 kDe DNA-binding suburit (Homo sapiens) 1.79 1 1 1 1 1 3 1.046 1 1.1460 1 203.46 1.79 3 3 3 3 3 4 1 1 1 1 1.046 1 1.1733 1 1 3 3 6.0 1.58 1 1 3 3 4 4 1 1 1 1 1 1.046 1 1 1.733 1 1 3 3 6.0 1.58 1 1 3 3 4 5 2 7 2 2 3 1 1 1 2 1.045 1 1 1.30 1 1 1 1.30 1 1 1 1.30 1 1 1 1.30 1 1 1 1.30 1 1 1 1.30 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5 64			7.1	9.99
SPEDICTED asy-conception Althoesterase 9, microhondrial lectors   1.58				54.6	5.07
Special Conference   PREDICTED: asyl-concurrgner Althoesterase 9, mitochnoridal isoform   1.88   4   1   1   1.046   1   1.733   1   1.33   1   1.34   2.70   2   2   2   319996622   putather RMA-binding protein   15 form   2   femors appliers   1.66   2   1   1   2   1.045   1   1.046   1   1.075   1.96   2   2   2   2   2   2   2   2   2	3 616			68.1	7.21
4905251   eular-polic translation intention factor 2 subunit E [Homo saplers]   2.70   1   1   2   1.05   1   0.70   2   1.05   1   1.07   1.05   1   1.07   1.05   1   1.07   1.05   2   1.05   1   1.05   1   1.07   1.05   1.05   2   1.05   1.05   1.05	1 379			43.2	7.08
1991-155/04	2 445			52.2	6.04
1991-15590   serime professe inhibitor Kazal-type is fordorm or precursor (Horno sa)   0.55   3   1   1   6   1.045   3   0.2   1.248   3   6.0   53.25   0.55   2				106.3	10.11
PREDICTED: elongulatin factor 1-delta boform XI4 [Homo saplems]   18.51   9   3   4   19   1.045   6   3.3   1.426   6   1.6,9   1.26,00   1.26,00   1.25,	6 916	916	10	103.9	8.35
4258279	13 644			74.4	5.53
PREDICTED: basement membrane-specific hepsare sulfate protec;   0.30   7   1   1   6   1.045   2   8.1   1.155   2   3.1   226.09   0.30   3   3   486   3   1   1   1   3   1.044   1   2   4.6   1.223   1   3   5.7   1768.61   24.14   3   2   276.3236   nitritises hormology 1 bedform 2 [brons sapiers]   7.00   7   1   1   3   1.044   1   1   1.066   1   20.14   3   2   276.3236   nitritises hormology 1 bedform 2 [brons sapiers]   7.00   7   1   1   3   1.044   1   1   1.066   1   20.14   3   2   2   2   2   2   2   2   2   2	19 281	281	2	31.1	5.01
487-2970 6 - phosphotructolistance, New type Rofform Delform sapering] 2.4-74 9 11 11 35 1.044 12 4.6 1.23 1.2 3.7 176.6 1 2.4.74 3.2 177-207-207-207-207-207-207-207-207-207-2	76 444	444	4	49.7	4.89
487-8970 6 - phosphortucolainae, liver type Isoform 1 [Horon sapers] 24-74 9 11 11 35 1.044 12 4.6 1.23 1.2 3.7 12 3.7 12 3.7 12 3.7 27 3.2 27 27 27 27 27 27 27 27 27 27 27 27 27	6 4057	4057	43	433.5	6.55
2976-322464 intifisace hormolog 1 knofrma (Phono saplers)	35 780	780	8	85.0	7.50
311893345 copine-1 barform C   Homo sapienc)   17.25   3 7 7 30 1.044 10 5.8 1.137 9 20 1.69.24 17.35 19 2070125 portion   Barford Source   Homo sapienc)   65.9 4 1 27 27 166 1.044 6.2 6.9 1.173 6.2 13.3 7657.05 65.94 178 530379112   PREDICTED: ris GTPase-activating-like protein IOGAP2 isoform X5 7.44 9 4 7 7 29 1.044 4 3.2 1.368 4 1 12.3 1303.14 7.44 21 22144279 beginners been modifie-activating-like protein IOGAP2 isoform X5 7.44 9 4 7 7 29 1.044 4 3.2 1.368 4 1 12.3 1303.14 7.44 21 22144279 beginners been modifie-activating-like protein IOGAP2 isoform X5 7.44 9 4 7 29 1.044 4 3.2 1.368 4 1 12.3 1303.14 7.44 21 1.09 1 1.09	3 243	243	7	26.3	6.27
20070125   protein disulfide-isomerase precursor [Homo saplens]   65.94   1   27   27   166   1.044   62   6.9   1.173   62   13.3   7057.05   65.94   78	30 536	536	5	58.9	5.83
S30379112   RPEDICIFED: ras GFless-earbounting-like protein LGAP2 bottom X;   7.44   9   4   7   29   1.044   3.2   1.388   4   12.3   130.314   7.44   21	166 508	508	5	57.1	4.87
22214/229				173.8	5.78
4885377 histone H1 3 [Homo saplems] 34.84 3 2 12 288 1.044 1 0.858 1 13781.38 34.84 34 5 3 2 12 288 1.044 1 0.858 1 13781.38 34.84 34 5 3 2 12 288 1.044 3 0.1 1.045 1 0.058 1 1 13781.38 34.84 34 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	6 623			68.6	6.48
530416138 PREDICTED: protein LSM14 homolog A isoform X3 [Homo saplers] 1.64 3 1 1 1 8 1.044 3 0.1 1.312 3 23.1 156.11 1.64 3 6/1907/48 Complement C4-A isoform 1 prepropriote [Homo saplers] 65.65 42 2 89 1298 1.044 6 12.6 1.207 5 5.8 5699,70 65.65 257 332329445 exikanyolic translation initiation factor 3 subunit B [Homo saplers] 3.93 1 3 3 9 1.044 3 5.2 1.105 3 8.0 25.0 3.80				22.3	11.02
67190748 complement C4-A kodorm 1 perproprotein [Homo sapiens] 65.65 42 2 89 1298 1.044 6 12.6 1.207 5 5.8 5699.70 65.65 257 323239445 eukaryotic translation initiation initiat	8 426			46.5	9.07
33239445 eukaryotic translation initiation factor 3 subunit B (Homo sapiens) 3.93 1 3 3 9 1.044 3 5.2 1.105 3 8.0 261.93 3.93 9 265403096 GRAM domain-containing protein TC isoform 2 (Homo sapiens) 1.09 5 1 1 1 3 1.044 1 1.127 1 33.11 1.09 3				192.7	7.08
285403096 GRAM domain-containing protein 1C isoform 2 (Homo sapiens) 1.09 5 1 1 3 1.044 1 1.127 1 33.11 1.09 3				92.4	5.00
				52.0	8.91
148539876   beta-adrenergic receptor kinase 1 [Homo sapiens]   13.06   6   8   8   39   1.044   12   5.6   1.249   12   17.8   1359.91   13.06   23	39 689			79.5	7.28
				27.7	4.78
3003277 19-3-3 pricetil interial (minimo Sapients) 97-30 1 0 14 152 1.043 14 0.1 1.059 15 1 (5.5 25/0-6.6 27.32) 44 1 1 1 1 1 1.043 1 1 0 0.059 15 1 29.29 4.48 1 1 1 1 1 1.043 1 1 0 0.059 15 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 134			15.1	10.46

								1											
Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]		A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)		.7) # Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs		calc. pl
123173757	ribonucleoprotein PTB-binding 1 [Homo sapiens]	1.72	1		1 1	2	1.043			1.841		1	82.51	1.72		2 2	756	5 79.5	5 8.92
530422336 530402178	PREDICTED: dedicator of cytokinesis protein 11 isoform X2 [Homo PREDICTED: sister chromatid cohesion protein PDS5 homolog B is	1.63	3		2 2	2 4	1 1.043		2 0.	1.028		2 0.2	78.11 2 508.85	1.07 1.63	,	4	2055		
	condensin complex subunit 2 isoform 4 [Homo sapiens]	1.16	7		2 2		3 1.043		t U.	1.136		2 0.2	90.34	1.16		9 9	605		
11056061	thymosin beta-4 [Homo sapiens]	56.82	1		7 9	91	1.043		7.		21	9 12.3		56.82	21	91	44		
	dystrophin Dp427p2 isoform [Homo sapiens]	0.51	44		1 3	3	1.042			1.387		1	190.55	0.51	-	9	3562		
10716563	calnexin precursor [Homo sapiens]	12.16	1		6 6	33			7.		1.2	2 9.9		12.16	18	33			
4502205	ADP-ribosylation factor 4 [Homo sapiens]	34.44	1		1 4	1 18	3 1.042		3.	5 1.439		5 18.7	631.59	34.44	10	18	180	20.5	5 7.14
578798834	PREDICTED: microtubule-actin cross-linking factor 1 isoform X27 [	0.47	40		3 3	5	1.042			10.102		1	93.77	0.47		5	4720	531.2	2 5.27
530393302	PREDICTED: cytosolic purine 5'-nucleotidase isoform X10 [Homo s.	12.43	6		3 3	21	1.042		5.	9 1.310		7 18.3	846.86	12.43		21	370	42.7	7 6.29
62420888	dipeptidyl peptidase 2 preproprotein [Homo sapiens]	6.50	3	:	2 2	2 6	1.042		4.		:	2 2.4		6.50		6	492		
5174529	S-adenosylmethionine synthase isoform type-2 [Homo sapiens]	2.78	1		1 1	1 3	1.042			1.116		1	116.95	2.78	1	3	395		
4759212	tubulin-specific chaperone A isoform 2 [Homo sapiens]	51.85	1	•	9 9	42		11	6.		15	5 8.4		51.85	26	42			
	long-chain-fatty-acidCoA ligase 1 isoform d [Homo sapiens]	3.04	14		2 2	? 6	1.042		5.			2 22.9		3.04		6	527		
530402403	PREDICTED: protocadherin-9 isoform X3 [Homo sapiens]	0.88	5		1 1	1 3	1.042		2.	7 1.271		2 5.9		0.88		2 3	1019		
145199237 7656952	RNA exonuclease 1 homolog [Homo sapiens]	0.41 5.70	2		1 1	1	1.041			1.168			25.21	0.41 5.70		1 18	1221		
7656952 530422392	calcyclin-binding protein isoform 1 [Homo sapiens] PREDICTED: coagulation factor IX isoform X2 [Homo sapiens]	13.64	1		1 2	2 18	1.041		1 8.			1 24.8	320.99 511.66	5.70 13.64		18	228 418		
	PREDICTED: coagulation factor IX isoform X2 [Homo sapiens]  PREDICTED: ubiquitin carboxyl-terminal hydrolase 3 isoform X3 [H		3		4 4	1	1.041		8.	1.292		4 24.8	23.33	13.64	1	11	351		
355594753	clusterin preproprotein [Homo sapiens]	42.09	7	1	3 13	105			5		3/	6 21.0		42.09	31	105			
	septin-5 isoform 2 [Homo sapiens]	15.03	2		3 3	11			7.		31	4 19.2		15.03	3.	11			
	nck-associated protein 1-like isoform 2 [Homo sapiens]	1.76	2		1 1		1 040			1 984		1	305.26	1.76		3 3	1077		
148536853	coatomer subunit alpha isoform 2 [Homo sapiens]	4.74	2		5 5	17	7 1.040		4.	4 1.258		6 5.6	5 593.98	4.74	14	1 17	1224		
154426278	muscular LMNA-interacting protein isoform 3 [Homo sapiens]	1.97	10		1 1	1	1.040			1.289		1	29.43	1.97		1	458		
	ADP-ribosylation factor 5 [Homo saplens]	38.89	1		1 5	25	1.040			2.239		1	1050.26	38.89	14	25			
	PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X7	9.82	9		5 5	14	1 1.040		8.			5 23.1	655.96	9.82	14	1 14			
212276104	leucine-rich repeat flightless-interacting protein 1 isoform 5 [Homo		73	1	1 11	36	1.040		7.		1:	3 8.7		17.95	28	36	752		
394953908	26S proteasome non-ATPase regulatory subunit 11 [Homo sapiens	3.08	1		1 1	1 2	1.040			1.391		1	129.92	3.08		2 2	422		
110611218	ribosome-binding protein 1 [Homo sapiens]	2.46	4	:	2 2	2 7	1.040		13.			3 1.6		2.46		7	977		
	caspase-1 isoform delta [Homo sapiens]	7.60	5		2 2	2 7	1.039		4.			3 6.5		7.60	5	7	263		
	protein FAM193A isoform 4 [Homo sapiens]	0.66	6		1 1	1	1.039			0.999		1	29.86	0.66		1	1211		
	26S proteasome non-ATPase regulatory subunit 9 isoform 1 [Homo		1		4 4	11	1.039		12.			4 15.5		41.26	10	11	223		
	60S ribosomal protein L15 isoform 2 [Homo sapiens]	6.21	2		1 1	2	2 1.039			0.948			58.99	6.21	-	2	145		
21237808	SWI/SNF complex subunit SMARCC2 isoform b [Homo sapiens]	1.15	7		1 1	3	1.039			1.227		1	124.99	1.15	3	3	1130		
22538467 14043026	proteasome subunit beta type-4 [Homo sapiens]	25.76 10.00	1		4 4	1 19	1.039		2.	1.123	1	8 14.7	7 908.11 195.49	25.76 10.00	10	19	264		
	vesicle-associated membrane protein 8 [Homo sapiens]		1		1 1				2 2.			2 20.9			-	3			
4504183	eukaryotic translation initiation factor 4H isoform 2 [Homo sapiens glutathione S-transferase P [Homo sapiens]	21.05 69.52	3	14	3 3 4 14	1 294	1.039				10			21.05 69.52	42	2 294	228		
25777713	S-phase kinase-associated protein 1 isoform b [Homo sapiens]	19.02	1		9 14	294	1.039	101	2 5.		10:	2 25.0		19.02	4.	294	163		
	PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X	23.31	7		4 7	1 3/	1 1.038		5.			7 12.3		23.31	21	34	429		
	complement component C8 alpha chain precursor [Homo sapiens]	30.99	1	1	3 13	75	3 1.038	21	7.		21	8 24.4		30.99	31	78	584		
4758012	clathrin heavy chain 1 isoform 1 [Homo sapiens]	16.24	14	19	9 20	92	1.038	3.			3:	2 18.1		16.24	5	92	1675		
197382664	eukaryotic translation initiation factor 4E type 3 isoform b [Homo s	14.41	2		1 1	. 6	1.038		2.	4 1.088		2 30.6	219.45	14.41	3	6	118	B 13.3	3 5.78
4507115	fascin [Homo sapiens]	6.29	- 1		2 2	2 6	1.038		9.	9 1.368		2 49.4	365.05	6.29		6	493	3 54.5	5 7.24
578831752	PREDICTED: probable helicase with zinc finger domain isoform X6	0.32	7		1 1	1	1.038			1.207		1	25.73	0.32		1	1578	B 177.5	5 8.10
	bifunctional glutamate/prolinetRNA ligase [Homo sapiens]	3.97	1		5 5	14	1.038		2.			5.5		3.97	14	1 14	1512		
	PREDICTED: apolipoprotein L1 isoform X2 [Homo sapiens]	20.00	4		7 7	30					10			20.00	21	30			
	PREDICTED: acyl-CoA synthetase family member 4 isoform X7 [Ho	1.11	8		1 1	11			1.			4 6.1		1.11	3	11	721		
	PREDICTED: dimethylaniline monooxygenase [N-oxide-forming] 4		4		1 1	1 1	1 1.037		1	1.255		1	0.00	1.31		1	381		
	beta-arrestin-2 isoform 2 [Homo sapiens]	11.93	11		4 5	14	1 1.037		3.			4 18.7		11.93	14	14	394		
46397403	OTU domain-containing protein 7A [Homo sapiens] centrin-3 isoform 2 [Homo sapiens]	4.19	2		1 1		1.037		2 8.	1.243 B 1.419		2 14.5	29.29	4.19		1	926		
5902076	serine/arginine-rich splicing factor 1 isoform 1 [Homo sapiens]	8.06	1		2 2	1 6	1.037		3 4.			3 8.6		8.06		5	248		
5453760	NEDD8 precursor [Homo sapiens]	34.57	2		2 2	11	2 1.037		4.			4 15.8		34.57		12	81		1 8.43
530386260	PREDICTED: colled-coil domain-containing protein 146 isoform X3	0.97	3		1 1		1.037			1.539		1	32.07	0.97		1 1	823		
578802932	PREDICTED: protein MEMO1 isoform X4 [Homo sapiens]	9.44	3		1 1	1 3	1.036			0.943		1	228.88	9.44		3	180		
167234419	thyroid hormone receptor-associated protein 3 [Homo sapiens]	1.36	1		1 1	. 6	1.036		5.	9 1.199		2 2.5		1.36	3	6	955	108.6	6 10.15
378744212	GTP-binding protein Rit1 isoform 3 [Homo sapiens]	4.37	3		1 1	9	1.036		2.	2.848		4 9.4	71.49	4.37	1	9	183	3 21.6	6 9.09
109148542	alaninetRNA ligase, cytoplasmic [Homo sapiens]	2.89	2		2 2		1.036		4.	3 1.055		2 19.6	302.18	2.89		5	968	B 106.7	7 5.53
578830584	PREDICTED: protein unc-13 homolog D isoform X1 [Homo saplens	6.44	3		5 5	18	1.036		3.	7 1.145	-	6 32.9	648.83	6.44	15	18	1071	1 120.6	6 6.40
255652953	zinc finger CCCH domain-containing protein 18 isoform 2 [Homo sa	0.84	2		1 1	1 2	1.036			1.045		1	31.12	0.84		2	953		3 8.32
4506193	proteasome subunit beta type-1 [Homo sapiens]	51.04	1	4	9 9	60					2:			51.04	26	60			
530372380	PREDICTED: acylamino-acid-releasing enzyme isoform X1 [Homo s	9.91	3		5 5	20	1.036		5.			7 3.9		9.91	14	20			
96304457	low molecular weight phosphotyrosine protein phosphatase isoform	16.07	2		1 1	3	1.036			1.318		1	339.62	16.07	3	3	112		
10835067	lupus La protein [Homo sapiens]	14.22	1		5 5	20	1.035		9.			7 13.6		14.22	14	20	408		
38201710 199562283	probable ATP-dependent RNA helicase DDX17 isoform 1 [Homo sa retrotransposon-like protein 1 [Homo sapiens]	10.01 0.44	6		0 7	19	1.035		6.	1.155		7 32.6	5 663.19 50.39	10.01 0.44	17	19	729 1358		
	retrotransposon-like protein 1 [Homo sapiens] keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	19.87	1		4 1	41	1.035		8.			1 11.1		19.87	20	5	1358		
73747917	antigen peptide transporter 2 isoform 2 [Homo sapiens]	3.06	20		2 2	41	1.035		0.			2 15.3		3.06	25	47	653		
	14-3-3 protein gamma [Homo sapiens]	60.73	1		9 17	189			7.		- 1			60.73	4	189	247		
	PREDICTED: dual specificity mitogen-activated protein kinase kinase		5		6 6	26					1			18.31	16				
	40S ribosomal protein S12 [Homo sapiens]	17.42	1		2 2		1.035		1.			2 23.9		17.42		6	132		
	phosphoserine aminotransferase isoform 1 [Homo sapiens]	7.03	4		2 3	8 8	3 1.035		1.			2 6.1		7.03		8	370		
153070260	myristoylated alanine-rich C-kinase substrate [Homo sapiens]	30.42	1		5 5	27	7 1.035	11	9.	0.979	10	0 12.5		30.42	14	27	332		
134288884	probable glutamatetRNA ligase, mitochondrial [Homo sapiens]	2.68	28		1 2	2 20				1.332		1	196.64	2.68		20	523	3 58.7	7 8.76
372266129	protein flightless-1 homolog isoform 3 [Homo sapiens]	5.44	25		6 6	15	1.034		i 3.			5 10.5		5.44	15	15	1214		
554790349	colled-coll domain-containing protein 90B, mitochondrial isoform e	6.47	5		1 1	2	1.034		12.			2 3.0		6.47		2	139		2 6.58
613410205	basic helix-loop-helix domain-containing protein KIAA2018 [Homo		1		1 1	1	1.034			2.644		1	23.13	0.31		1	2245		
530403051	PREDICTED: putative ATP-dependent RNA helicase TDRD9 isoform		4		1 1	2	1.034		4.			2 7.5		0.83		2	1330		
	zinc finger protein 142 [Homo sapiens]	0.30	2		1 1	3	1.034			1.126		1	27.64	0.30		3	1687		
340138932	apolipoprotein B receptor [Homo sapiens]	10.94	1	1	8	29	1.034		7.	2 1.148 1.039	10	3.8		10.94	24	29	1097		
567316026	rho GTPase-activating protein 30 isoform 4 [Homo sapiens]	2.71	4		1 1	2	1.034		6.			1 1.0	89.22	2.71		2	924		
	poly(U)-binding-splicing factor PUF60 isoform h [Homo sapiens] popeye domain-containing protein 3 [Homo sapiens]	1.60 2.75	8		1		5 1.034 3 1.034		6.	1.690		1.0	56.42 55.36	1.60 2.75		5	499		
	PREDICTED: transcription elongation factor SPT6 isoform X3 [Hom	0.62	1		1		1.034		6			2 40		0.62		3	1603		
	PREDICTED: transcription elongation factor SPT6 isoform X3 [Hom proteasome subunit alpha type-6 isoform a [Homo saplens]	0.62 26.83	2		6 /	39					1			0.62 26.83	18	3 39			
	brocesoure seemit aibita tabe a poronti a fuonto gabienzi	2.83	3		1 1	39	2 1.033		5.			2 4.8		20.03	10	39	318		
23110944 89353285	death effector domain-containing protein [Homo saniens]		2		2 2		1.033		2 2.			2 26.3		9.79		6	327		
	death effector domain-containing protein [Homo saplens] vacuolar protein sorting-associated protein 26A isoform 1 [Homo s	9.79	2									20.0							
89353285	vacuolar protein sorting-associated protein 26A isoform 1 [Homo s		1	:	1 1	3				1.117		1	52.86	3.53		3			7 6.79
89353285 17978519		9.79 3.53 6.87	1 2		2 2 1 1 2 2	1 3	3 1.033 5 1.033		2 6.	1.117 5 0.992		1 14.6	52.86	3.53 6.87	3	3 3	255 611	5 26.7	
89353285 17978519 58801559 50053795 4759140	vacuolar protein sorting-associated protein 26A Isoform 1 [Homo s complement C1q-like protein 3 precursor [Homo sapiens] eukaryotic translation initiation factor 4B [Homo sapiens] Na(+)/H(+) exchange regulatory cofactor NHE-RFT [Homo sapiens]	3.53 6.87 29.89	1 2 1		2 2 1 1 2 2 7 7	48	1.033 1.033 1.033	1	7.	5 0.992 3 1.299	1	7 12.1	52.86 228.63 2332.86	6.87 29.89	3 5 21	3 3 5 5 48	255 611 358	5 26.7 1 69.1 8 38.8	1 5.73 8 5.77
89353285 17978519 58801559 50053795 4759140 578830426	vacuolar protein sorting-associated protein 26A isoform 1 [Homo s complement C1q-like protein 3 precursor [Homo sapiens] eukaryotic translation initiation factor 4B [Homo sapiens] Na(-\f)H(-\f) exchange regulatory cofactor NHE-RF1 [Homo sapiens PREDICTED: collagen alpha-1()) chain isoform X3 [Homo sapiens]	3.53 6.87 29.89 10.20	1 2 1 6		2 2 1 1 1 2 2 7 7 7 8 8 8	48 3 61	3 1.033 5 1.033 8 1.033	11	7. i 11.	0.992 3 1.299 5 1.079	1: 2:	7 12.1 5 12.3	52.86 228.63 1 2332.86 3 2130.55	6.87 29.89 10.20	21 21	61	255 611 358 1020	5 26.7 1 69.1 8 38.8 0 99.7	1 5.73 8 5.77 7 5.50
89353285 17978519 58801559 50053795 4759140 578830426 4504483	vacuolar protein sorting-associated protein 26A Isoform 1 [Homo s complement C1q-like protein 3 precursor [Homo sapiens] eukaryotic translation initiation factor 4B [Homo sapiens] Na(+)/H(+) exchange regulatory cofactor NHE-RFT [Homo sapiens]	3.53 6.87 29.89	2 1 2 1 6		2 2 2 7 7 7 8 8 8 6 6 6	48 48 3 61 3 15	3 1.033 5 1.033 3 1.033 1 1.033 5 1.033	11 21	7.	5 0.992 3 1.299 6 1.079 1 1.077	1: 2: 4	7 12.1 5 12.3 6 1.9	52.86 5 228.63 1 2332.86 3 2130.55 766.26	6.87 29.89	2° 2° 16	3 3 5 5 48 61 61 34	255 611 358 1020 218	5 26.7 1 69.1 8 38.8 0 99.7 8 24.6	1 5.73 8 5.77 7 5.50 6 6.68

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/114	A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116	A8: 117/116 Count #	A8: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7	7) # Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs		calc. pl
578799388	PREDICTED: ribonucleoprotein PTB-binding 2 isoform X1 [Homo s		2		1 1	2	1.03	2	1	1.674	1		42.08	0.77	2	2	2 647		
189181666	beta-hexosaminidase subunit alpha preproprotein [Homo sapiens]	4.16	1		2 2		1.03		2 5.	1.199	2	8.4	208.03	4.16			5 529		
	26S protease regulatory subunit 8 isoform 2 [Homo sapiens]	10.55	3	3	3 3	15	1.03 1.03		5 3.:	1.125	5	7.0	725.80 274.29	10.55 2.48	9	15	5 398 3 848		
321267473 148596990	scaffold attachment factor B1 isoform 4 [Homo sapiens] copper homeostasis protein cutC homolog [Homo sapiens]	2.48 8.06	5		1 1	3	1.03		1	1.105	1		43.15	2.48 8.06	3	3	2 273		
530374901	PREDICTED: protein CDV3 homolog isoform X4 [Homo sapiens]	7.62			2 2		1 1.03		2 4.		1	4.4		7.62		4	4 210		
	E3 ubiquitin-protein ligase TRIM21 [Homo sapiens]	7.58	2		2 2		7 1.03		3 0.		3	29.5		7.58		,	7 475		
530380541	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotra		5		1 1	24			8 2.1		8	20.9		1.49		24			
	PREDICTED: PHD finger protein 21A isoform X9 [Homo sapiens]	1.47	6		1 1	11			4 0.1		4	1.6		1.27	1	11			
	PREDICTED: protein Z-dependent protease inhibitor isoform X1 [F		2	1	1 1		3 1.03		1	1.074	1	1.0	198.54	3.60		3 3	3 444		
	PREDICTED: 60 kDa heat shock protein, mitochondrial isoform X1	5.76	1		2 2		1.03		2 19.1		2	12.3		5.76			5 573		
	nudC domain-containing protein 2 [Homo sapiens]	5.73	1		1 1	3	1.03		1	1.250	1		80.91	5.73			3 157		
18105048	histone H2B type 1-K [Homo sapiens]	69.84	23		2 12	205			4 11.		14	18.4		69.84	34	205			
530355690	PREDICTED: keratin, type II cuticular Hb3 isoform X2 [Homo sapi	3.13	9	1	1 2	10	1.03		3 5.		3	1.8	162.70	3.13	4	1 10	447	7 49.7	7 5.54
578799625	PREDICTED: NAD kinase isoform X5 [Homo sapiens]	11.98	5	1	3 3	9	1.03		3 17.	1.355	3	4.2	450.68	11.98	9	9	9 359	9 39.6	6 5.80
530385393	PREDICTED: nicotinamide phosphoribosyltransferase isoform X1 [	68.64	13	28	8 28	223	1.03	8	4 8.	1.171	84	13.0	9194.59	68.64	79	223			
578803933	PREDICTED: UBX domain-containing protein 4 isoform X1 [Homo		2	1	1 1	3	1.03		1	1.249	1		63.02	2.80	3	3	3 322		
578802939	PREDICTED: vacuolar protein sorting-associated protein 54 isoform	r 0.53	3	1	1 1	3	1.03		1	2.056	1		34.56	0.53	3	3	941	1 106.3	
530428415	PREDICTED: proteasome subunit beta type-8 isoform X1 [Homo s		3	8	8 8	46					16	8.5		36.63	24	1 46			
	N-acetyl-D-glucosamine kinase [Homo sapiens]	23.59	3	8	8 8	34			3 12.0		13	15.5		23.59	22				
	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isol		7	10	0 10	65			4 5.:		24	11.1		33.11	28				
	non-histone chromosomal protein HMG-14 [Homo sapiens]	61.00	1		6 6	31			3 6.0		13	10.6		61.00	15	31			
	CAP-Gly domain-containing linker protein 2 isoform 2 [Homo sapie	0.89	2	1	1 1	1	1.03		1	0.971	1		29.31	0.89	1	1	1 1011		
	PREDICTED: apolipoprotein C-I isoform X1 [Homo sapiens]	30.12	43	3	3 4	33			0 5.0		10	10.6		30.12	12				
	ubiquitin carboxyl-terminal hydrolase isozyme L3 isoform 1 [Homo	15.98	4	3	3 3	10			4 2.		4	12.7		15.98	3	3 10			
54792071 56711324	small ubiquitin-related modifier 2 isoform b precursor [Homo sapid	30.99	7		2 2	14	1 1.03 3 1.03		5 1.8 2 4.		5	7.7 5.1		30.99	6	14	4 71 3 603		
56711324 12667788	HAUS augmin-like complex subunit 3 [Homo sapiens]	1.66	1	121	1 1	1476					475			1.66 67.09	200	1476			
12667788 578837053	myosin-9 [Homo saplens] PREDICTED: calcineurin-binding protein cabin-1 isoform X11 [Hon		22	121	141	1476	5 1.03 5 1.03		2 3.		4/5	16.4	68159.51	67.09 0.29	396	1476	5 1960 5 2103		
	RNA-binding protein EWS isoform 4 [Homo sapiens]	4.50	9	-	2 2		1.03		2 3.		2	2.7		4.50	3		5 600		
4503477	elongation factor 1-beta [Homo sapiens]	19.56	1		3 4	24	1.03		8 3.		2 8	15.2		19.56	10	2 26			
	cytosol aminopeptidase [Homo sapiens]	6.94	1		3 3	10	1.03		4 11.		4	7.3		6.94	12	3 10			
	double-stranded RNA-specific editase 1 isoform 7 [Homo sapiens]	1.34	9	1	1 1	12			5 9.1		3	11.7		1.34	3	12			
	SPARC-like protein 1 isoform 1 precursor [Homo sapiens]	8 28	2		2 2		1.02		2 10		2	78.0		8 28	5		5 664		
	metal transporter CNNM4 precursor [Homo sapiens]	0.90	5		1 1		1.02		2 15.	1.290	2	24.6	97.11	0.90			5 775	5 86.6	6 6.07
5031595	actin-related protein 2/3 complex subunit 4 isoform a [Homo sapi	69.64	4	11	1 11	99	1.02	3	6 5.0	1.133	36	16.3	3825.25	69.64	33	99	9 168	8 19.7	7 8.43
11386183	wiskott-Aldrich syndrome protein family member 2 isoform 1 [Hon	5.42	2		2 2	6	1.02		2 5.	1.081	2	16.8	211.39	5.42	6	i 6	6 498	8 54.3	3 5.53
236461719	potassium voltage-gated channel subfamily KQT member 5 isofori	r 0.76	4	1	1 1	- 2	1.02		1	1.188	1		31.63	0.76	2	2 2	923	3 101.2	2 9.50
530391071	PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform )	26.42	4	10	0 10	60	1.02	2	2 6.	1.109	22	15.9	2729.64	26.42	26	60	439	9 48.5	5 5.92
40254844	receptor-interacting serine/threonine-protein kinase 3 [Homo sapi	0.97	1	1	1 1	4	1.02		1	1.137	1		68.07	0.97	3	3 4	4 518		
189163485	lysosomal protective protein isoform b precursor [Homo sapiens]	8.96	3	1	3 4	9	1.02		3 11.		3	4.9		8.96	9	9	9 480		
	phosphoglycerate mutase 1 [Homo sapiens]	82.28	30	19	9 19	322					110	16.1		82.28	56	322			
8051584	ficolin-1 precursor [Homo sapiens]	27.30	9	1	7 7	37			2 4.:		12	13.9		27.30	21	37			
	PREDICTED: t-SNARE domain-containing protein 1 isoform X2 [Ho		1	1	1 1	1	1.02		1	1.259	1		35.09	1.14	1	1	1 878		
	WD repeat-containing protein 1 isoform 1 [Homo sapiens]	59.74	3	28	8 28	257			3 7.		92	13.7		59.74	81	257			
	neuron-specific calcium-binding protein hippocalcin [Homo sapien	4.15	3		1 1	3	1.02		1	1.155	1		70.76	4.15	3	3	3 193		
30181236 5453567	copine-2 [Homo sapiens]	13.32	17	4	4 5	36			4 2.		4	8.7 18.1		13.32	15	36	548		
	craniofacial development protein 1 [Homo sapiens]	2.34	1		1 1	3	1.02				2			2.34		2			
	PREDICTED: lamin-B receptor isoform X1 [Homo sapiens]	9.95 t 3.37	2		5 5	39	9 1.02 3 1.02		5 5.1	1.118	15	6.3	1294.43 55.17	9.95 3.37	16	39	9 573 3 208		
6912494	PREDICTED: proline-serine-threonine phosphatase-interacting pro microtubule-associated protein RP/EB family member 1 [Homo sa		4		0 0	30			1 6.		11	5.0		34.33	22	2 30			
578815682	PREDICTED: phosphoprotein associated with glycosphingolipid-en		1		2 2	11	1.02		4 5.1		- 11	5.6		6.48	- 22	11			
	glycogen phosphorylase, liver form isoform 2 [Homo sapiens]	55.10	- 4	3/	4 30	376					120	15.6		55.10	11/	376			
55770842	C-reactive protein precursor [Homo sapiens]	34.38	1		7 7	70	1.02				25	22.0		34.38	19	70			
	DENN domain-containing protein 1A isoform 2 [Homo sapiens]	1.25	6	1	1 1		1.02		3 1.		3	30.8		1.25			3 559		
578819702	PREDICTED: MMS19 nucleotide excision repair protein homolog is		7		1 1	1	1.02		1	1.166	1		28.83	1.20			1 666		
	keratin, type II cytoskeletal 6A [Homo sapiens]	24.82	16		1 16	85	1.02		1	1.073	1		2903.28	24.82	43	85			
4759270	translin isoform 1 [Homo sapiens]	38.60	2	6	6 6	30	1.02	1	0 5.	1.182	10	13.7	1238.88	38.60	18	30	228	8 26.2	2 6.44
530364307	PREDICTED: farnesyl pyrophosphate synthase isoform X2 [Homo	14.45	3	4	4 4	12	1.02	3	4 5.1	1.113	4	33.6	421.93	14.45	12	12	2 353	3 40.5	5 5.17
	ras-related protein Rab-11A isoform 2 [Homo sapiens]	20.65	3	1	3 3	21	1.02	3	7 3.1	1.210	7	11.0	856.51	20.65	9	21	1 155	5 17.6	6 8.85
635574580	hematopoietic lineage cell-specific protein isoform 2 [Homo sapier	18.26	7	8	8 8	34	1.02	1	3 6.9	1.132	13	3.4	1108.07	18.26	21	34	4 449	9 49.7	7 4.74
4504901	importin subunit alpha-3 [Homo sapiens]	2.69	1	1	1 1	1	1.02		1	1.172			67.44	2.69	2	2 2	2 521		
	PREDICTED: complement factor I isoform X4 [Homo sapiens]	42.00	6	22	2 22	164					64	14.9		42.00	61	164			
5031789	Inositol monophosphatase 1 isoform 1 [Homo sapiens]	20.94	3	5	5 5	12			5 3.		5	33.2		20.94	12	12			2 5.26
11559925	probable Xaa-Pro aminopeptidase 3 isoform 1 [Homo sapiens]	2.76	1	1	1 2	6	1.02		1	1.380	1		99.40	2.76	4	1 6	6 507		
217330646	activated RNA polymerase II transcriptional coactivator p15 [Hom	28.35	3		5 5	16	1.02		6 3.1		6	8.8		28.35	13	16	6 127		
578821284	PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase	9.50	4		3	12	1.02		4 2.1		4	18.3		9.50	9	12			
205277441	thyroxine-binding globulin precursor [Homo sapiens]	20.96	3	1	7	36	1.02		2 9.		12	14.2		20.96	21	36	6 415		
10863977	U6 snRNA-associated Sm-like protein LSm2 [Homo sapiens]	27.37	1	-	2 2		1.02		2 9 7.		2	28.4		27.37	6	5 6 3 113	6 95		
578813850 4507951	PREDICTED: actin-related protein 2/3 complex subunit 1B isoform	44.09	3	13	3 13	113					39	15.7 17.3		44.09	38				
	14-3-3 protein eta [Homo sapiens]	65.45	1	11	18	180			0 7.:		20	17.3		65.45	50	180			
530364909 4507125	PREDICTED: phosphatidylinositol 4-phosphate 3-kinase C2 domain small nuclear ribonucleoprotein-associated proteins B and B' isofor		2		. 1	14			5 2.		8	5.6		0.31	15				
	V-type proton ATPase subunit E 1 isoform b [Homo sapiens]	22.51	3		5	15			5 2.: 4 12.:		5	6.5		22.51	15	15			
538917488	socitrate dehydrogenase [NADP] cytoplasmic [Homo sapiens]	58.94	3	16	S 3	78					25	14.9		21.57 58.94	5	78			
	delta-aminolevulinic acid dehydratase [Homo sapiens]	22.42	2	10	5 5	21	1.02		7 3.0		7	32.9		22.42	15	21			
	PREDICTED: zinc finger CCCH domain-containing protein 13 isofor		5	-	1 1	14			0 2.		10	13.1		0.38	10	2 14			
13569879	acidic leucine-rich nuclear phosphoprotein 32 family member E isc		9	,	6 6	25	1.02		7 7.		7	10.4		33.96	17	22			
	erythrocyte band 7 integral membrane protein isoform a [Homo s	7.64	2		2 2	7	7 1.02		3 5.		3	7.0		7.64	5		7 288		
60279268	splicing factor U2AF 65 kDa subunit isoform b [Homo sapiens]	6.37	3	3	3 3	8	1.02		3 3.:		3	1.5		6.37	8	8	B 471		
530376357	PREDICTED: ADP-ribosyl cyclase 2 isoform X3 [Homo sapiens]	13.84	4	1	3 3	7	7 1.02		3 8.		3	9.2		13.84	7	7	7 289		
187608516	arf-GAP with coiled-coil, ANK repeat and PH domain-containing pr	3.60	3	1	2 2	6	1.02	1	2 0.	0.939	2	24.7	188.95	3.60	6	5 6	6 778	88.0	0 6.80
5729953	nuclear migration protein nudC [Homo sapiens]	2.42	1	1	1 1	3	1.02	1	1	1.121	1		120.02	2.42	3	3	3 331	11 38.2	2 5.38
294489346	motile sperm domain-containing protein 2 isoform 2 [Homo sapier	2.20	4	1	1 1	- 2	2 1.02	1	1	1.287	1		102.28	2.20	2	2 2	2 455	5 52.1	1 6.14
73808090	BUB3-interacting and GLEBS motif-containing protein ZNF207 isof	2.81	6	1	1 1	- 2	1.02	5	1	1.501	1		52.64	2.81	2	2 2	2 463	3 49.7	7 9.10
50593002	U2 small nuclear ribonucleoprotein A' [Homo sapiens]	15.69	1	3	3 3	8	1.02		3 6.		3	0.2		15.69	8	8 8	B 255		
578831041	PREDICTED: cytokine receptor-like factor 3 isoform X1 [Homo sap	5.50	2		2 2		1.02		2 0.0		2	24.0		5.50	5	5 5	5 400		
515869342	hsc70-interacting protein isoform 2 [Homo sapiens]	18.11	2		6 6	21			8 2.1		8	9.6		18.11	16	21			
115430223	galectin-3 isoform 1 [Homo sapiens]	28.40	2		6 6	48			7 6.		17	13.9		28.40	18	48			
	PREDICTED: protein diaphanous homolog 1 isoform X1 [Homo sa		3	1	7 7	23			8 5.		8	14.9		8.88	20	23			
530380424			6		5 5	14	1.02		5 4.1		5	5.0		11.44	14	1 14	4 647	71.4	
530421064	PREDICTED: SH3 domain-containing kinase-binding protein 1 isofe	11.44	0																
530421064 377520143	protein FAM49B [Homo sapiens]	47.22	4	12	2 12	63	1.02				23	31.1		47.22	34	1 63		4 36.7	
530421064 377520143 4506205	PREDICTED: SH3 domain-containing kinase-binding protein 1 isof- protein FAM498 [Homo sapiens] proteasome subunit beta type-9 proprotein [Homo sapiens] superoxide dismutase [Mn], mitochondrial isoform A precursor [Hi	47.22 21.00	4	12	2 12 4 4	63 26 45	1.02	5	3 7.: 9 3.: 6 7.:	1.181	23	31.1 20.5 9.4	949.62	47.22 21.00 46.85	34 12		6 219	9 23.2	2 5.03

	- · · ·															1			
Accession 23065544	Description  [qlutathione S-transferase Mu 1 isoform 1 [Homo sapiens]	ΣCoverage 41.28	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/114 1.02	A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116 1 1.192	A8: 117/116 Count A8	8: 117/116 Variability [%]	Score A(3,6,7) 1425.87	Coverage A(3,6, 41.28	7) # Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs		
9966777	resistin precursor [Homo sapiens]	51.85	10		4 4	54	1.02	12	5.		12	27.6		51.85	1	2 54			
	AT-rich interactive domain-containing protein 1A isoform b [Homo	0.73	2		1 1	3	1.02		J.	1.332	17	27.0	266.77	0.73		3 3	206		
	colled-coil domain-containing protein 88B precursor [Homo sapiens		3	:	2 2	7	1.02		6.			8.1	219.91	1.29		5 7	147		
	actin, cytoplasmic 2 [Homo sapiens]	86.40	4		2 32	3749	1.02	5 60	10.	4 1.202	60	31.6	165236.20	86.40	9	5 3749	37!		
530415478	PREDICTED: zinc finger protein 256 isoform X1 [Homo sapiens]	1.69	2		1 1	1	1.02	5 1		4.743	1		32.36	1.69		1 1	47-	4 54.8	8 8.98
	PREDICTED: RNA-binding protein Raly isoform X3 [Homo saplens]	14.48	4	:	3	11	1.02		18.			20.3		14.48		8 11	291		
	peptidyl-prolyl cis-trans isomerase A [Homo sapiens]	78.79	15	13	2 15	329						16.8		78.79		4 329			
	carbonyl reductase [NADPH] 1 isoform 2 [Homo sapiens]	30.06	3		4 4	13			0.			23.3		30.06	1	0 13			
	PREDICTED: protein PRRC1 isoform X1 [Homo sapiens]	3.15	2		1 1	2	1.02			1.382			64.14	3.15		2 2	44		
375493534 530418095	casein kinase 2, alpha 1 polypeptide-like [Homo sapiens]	9.97	9		3 3	8	1.02		5.			8.0		9.97		8 8	39		
	PREDICTED: glutathione synthetase isoform X2 [Homo sapiens]	10.13	1		4 4	10			4.			7.9 3.4		10.13	1	0 10			
	ATP-binding cassette sub-family C member 8 isoform 2 [Homo sap		3		1 1	5	1.02		6.			3.4		0.32 23.87		3 E	158		
4506203	PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform proteasome subunit beta type-7 proprotein [Homo sapiens]	8.30	/		7	34	1.02		4.			25.6		8.30	2	0 34	27		
578808207	PREDICTED: lateral signaling target protein 2 homolog isoform X4	0.85	1		2 2	3	1.02		2.			7.3		0.85		3	93		
24307939	T-complex protein 1 subunit epsilon [Homo sapiens]	30.68	1	1:	3 13	40	1.02		5.		15	14.4		30.68	3	5 40			
	proline-serine-threonine phosphatase-interacting protein 2 [Homo	9.88	1		3 3	9	1.02		3.		3	12.9		9.88		9 9	33		
	60S ribosomal protein L27 [Homo sapiens]	5.88	1		1 1	3	1.02			2.110	1		76.00	5.88		3 3	13		8 10.56
530410446	PREDICTED: alpha-2-antiplasmin isoform X6 [Homo sapiens]	39.66	7	1:	3 13	79	1.02	1 28	7.	7 1.137	27	23.1	3459.87	39.66	3	9 79	46	4 51.7	7 6.29
58219792	ras-related protein Rap-1b isoform 1 precursor [Homo sapiens]	55.43	5		7 8	37	1.024	1 11	6.	1.069	11	14.2	1420.15	55.43	2	2 37	18-	14 20.8	8 5.78
	PREDICTED: fermitin family homolog 3 isoform X1 [Homo sapiens]	36.65	4	11	8 18	80	1.024	1 28	5.	1.202	28	20.5	3684.67	36.65	5	1 80	66	3 75.4	4 6.77
578798632	PREDICTED: tyrosine-protein kinase Fgr isoform X1 [Homo sapiens	17.20	92		6 7	28			3.			13.0	1139.47	17.20	2	1 28			
555290081	3'(2'),5'-bisphosphate nucleotidase 1 isoform 2 [Homo sapiens]	6.32	6	:	2 2	8	1.02		2.			1.3		6.32		5 8	25:		
	RNA-binding motif protein, X chromosome isoform 1 [Homo sapier	11.00	4	:	3 4	18			1.			5.0		11.00	1				
	PREDICTED: spectrin beta chain, non-erythrocytic 1 isoform X2 [H		7	21	8 29	103			5.			21.6		15.74	7	9 103			
4502161	apolipoprotein C-IV precursor [Homo sapiens]	5.51	1		1 1	2	1.02			0.959			73.89	5.51		2 2	12		
6715607 4505891	hemoglobin subunit gamma-2 [Homo sapiens]	65.31	1		1 8	240	1.02		2.		2	7.4	6354.71 31.49	65.31	2	4 240	73		
	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 precursor [Homesquiater complex protoin LAMTOR3 inform 1 [Homesquiater]	0.95	1		1 1	2	1.02		12.			26.9	31.49 309.27	0.95 32.00		2	731		
	ragulator complex protein LAMTOR2 isoform 1 [Homo sapiens] pyridoxal kinase [Homo sapiens]	32.00 41.99	2		3 3	8	1.02		8.		3	26.9 14.8		32.00 41.99	-	8 E			
	uncharacterized protein C9orf172 [Homo sapiens]	0.61	5	-	2 2	4/	1.02		6.	1.12:		14.8	2519.26 113.36	0.61	2	4	97		
	PREDICTED: leucine-rich repeat transmembrane protein FLRT1 iso		1		1 1	1	1.02			1.322			22.19	1.34		1	67		
4504111	growth factor receptor-bound protein 2 isoform 1 [Homo sapiens]	37.33	2		7 7	26			3			23.6		37.33	2	0 26			
	PREDICTED: deoxynucleoside triphosphate triphosphohydrolase S/		2		3 3	12			8.			10.0		6.77	-	9 12			
578818565	PREDICTED: vimentin isoform X1 [Homo sapiens]	55.79	51	3:	3 35							12.2		55.79	10				
6598323	rab GDP dissociation inhibitor beta isoform 1 [Homo sapiens]	68.76	2	11	9 27	201			6.	5 1.142	53	14.0	9147.25	68.76	7	8 201	445	5 50.6	
108773810	leucinetRNA ligase, cytoplasmic [Homo sapiens]	1.02	1		1 1	3	1.02			1.475	1		205.08	1.02		3 3	117	6 134.4	
5031695	complement factor H-related protein 2 precursor [Homo sapiens]	25.93	3		4 6	32	1.02		10.	1 1.225	9	15.3		25.93	1	8 32			
295821193	serum amyloid A-1 protein preproprotein [Homo sapiens]	77.05	18		5 11	118			5.		24	19.2		77.05	2	8 118			
380837121	vesicle-trafficking protein SEC22b precursor [Homo sapiens]	12.56	1	:	2 2	5	1.02		7.		2	26.5	124.27	12.56		5 5	21!		
14210504	AP-1 complex subunit mu-1 isoform 2 [Homo sapiens]	1.89	4		1 1	3	1.02			1.119	1		136.78	1.89		3 3	42		
	tubulin alpha-1C chain [Homo sapiens]	42.98	6		5 15	135			5.		9	12.8		42.98	4	2 135			
	probable G-protein coupled receptor 179 precursor [Homo sapiens	0.51	1		1 1	9	1.02		5.		6	29.5		0.51		3 9	236		
530391036 4504061	PREDICTED: solute carrier family 2, facilitated glucose transporter N-acetylolucosamine-6-sulfatase precursor [Homo sapiens]	2.55	4		1 1	10	1.02		5	1.277	1	7.9	0.00 772.42	2.55 14.31	1	8 18	31-		
124494254	n-acetyglucosamine-o-surratase precursor [Homo sapiens]	32.74	1	10	0 10	18			-			7.9		32.74	1				
375477430	T-complex protein 1 subunit delta isoform b [Homo sapiens]	22.99	1	- 10	0 0	43			10			13.1		32.74 22.99	2				
4502101	annexin A1 [Homo sapiens]	77.46	2	3	1 32							17.7		77.46	8				
	PREDICTED: ceruloplasmin isoform X3 [Homo sapiens]	74.93	4		1 62				7.	1.033		17.7	36732.88	74.93	17				
	PREDICTED: putative V-set and immunoglobulin domain-containing		2		1 3	101			0.			4.3		22.83		9 101			
24430192	keratin, type I cytoskeletal 16 [Homo sapiens]	36.36	17		7 17	69	1.02		6.	1.056	7	11.2		36.36	4	8 69			
5031877	lamin-B1 isoform 1 [Homo sapiens]	29.01	2	15	5 15	58	1.02	2 21	6.	1 1.135	21	14.3	2688.70	29.01	4	2 58	58	6 66.4	4 5.16
586946397	roundabout homolog 2 isoform 5 [Homo saplens]	0.76	6		1 1	1	1.02			1.247	1		35.50	0.76		1 1	78		
	lymphocyte-specific protein 1 isoform 1 [Homo sapiens]	48.08	6	1	1 11	70	1.02		8.			15.4		48.08	3	1 70	33		
4507789	ubiquitin-conjugating enzyme E2 L3 isoform 1 [Homo sapiens]	64.94	3		8	33						12.3		64.94	2	1 33			
	eukaryotic initiation factor 4A-III [Homo sapiens]	7.79	1	:	2 3	11	1.02		0.			3.3		7.79		9 11	41		
	60 kDa SS-A/Ro ribonucleoprotein isoform 4 [Homo sapiens]	2.12	5		1 1	2	1.02			1.538			96.05	2.12		2 2	511		
	complement C1q subcomponent subunit C precursor [Homo saple <sub>r</sub>	20.41	1		4 4	44						20.4		20.41		2 44			
40068518	6-phosphogluconate dehydrogenase, decarboxylating [Homo saple	66.46	1	31								20.0		66.46	8				
	tubulin beta chain isoform b [Homo sapiens]	64.41	8		5 20							21.0		64.41		7 166			
	PREDICTED: sulfotransferase 1A1 isoform X1 [Homo sapiens]	42.03	7	10	10	55			5.			25.1	2053.88	42.03	2	9 55			
578814724 37577157	PREDICTED: maltase-glucoamylase, intestinal isoform X1 [Homo s. calpain-5 [Homo saplens]	1.09	2		1 1	3	1.02			1.187			116.64 41.12	0.73 1.09		3	275		
88999583	myosin light polypeptide 6 isoform 2 [Homo sapiens]	74.83	1		. I	168	1.02		7.			14.1	7156.22	74.83	,	0 168			
4557351	cholinesterase precursor [Homo sapiens]	1.83	2	-	1 1	100	1.02		1.	1.124		14.1	191.75	1.83	3	3 3	60:		
	calponin-2 isoform a [Homo sapiens]	34.95	4		7 7	68	1.02		6.		25	28.8		34.95	1	8 68			
	collagen alpha-1(III) chain preproprotein [Homo sapiens]	3.62	1		4 4	12			8.		4	1.3		3.62	1	2 12	146	6 138.5	
16306550	selenium-binding protein 1 isoform 1 [Homo sapiens]	8.69	3		4 4	20	1.02	1 7	7.	2 1.073	7	4.2		8.69	1	0 20	47:	2 52.4	4 6.37
	V-type proton ATPase subunit F isoform 1 [Homo sapiens]	10.08	3		1 1	3	1.020			1.031	1		158.38	10.08		3 3	111		
	PREDICTED: spartin isoform X2 [Homo sapiens]	1.80	1		1 1	3	1.020			1.365			149.63	1.80		3 3	66		
	D-dopachrome decarboxylase [Homo sapiens]	43.22	6		5 5	38			-			10.9		43.22		4 38			
5174539	malate dehydrogenase, cytoplasmic isoform 2 [Homo sapiens]	38.62	3	1	1 11							15.2		38.62	3				
321400142	CD44 antigen isoform 8 precursor [Homo sapiens]	10.54	19		3 3	21			4.			1.8		10.54		9 21			
4502107	annexin A5 [Homo sapiens]	72.81	1	11	8 20							13.3		72.81	5				
	proteasome subunit alpha type-7 [Homo sapiens]	44.76	5	•	9 9	48						6.5		44.76	2				
10834978	Interleukin-8 precursor [Homo sapiens]	31.31	1		3 3	14			2.		6	18.4		31.31		6 14			
4758950	peptidyl-prolyl cis-trans isomerase B precursor [Homo sapiens]	49.54	1	1	1 11	68	1.020		6.		24	9.1	3060.14	49.54	3				
578823780	PREDICTED: nascent polypeptide-associated complex subunit alph	18.60	7		3 3	10	1.020		2.		3	7.1	482.64	18.60		8 10			
	60S ribosomal protein L21 [Homo sapiens] protein S100-A7A [Homo sapiens]	4.38 42.57	1		1	2	1.020			1.100	1		63.96 2323.05	4.38 42.57		2 2	160		
28827815 71361688		42.57 32.81	1		4	122			8.			18.8		42.57 32.81		7 122			
	myeloblastin precursor [Homo sapiens]  V-type proton ATPase 116 kDa subunit a isoform 1 isoform c [Hom		1		. 6	122	1.020		8.	1 1.329		18.8	5196.98 30.24	32.81 0.96	1	122	83		
	rho GDP-dissociation inhibitor 2 [Homo sapiens]	80.10	4	16	1 1	336			9.			18.0		80.10		8 336			
	PREDICTED: protein CLEC16A isoform X8 [Homo sapiens]	0.79	0	10	1 1	336			9.	1.091		18.0	14404.86 75.46	0.79	4	3 336	88		
	GTP-binding nuclear protein Ran isoform 1 [Homo sapiens]	39.81	8		. I	68			7.			11.7		39.81	2	3 65			
5453555		1.45	12		1 1	3	1.020		7.	1.332		11.7	185.64	1.45	-	3 3	89		
	PREDICTED: protein transport protein Sec31A isoform X23 (Homo		12		8 8	197			6.			16.3		59.22	2	2 197			
	PREDICTED: protein transport protein Sec31A isoform X23 [Homo histone H4 [Homo sapiens]	59.22	1																
578808923 4504301	histone H4 [Homo sapiens]	59.22 44.91	5		8 8	56		9 19	8.	1 1.122	19	11.0	2570.91	44.91	2	3 56	28		
578808923 4504301			5		8 8 5 5	56	1.01		8.			11.0 4.2		44.91 7.76	2	3 56 5 18		5 30.3	3 7.52
578808923 4504301 354983501 16757970 194688133	histone H4 [Homo sapiens] protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 1 protein Niban [Homo sapiens] high mobility group protein B2 [Homo sapiens]	44.91 7.76 58.37	1 5 1	1	8 8 5 5	56	1.01 <sup>4</sup> 1.01 <sup>4</sup> 1.01 <sup>4</sup>	9 6 9 55		5 1.189 6 1.171	6 55		712.12 6897.31	7.76 58.37	2 1 4		92	15 30.3 18 103.1 19 24.0	3 7.52 1 4.78 0 7.81
578808923 4504301 354983501 16757970 194688133 5174661	histone H4 [Homo sapiens] protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 1 protein Niban [Homo sapiens] high mobility group protein 82 [Homo sapiens] protein \$100-A2 [Homo sapiens]	44.91 7.76 58.37 9.28	1 5 1 1	1	8 8 5 5 1 16	56 18	1.01 <sup>4</sup> 1.01 <sup>4</sup> 1.01 <sup>4</sup> 1.01 <sup>4</sup>	9 6 9 55 9 1	5.	5 1.189 6 1.171 1.034	6 55 1	4.2 14.1	712.12 6897.31 164.46	7.76 58.37 9.28	1 4	5 18 2 188 3 3	920	15 30.3 18 103.1 19 24.0 17 11.0	3 7.52 1 4.78 0 7.81 0 4.78
578808923 4504301 354983501 16757970 194688133 5174661 11761621	histone H4 [Homo sapiens] protein-L-isoaspartate(D-aspartate) O-methyltransferase isoform 1 protein Niban [Homo sapiens] high mobility group protein B2 [Homo sapiens]	44.91 7.76 58.37 9.28 10.56	1 5 1 1 1 2	1	8 8 8 5 5 1 16 1 1	56 18	1.01 <sup>4</sup> 1.01 <sup>4</sup> 1.01 <sup>4</sup>	9 6 9 55 9 1 9 6	5.	5 1.189 6 1.171 1.034	6 55 1 6	4.2	712.12 6897.31 164.46	7.76 58.37	1 4	5 18	920	15 30.3 18 103.1 19 24.0 17 11.0 10 39.8	3 7.52 1 4.78 0 7.81 0 4.78 8 6.79

A	Description	50	T# Destains	Ed Halana Dantidas	7# Dsld	F# 0014-	40-115/114	AD: 11F/114 Carret	A0: 115/114 Veslebille: 50/1	AD: 117/11/	AO. 117/11/ Count	AO. 117/11/ Mariabilla. (0/1	C 1/2 / 2	C A(2 / 7)	# DHd 8/2 / 70	# PSM A(3,6,7)	# 44-	MW D-D-1	
Accession 16507237	Description  78 kDa qlucose-regulated protein precursor [Homo sapiens]	ΣCoverage 39.45	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/114 1.019	A8: 115/114 Count	A8: 115/114 Variability [%]			A8: 117/116 Variability [%]			# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs 5 654	MW [kDa]	calc. pl
530406263	PREDICTED: ras-related protein Rab-27A isoform X3 [Homo sapien	25.60	3	23	5 2	5 20	1.019	4.	1 4		**	7 13			,	1 2		72.5	5.10
111154090		0.77	4			1 0	1.019		4.1			6 3				2	9 653		
4503481	rho GTPase-activating protein 24 isoform 3 [Homo sapiens]	37.53	4	13	3 1:	8 67	1.019					26 14				6			
5454088	elongation factor 1-gamma [Homo sapiens]	28.69	13	13	3 1.	72	1.019	11				20 14.			31	7			
311771535	acidic leucine-rich nuclear phosphoprotein 32 family member B [Hc	20.09	13	3	3	5 22	1.019		7			7 6			1			20.0	
6005942	T-complex protein 1 subunit beta isoform 2 [Homo sapiens]	57.32	54	34		7 179	1.019	Af		1.0	**	55 15.			10			UZ,	0.44
530368148	transitional endoplasmic reticulum ATPase [Homo sapiens]	69.25	54	14	, ,		1.019	0.	,			12 14.			4			89.3	
	PREDICTED: macrophage-capping protein isoform X1 [Homo saple		2	14	1 1	1 123													
23110942	proteasome subunit alpha type-5 isoform 1 [Homo sapiens]	30.29	2	5	5 .	5 25	1.019		6.			9 10.			11	2			
530393330	PREDICTED: zinc finger SWIM domain-containing protein 8 isoform	0.61	10	1	1	1 8	1.018		3.0			3 1.				3	8 1800		
40385883	ribulose-phosphate 3-epimerase isoform 1 [Homo sapiens]	22.81	6	4	1 .	1 14	1.018		1.			5 3.			1	1			
20357529	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [	11.47	7	3	3	3 7	1.018		0.1			2 6.				,	7 340		
24119203	tropomyosin alpha-3 chain isoform 2 [Homo sapiens]	69.76	20				1.018					19 13.			8				
20149675	EF-hand domain-containing protein D2 [Homo sapiens]	40.83	4	11		1 57	1.018					22 10.			31	5			
5453990	proteasome activator complex subunit 1 isoform 1 [Homo sapiens]	71.49	4	14	1 1	1 62	1.018					25 17.			3	6			
530397175	PREDICTED: signal-induced proliferation-associated protein 1 isofo	2.50	1	2	2	2 6	1.018		2 3.0			2 14.				i i	6 1042		
530387889	PREDICTED: serine/threonine-protein phosphatase 2A 55 kDa regu	7.99	15	2	2	2 8	1.018		6.			3 15.				5	8 288		
578826102	PREDICTED: tryptophantRNA ligase, cytoplasmic isoform X4 [Hor	43.52	2	16	5 16	5 50	1.018		5.9			20 13.			4	5			
57634536	la-related protein 4B [Homo sapiens]	0.68	2	1	1	1 1	1.018			1.2		1	30.8				1 738		
66932947	alpha-2-macroglobulin precursor [Homo sapiens]	71.71	23	78	3 8	7 2369	1.018								24	236			
347543829	dihydropyrimidinase-related protein 2 isoform 3 [Homo sapiens]	12.69	11	5	5 !	5 16	1.018		2.0	1.2	93	6 5.	6 769.5	12.69	10	1	6 536	58.1	6.15
34577063	adenylosuccinate synthetase isozyme 2 [Homo sapiens]	31.80	4	12	2 1:	2 69	1.018	26	8.1	3 1.2	24 2	26 24.	2 3072.8	3 31.80	3:	6	9 456	50.1	6.55
30410792	proteasome activator complex subunit 2 [Homo sapiens]	38.91	3	7	7	7 30	1.018	11	3.0	1.1	18 1	11 10.	3 1535.3	4 38.91	21	3	0 239	27.4	5.73
188536004	zinc finger protein 469 [Homo sapiens]	0.23	1	1	1	1 1	1.018			0.8	14	1	34.3	7 0.23			1 3925	409.9	7.72
662236841	mitogen-activated protein kinase kinase kinase 6 isoform 2 [Homo	0.47	2	1	1	1 6	1.018		6.:			2 8.				3	6 1280		
320202986	alcohol dehydrogenase [NADP(+)] [Homo sapiens]	31.69	2	8	3	3 26	1.017		2.9			8 15.			2:	2			
578818655	PREDICTED: glycylpeptide N-tetradecanoyltransferase 2 isoform X:	4.31	6	1	1	2 5	1.017			0.9		1	156.3				5 441	50.5	
4507903	serine/threonine-protein kinase VRK1 [Homo sapiens]	3.54	3	1	1	1 3	1.017			1.3		1	195.3			3	3 396	45.4	
4505257	moesin [Homo sapiens]	79.03	28	43	3 5	729	1.017	203	8.1			98 16.			16	72		67.8	
10863945	X-ray repair cross-complementing protein 5 [Homo sapiens]	27.46	3	13	3 1:		1.017	28							31				
19923483	ras-related protein Rab-14 [Homo sapiens]	31.63	16	3	3	1 15	1.017		6.3			4 16.			11	-			
530406418	PREDICTED: tropomyosin alpha-1 chain isoform X18 [Homo sapier	40.41	29	4	1 1	5 113	1.017		7.			5 11.			4				
530403015	PREDICTED: WD repeat and HMG-box DNA-binding protein 1 isofo	1.09	1	1		1 2	1.017		,,	1.1		1	40.9		-	11	2 825		
530396910	PREDICTED: w/o repeat and nine-box braventaing protein 1 isolo PREDICTED: synaptotagmin-like protein 2 isoform X3 [Homo saple	0.37	- 4			1 2	1.017			1.9		1	35.3				2 1602		
530384472	PREDICTED: synapiotagrini-like protein 2 foliorm x3 (nomo sapie PREDICTED: chromobox protein homolog 3 isoform X1 (Homo sapi	55.74	9	1	7	R 46	1.017	14	8.1			15 15.			2	4			
4758638	peroxiredoxin-6 [Homo sapiens]	70.98	3	15	1	5 105	1.017	40				39 9.			2.	3 10			
133925809	inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Homo s	23.71		14	. 1	5 111	1.017	41				11 16.			4	11		99.8	
530426021	PREDICTED: attractin isoform X2 [Homo sapiens]	9.99				20	1.017	14				14 10.			2	3		122.9	
4502133		29.60	- 1	,	,	39	1.017	33							21	3	6 223		
296011003	serum amyloid P-component precursor [Homo saplens] abl interactor 1 isoform I [Homo saplens]	3.34	17	,	,	00	1.017	3.	5.0	1.1		33 11.	124.8		2	0	3 329		
260436922		9.15	17		1	3	1.017		8.			2 6.					6 590	60.5	
4506003	suprabasin isoform 1 precursor [Homo sapiens] serine/threonine-protein phosphatase PP1-alpha catalytic subunit is	29.70	1		2	2 50	1.017		2.			5 4.			2		0 330		
				3	5 1	1 105	1.017	3							2.	1 10			
10947139	arginase-1 isoform 2 [Homo sapiens]	66.15	2	14	1	1 105		3.	4.1			37 15.			4	10:			
662033927	astrocytic phosphoprotein PEA-15 isoform c [Homo sapiens]	9.26	3	1	1	1 2	1.017			0.9		1	102.6			2	2 108	12.5	
216548487	protein-arginine deiminase type-4 [Homo sapiens]	50.23	5	25	5 20	5 263	1.017	90	7.0			90 16.			7	26			
635372916	enolase-phosphatase E1 isoform 2 [Homo sapiens]	12.72	2	1		1 3	1.017			1.2		1	207.1			3	3 173		
555943829	solute carrier family 2, facilitated glucose transporter member 14 is	2.68	5	1	1	1 3	1.017			0.8		1	102.2			3	3 411		
112421122	dnaJ homolog subfamily C member 13 [Homo sapiens]	0.85	2	2	2	2 5	1.016		3.0			2 19.					5 2243		
19923142	importin subunit beta-1 isoform 1 [Homo sapiens]	12.21	2	9	9 1	39	1.016		5.			14 16.			2	3	9 876		
578815934	PREDICTED: triple QxxK/R motif-containing protein isoform X1 [Ho	6.98	1	1	1	1 3	1.016			1.2		1	101.7			3	\$ 86	9.7	
578815687	PREDICTED: 60S ribosomal protein L7 isoform X1 [Homo sapiens]	9.13	2	1	1	1 5	1.016		2.			2 11.				3	5 208	24.4	
4505763	phosphoglycerate kinase 1 [Homo sapiens]	81.77	1	26	5 3:	548	1.016	155	9.			55 13.			9:	54		44.6	
282721079	sushi repeat-containing protein SRPX isoform 4 precursor [Homo si	1.58	4	1	1	1 1	1.016			1.7		1	23.1				1 379		
578819848	PREDICTED: calcium/calmodulin-dependent protein kinase type II	2.67	22	1	1	1 2	1.016			1.1		1	73.4			2	2 337	36.7	
88703045	proline-rich protein 11 [Homo sapiens]	1.94	1	1	1	1 1	1.016	1		2.6		1	23.4				1 360	40.1	
5803013	endoplasmic reticulum resident protein 29 isoform 1 precursor [Ho	31.03	2	6	5 (	5 38	1.016	14	5.1			14 13.			10	3	8 261	29.0	
578822199	PREDICTED: neutrophil collagenase isoform X1 [Homo sapiens]	43.24	2	15	5 1	5 186	1.016	65				64 11.			4:	18		50.8	
4826686	ATP-dependent RNA helicase DDX1 [Homo sapiens]	2.84	1	1	1	1 11	1.016	4	3.	1.1	34	4 16.	9 678.8	2 2.84		1	1 740	82.4	7.23
194394158	nicotinate phosphoribosyltransferase isoform 1 [Homo sapiens]	44.24	2	16	5 16	5 80	1.015	30	6.0	1.1	33 3	30 19.	9 3943.0	8 44.24	4:	8	0 538	57.5	5.68
5031635	cofilin-1 [Homo sapiens]	80.12	20	22	2 2:	2 275	1.015	99	10.:	1.1	57 9	99 12.	6 10448.4	5 80.12	6	27	5 166	18.5	8.09
51873067	sulfhydryl oxidase 1 isoform b precursor [Homo sapiens]	22.68	2	11	1 1	1 46	1.015	16	6.	1.1	76 1	16 18.	9 1742.1	5 22.68	3:	2 4	6 604	66.8	8.56
11496277	ragulator complex protein LAMTOR3 isoform 1 [Homo sapiens]	41.13	2	2	2 :	2 6	1.015		7.1	1.1	11	2 3	6 388.1	8 41.13		i i	6 124	13.6	7.34
4506381	ras-related C3 botulinum toxin substrate 2 [Homo sapiens]	53.65	6	4	1 1	73	1.015	18	4.1	1.6	17 1	16 21	2 2942.7	53.65	2:	7	3 192	21.4	7.61
4501891	alpha-actinin-1 isoform b [Homo sapiens]	74.89	44	38	6	1 592	1.015	116	6.	1.1	30 11	12 16	6 25616.8	74.89	17:	59:	2 892	103.0	5.41
4507877	vinculin isoform VCL [Homo sapiens]	59.10	4	53	3 5:	3 283	1.015	103							15:	28:		116.6	6.09
6912586	6-phosphogluconolactonase [Homo sapiens]	42.25	2	8	3 1	3 43	1.015	16		1.1			2 1964.0	1 42.25	2:				
144226251	chitinase-3-like protein 1 precursor [Homo sapiens]	41.78	1	12	2 1	2 67	1.015	24	4.1	1.3	05 2	23 29.	4 3595.5	2 41.78	3!	6	7 383	42.6	8.46
4502261	antithrombin-III precursor [Homo sapiens]	68.32	2	32	2 3:	2 298	1.015								9.				
4507793	ubiquitin-conjugating enzyme E2 N [Homo sapiens]	36.84	2	5	5 !	5 25	1.015		7.1	1.1		9 12			11	2			
115430227	LYR motif-containing protein 5 [Homo sapiens]	12.22	1	1		1 1	1.015			1.1		1	29.1			_	1 90	10.9	
11128019	cytochrome c [Homo saplens]	36.19	1	4	1	1 17	1.015		2.1			6 14.			1	1	7 105	11.7	
530422768	PREDICTED: high mobility group protein B3 isoform X3 [Homo sap	18.50	3	3	3	1 13	1.015		5.1			3 0.				1			
4503971	rab GDP dissociation inhibitor alpha [Homo sapiens]	36.69	1	4	1	1 80	1.015		9 4.			9 22			4				
4505591	peroxiredoxin-1 [Homo sapiens]	46.73	2			61	1.015					17 7.			21				
4503689	fibringgen alpha chain isoform alpha-E preproprotein [Homo sapier	54.04	56	46	5 41		1.015								13:				
530389317	PREDICTED: 14-3-3 protein zeta/delta isoform X2 [Homo sapiens]	81.22	17			5 282	1.015					58 11.			71				
5031855	lymphocyte cytosolic protein 2 [Homo sapiens]	8.44	17	10	. 2	1 15	1.015					6 14.			/	20.			
5453908	phosphatidylinositol transfer protein alpha isoform [Homo sapiens]	5.56	1	4		. 15	1.015		2			2 3.				1	4 270		
178557739	complement C4-B preproprotein [Homo sapiens]	66.40	42		1 0	1 1339	1.015					2 3.			26:	133			
402478626		20.37	42	4	, ,	1 1339	1.015		13.			6 10			26.				
402478626	low affinity immunoglobulin gamma Fc region receptor III-B isoforr aminopeptidase B (Homo sapiens)	20.37	18	14		1 57	1.015					24 17.			31				
56788356	tuftelin-interacting protein 11 [Homo sapiens]	0.84	4	14	1	. 5/	1.015	24	6.1	1.6		1/.	8 2527.8		31	5	1 837		
5032059	protein S100-A12 [Homo sapiens]	90.22		10		0 445	1.015	159	81			54 26.			21	3 44			
			1	10	. 10	445		159							21	44			
10947135	ATP-binding cassette sub-family F member 1 isoform b [Homo sapl	1.36	2	1		6	1.015		4.			2 12					6 807	91.6	
530395344	PREDICTED: rho-related GTP-binding protein RhoG isoform X1 [Ho	30.89	5	4		5 32	1.015		4.1			5 16.			11	3.	2 191	21.3	
256818825	THAP domain-containing protein 4 isoform 1 [Homo sapiens]	1.04	2	1		1 3	1.015			1.2		1	82.1				3 577		
	small nuclear ribonucleoprotein Sm D3 [Homo sapiens]	7.94	1	1		3	1.015			1.0		1	122.5			3	3 126		
4759160	protein S100-A10 [Homo sapiens]	23.71	1	2	2 :	2 5	1.014		5.			2 0.					5 97	11.2	
4506761	apolipoprotein B-100 precursor [Homo sapiens]	49.92	7	193			1.014								55				
4506761 105990532			18		5 1	1 67	1.014	8	5.1	1.1	31	8 12.	2 2489.7	4 71.31	2	6	7 122	13.5	9.14
4506761 105990532 188497671	serum amyloid A-2 protein isoform a precursor [Homo sapiens]	71.31	10																
4506761 105990532 188497671 71284108	serum amyloid A-2 protein isoform a precursor [Homo sapiens] nuclear distribution protein nudE-like 1 isoform A [Homo sapiens]	3.35	8	1	1	1 3	1.014			1.0	74	1	144.5	4 3.35		3	3 328	37.0	5.24
4506761 105990532 188497671 71284108 4504445	serum amyloid A-2 protein isoform a precursor [Homo sapiens] nuclear distribution protein nudE-like 1 isoform A [Homo sapiens] heterogeneous nuclear ribonucleoprotein A1 isoform a [Homo sapiens]	3.35 43.13	8	1	1	1 3	1.014	21		1.1	74	1 22 10.	8 3255.9	4 3.35 3 43.13	4	3	3 328 1 320	37.0 34.2	5.24 9.23
4506761 105990532 188497671 71284108 4504445 530406071	serum amyloid A-2 protein isoform a precursor [Homo sapiens] nuclear distribution protein nudE-like 1 isoform A [Homo sapiens]	3.35	8	11	1 10	1 3		22	10.0	5 1.1 3 1.0	74 53 2 50	1 22 10. 2 7. 20 7.	8 3255.9 7 57.4	4 3.35 3 43.13 8 0.35		3	3 328 1 320 6 1443	37.0 34.2 165.9	5.24 9.23 7.74

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Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]		A8: 117/116 Count				6,7) # Peptides A(3,6,7)	# PSM A(3,6,7)			calc. pl
10835063	nucleophosmin isoform 1 [Homo saplens]	36.73	5	9	9 9	58	1.014	21	6.	6 1.183	21	15.4		36.73	2	4 58	3 294		
530360487	PREDICTED: protein DJ-1 isoform X1 [Homo sapiens]	77.78	1	14	4 14	153	1.014	53	8.		53	10.0		77.78	4	10 153			
32313593 4507725	olfactomedin-4 precursor [Homo sapiens]	18.63 77.55	2	9	9 9	37	1.014	13 156	4. 10.		13 154	16.1 23.3		18.63 77.55	2	26 37 35 448			
	transthyretin precursor [Homo sapiens]  ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1 [Homo sapiens]	2.67	5	12	2 12	448	1.014	156	10.		154	23.3		2.67	3	3 448	3 147		
530397480	PREDICTED: phosphatidylinositol-binding clathrin assembly protein	10.79	26		5 5	18	1.014	- 6	6.		- 4	17.2		10.79	1	15 18			
29789283	WD repeat-containing protein 75 [Homo sapiens]	1.08	1		1 1	1	1.014	1	0.	2.470	1	17.2	40.29	1.08		1 1	830		
	heat shock 70 kDa protein 1A/1B [Homo sapiens]	63.03	1	29	9 33	581	1.014	184	7.		179	15.9		63.03	9	5 581			
4826659	F-actin-capping protein subunit beta isoform 1 [Homo sapiens]	67.65	5	18	8 18	165	1.014	62	6.	5 1.253	62	18.3	7312.89	67.65	5	165	272	2 30.6	6.00
	serine/threonine-protein kinase D1 [Homo sapiens]	0.55	2	1	1 1	5	1.014	2	6.	9 1.683	2	22.4	48.32	0.55		3 5	912	2 101.6	6.62
87196339	collagen alpha-1(VI) chain precursor [Homo sapiens]	10.51	2	8	8 8	34	1.014	12	4.	7 1.074	12	4.6	1277.58	10.51	2	24 34	1028	8 108.5	5 5.43
578813403	PREDICTED: glycinetRNA ligase isoform X1 [Homo sapiens]	3.73	2		2 2	12	1.014	4	3.	1 1.063	4	10.7	452.12	3.73		6 12	616	6 69.9	
	PREDICTED: LOW QUALITY PROTEIN: double homeobox protein 4	1.67	3	1	1 1	11	1.014	6	2.		6	2.6		1.67		3 11			
4885393	hemoglobin subunit epsilon [Homo sapiens]	18.37	1	1	1 3	218	1.013	5	7.		5	5.4	5218.29	18.37		9 218			
530382704	PREDICTED: serine/threonine-protein kinase RIO1 isoform X2 [Hor	1.51	2	1	1 1	1	1.013	1		1.919	1		21.34	1.51		1 1	464		
530380520	PREDICTED: annexin A6 isoform X2 [Homo sapiens]	67.62	11	40	0 41	408	1.013	146	6.		143	12.3		67.62	12	20 408			
	Junctional adhesion molecule A precursor [Homo sapiens]	4.01	1	1	1 1	2	1.013	2	6.				45.84	4.01		1 2	299		
	keratin, type I cytoskeletal 17 [Homo sapiens]	28.01	15	4	4 12	54	1.013	5	2.		5	11.0		28.01	3	3 54	432		
	ragulator complex protein LAMTOR5 [Homo sapiens]	17.34	1	-	2 2	18	1.013	6	3.		6	3.9		17.34		6 18			
18491024 40317626	dipeptidyl peptidase 3 isoform 1 [Homo sapiens] thrombosopodin-1 precursor [Homo sapiens]	10.04 2.31	2		0 0	26	1.013	9	5. 4.		9	3.4 10.8		10.04 2.31	1	16 26	737		
68303549	argininosuccinate lyase isoform 3 [Homo sapiens]	6.16	- 1		2 2	16	1.013	2	4.		2	10.0		6.16		9 16			
	PREDICTED: DEP domain-containing protein 5 isoform X10 [Homo	0.34	4		3 3	20	1.013	19	3.		19	31.9		0.34		1 20			
55749504	syntenin-1 isoform 2 [Homo saplens]	2.05			1 1	20	1.013	19	Z.	1.302	19	31.9	79.02	2.05		2 20	3 292		
	S-methyl-5'-thloadenosine phosphorylase [Homo sapiens]	22.61	1		4 4	18	1.013		7.		6	4.5		22.61	1	12 18			
6912388	grancalcin [Homo sapiens]	44.70	6		9 9	60	1.013	20	4.		20	17.0		44.70	2	25 60			
578838327	PREDICTED: nik-related protein kinase isoform X4 [Homo sapiens]	0.33	4	1	1 1	2	1.013	1		1.116	1	17.0	33.89	0.33		2 :	1526		
154146191	heat shock protein HSP 90-alpha isoform 2 [Homo sapiens]	50.82	16	23	3 39	344	1.013	68	9.	1 1.143	66	14.4	15165.21	50.82	10	08 344	732	2 84.6	5.02
4758304	protein disulfide-isomerase A4 precursor [Homo sapiens]	4.50	2	1	3 3	11	1.013	4	0.	8 1.141	4	12.3	496.62	4.50		9 11	645	5 72.9	9 5.07
546232005	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2	1.71	30	3	3 3	4	1.012	1		1.265	1		49.60	1.71		4 6	1170		
589908406	dipeptidyl aminopeptidase-like protein 6 isoform 5 [Homo sapiens]	1.42	10	1	1 1	9	1.012	4	3.		4	10.1		1.42		3 9	353	3 38.7	
	acyl-CoA-binding protein isoform 3 [Homo saplens]	62.07	7	5	5 5	45	1.012	18	4.		18	9.9		62.07		14 45			
530402312	PREDICTED: high mobility group protein B1 isoform X1 [Homo sap	52.09	2	8	8 14	126	1.012	31	5.		30	8.9		52.09	3	35 126			
	PREDICTED: sorting nexin-1 isoform X2 [Homo sapiens]	2.76	7	1	1 1	3	1.012	1		1.065	1		221.55	2.76		3 3			
	histone H2B type 1-B [Homo sapiens]	69.84	14		2 12		1.012	7	4.		7	15.4		69.84	3				
	calmodulin (Homo sapiens)	52.35	4	11	1 11		1.012	44	7.		44	11.4		52.35		32 117			
7706441	vacuolar protein sorting-associated protein 29 isoform 1 [Homo sap	29.12	5		5 5	20	1.012	6	6.		6	7.5		29.12		15 20			
4505029	leukotriene A-4 hydrolase isoform 1 [Homo sapiens]	66.45	6	40	0 40	290	1.012	105	6.		104	21.0		66.45	11				
16418467 15149476	leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	49.86 1.21	2	13	3 14	146	1.012	48	7.	4 1.206 1.248	48	16.7	6171.03 81.56	49.86 1.21	4	11 146	347		
530384149	argininetRNA ligase, cytoplasmic [Homo sapiens]	29.36	1		1 1	3	1.012	1	2.		1	9.0		29.36		3 3	218		
578823404	PREDICTED: ribonuclease T2 isoform X1 [Homo saplens] PREDICTED: ETS domain-containing protein Elk-3 isoform X1 [Hom	1.47	1		1 1	3	1.012	2	3.		2	16.2		1.47		2 10	3 407		
5454158	valinetRNA ligase [Homo sapiens]	2.37	3		3 3	6	1.012	3	2.		3	7.1		2.37		6 6	1264		
	fructose-bisphosphate aldolase A isoform 1 [Homo sapiens]	93.96	2	26	6 33	518	1.012	161	8.		160	18.5		93.96	9	8 518			
	ras-related protein Rab-44 [Homo sapiens]	4.41	1		2 2	6	1.012	2	8.		2	6.2		4.41		6 6	1021		
	PREDICTED: glucose-6-phosphate isomerase isoform X2 [Homo sa	67.92	6	32	2 33	539	1.012	200	7.		199	18.9		67.92	9	95 539			
16579888	fructose-1,6-bisphosphatase 1 [Homo sapiens]	17.16	3		4 4	19	1.012	7	9.	3 1.092	7	16.3	994.38	17.16	1	12 19	338	8 36.8	B 6.99
4505185	macrophage migration inhibitory factor [Homo sapiens]	65.22	1	3	3 3	23	1.012	8	3.	8 1.148	8	9.6	634.24	65.22		9 23	115	5 12.5	5 7.88
530420291	PREDICTED: gamma-parvin isoform X2 [Homo sapiens]	3.63	1	1	1 1	6	1.012	2	7.	6 1.313	2	5.4	256.85	3.63		3 €	331	1 37.5	5.49
156139127	uncharacterized protein C10orf88 [Homo sapiens]	1.12	7	1	1 1	44	1.012	18	9.	0 1.273	18	23.8	468.90	1.12		3 44		5 49.2	2 6.25
4505529	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	51.24	1	8	8 14	524	1.012	125	7.	7 1.238	125	19.2	18538.23	51.24	4	12 524	201	1 23.6	6 5.11
13324688	WD repeat-containing protein 11 [Homo sapiens]	0.65	1	1	1 1	1	1.012	1		1.294	1		34.55	0.65		1 1	1224		
530388884	PREDICTED: zinc finger protein ZFPM2 isoform X1 [Homo sapiens]	0.46	2	1	1 1	1	1.012	1		1.128	1		32.83	0.46		1 1	1 1082		
530401389	PREDICTED: 60S ribosomal protein L6 isoform X1 [Homo sapiens]	5.08	2	1	1 1	3	1.012	1		1.226	1		65.80	5.08		3 3	3 177		
	puromycin-sensitive aminopeptidase [Homo sapiens]	18.39	8	13	3 13	52	1.011	19	5.		19	9.4		18.39	3	52			
530418357	PREDICTED: serine/threonine-protein kinase 4 isoform X4 [Homo s	3.46	5		1 1	3	1.011	1		1.219	1		196.14	3.46		3	462		
	L-lactate dehydrogenase A chain isoform 1 [Homo sapiens]	78.61	10	24	4 26	447	1.011	141	7.		140	16.0		78.61	7	17 447			
	adenylyl cyclase-associated protein 1 [Homo sapiens]	80.42 7.53	3	32	2 32	4/0	1.011	179	8.		1/1	17.7		80.42 7.53	9	93 470	475		
4758092 6912516	di-N-acetylchitobiase precursor [Homo sapiens] mitochondrial peptide methionine sulfoxide reductase isoform a pre	7.53	1		2 2	18	1.011	2	12.		2	22.0		7.53		4 4			
		0.50	4		5 5	18	1.011	,	12.	1.059	1	8.8	68 11	0.50	1	8 18	3186		
	PREDICTED: dystonin isoform X17 [Homo sapiens] nucleolar and colled-body phosphoprotein 1 isoform 2 [Homo sapie	0.50	1		1 1	6	1.011	1	3.		1	1.5		0.50		3	5 699		
	PREDICTED: heterochromatin protein 1-binding protein 3 isoform 2	15.34	4		. 1	33	1.011	14	3.		14	7.5		15.34	2	22 33			
	NME1-NME2 protein [Homo sapiens]	71.54	7	`	6 15	151	1.011	15	6.		15	11.5	1247.70	71.54		11 151			
4502149	apolipoprotein A-II preproprotein [Homo sapiens]	74.00	6	10	2 12	248	1.011	91	9.		89	22.6		74.00	3	34 248			
578833114	PREDICTED: microtubule-associated serine/threonine-protein kinas	0.53	4	1	1 1	1	1.011	1		1.662	1	22.0	20.18	0.53		1 ,	1 1314		
578800587	PREDICTED: roquin-1 isoform X5 [Homo sapiens]	0.73	4	1	1 1	1	1.011	1		1.361	1		30.72	0.73		1 7	1101		
	serine/threonine-protein phosphatase 2B catalytic subunit alpha isc	12.15	10	4	4 4	11	1.011	4	8.		4	19.3		12.15	1	1 17	469		
	phosphoglucomutase-2 [Homo sapiens]	36.60	2	19	9 19	87	1.011	34	4.		34	19.3		36.60	5	50 87			
116063573	filamin-A isoform 1 [Homo sapiens]	50.21	2	89	9 98	743	1.011	252	7.		249	13.7		50.21	28				
	PREDICTED: fructose-bisphosphate aldolase C isoform X3 [Homo s	46.98	3	ç	9 16	125	1.010	15	10.		15	17.0		46.98		18 125			
	PREDICTED: plasma kallikrein isoform X2 [Homo sapiens]	24.00	3	14	4 14	51	1.010	19	6.		19	15.0		24.00		39 51			
	PREDICTED: ADP-ribosylation factor 3 isoform X1 [Homo sapiens]	54.70	3	4	4 8	49	1.010	10	8.		10	31.1		54.70		23 49			
9910460	omega-amidase NIT2 [Homo sapiens]	21.74	1		5 5	18	1.010	6	4.		6	2.2		21.74		15 18			
21071008	transcobalamin-1 precursor [Homo saplens]	18.48	1		5	17	1.010	6	10.		6	25.6		18.48		15 17			
	26S protease regulatory subunit 6A [Homo sapiens]	20.27 5.70	1		5	14	1.010	5	7.		5	25.4 2.7		20.27 5.70	1	14 14			
513126877 170763500	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens] protein SET isoform 1 [Homo sapiens]	5.70 35.17	5	-	2 2	9	1.010	3	1.		3	2.7		5.70 35.17		6 9	386		
		35.17 59.33	5		1 40	27	1.010	163	3.		157	12.4		35.17 59.33	11				
	inter-alpha-trypsin inhibitor heavy chain H4 isoform 2 precursor [H	59.33 18.71	50	41	1 42	148	1.010	163	6.	1.181	157	19.7	19386.47 5073.55	59.33 18.71	11	19 443 19 148			
	phosphoglycerate kinase 2 [Homo sapiens] inter-alpha-trypsin inhibitor heavy chain H1 isoform a precursor [Hi	31.61	76	10	. / R 10	148	1.010	40	5.		67	19.5		31.61		6 197			
109148508	ubiquitin thioesterase OTUB1 [Homo sapiens]	16.97	75	10	4 4	20	1.010	7	4.		7	7.5		16.97	1	11 20			
	U6 snRNA-associated Sm-like protein LSm4 isoform 2 [Homo saple	5.60	2		1 1	1	1.010	1	*	0.912	1	7.0	24.37	5.60		1	1 125		
	26S protease regulatory subunit 6B isoform 1 [Homo sapiens]	13.64	2		4 4	23	1.010	9	7.		9	7.4		13.64	1	12 23			
	uncharacterized protein C10orf12 [Homo sapiens]	0.40	1	1	1 1	6	1.010	3	6.		3	5.1		0.40		2 (	1247		
	actin-related protein 2/3 complex subunit 5 isoform 1 [Homo sapie	78.15	2	8	8 10	115	1.010	37	5.		37	20.7		78.15	2	27 115			
544711070	T-complex protein 1 subunit theta isoform 3 [Homo sapiens]	26.16	4	11			1.010	17	3.		17	10.0		26.16	3				
296040505	glycogenin-1 isoform 2 [Homo sapiens]	21.02	3	7	7 7	36	1.010	14	3.		14	8.0	1409.20	21.02	1	18 36	333	3 37.5	
	PREDICTED: amyloid beta A4 precursor protein-binding family B m	7.81	1		5 5	15	1.010	5	6.		5	10.5		7.81	1	15 15	666	6 73.1	
578818421		51.70	0	20	0 31	398	1.010	91	8.		91	15.2	18045.08	51.70	8	37 398			9 5.52
578822169	PREDICTED: heat shock cognate 71 kDa protein isoform X1 [Homo	51.70																	
578822169 530370916	PREDICTED: tubulin alpha-4A chain isoform X1 [Homo sapiens]	45.50	5		5 15	145	1.010	12	3.		12	25.7		45.50	4	13 145			
578822169 530370916 156616273	PREDICTED: tubulin alpha-4A chain isoform X1 [Homo sapiens] pleckstrin [Homo sapiens]	45.50 33.14	5	5	5 15 9 9	39	1.009	12 14	8.	8 1.163	12 13	6.2	1597.46	33.14	2	23 39	350	0 40.1	1 8.28
578822169 530370916 156616273 4507669	PREDICTED: tubulin alpha-4A chain isoform X1 [Homo sapiens]	45.50	5 5 6	5 9	5 15 9 9 5 5	39		12 14 9		8 1.163 2 1.226	12 13 9		1597.46 708.24		2		350	0 40.1 2 19.6	1 8.28 6 4.93

	T																	
Accession 55743122	Description retinol-binding protein 4 precursor [Homo sapiens]	ΣCoverage 72.64	2# Proteins	∠# Unique Peptides	∠# ⊬eptides	2# PSMS A8:	1.000	AD: 115/114 Count A8: 115/114	4 variability [%] A8	1.141	A8: 117/116 Count A8: 117/116 Variability [%	bj Score A	(3,6,7) Cov 608.45	rerage A(3,6,7) # Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa] 23.0	calc. pl
530402335	PREDICTED: plastin-2 isoform X2 [Homo sapiens]	87.40	15	50	50	867	1.009	301	8.0	1.141	300 1		935.55	87.40 1	47 867	621		5.43
	rho GTPase-activating protein 4 isoform 2 [Homo sapiens]	12.26	2	7	7	20	1.009	7	7.3	1.161	7		122.18	12.26	20 20			
94536842	ribose-5-phosphate isomerase [Homo sapiens]	17.36	1	4	4	12	1.009	5	0.9	1.079	5 1	13.9	546.15	17.36	11 12	311	33.2	
	catechol O-methyltransferase isoform S-COMT [Homo sapiens]	6.79	2	1	1	3	1.009	1		1.118	1		180.08	6.79	3 3	221		
	carboxypeptidase N catalytic chain precursor [Homo sapiens]	14.41	1	4	4	60	1.009	8	6.9	1.268			930.09 767.69	14.41	12 23			
4502565 169636415	calpain small subunit 1 [Homo sapiens]  complement component C6 precursor [Homo sapiens]	37.31 32.12	5	23	23	102	1.009	36	6.2 9.4	1.207			429.34		24 60 57 102			
	PREDICTED: calpain-1 catalytic subunit isoform X1 [Homo sapiens]	24.93	1	15	15	64	1.009	23	7.2	1.214			348.23		45 64			
23238211	actin-related protein 2/3 complex subunit 2 [Homo sapiens]	73.00	2	21	21	248	1.009	90	7.9	1.162	90 1	14.9 9	851.15	73.00	59 248	300	34.3	
4507521	transketolase isoform 1 [Homo saplens]	69.50	14	39	40	654	1.009	234	8.7	1.173			764.91		15 654			
	T-complex protein 1 subunit alpha isoform a [Homo sapiens]	32.37	2	14	14	51	1.009	18	4.7	1.079			069.42	32.37	39 51			
27544941 207029439	unconventional myosin-If [Homo sapiens] histone-binding protein RBBP4 isoform c [Homo sapiens]	25.87 3.85	5	19	19	101	1.009	36	6.5	1.228 0.825	36 2	20.7 4	898.04 39.96	25.87 3.85	55 101	1098		
	charged multivesicular body protein 2b isoform 2 [Homo sapiens]	5.81	2	1	1	3	1.009	1		1.149	1		133.27	5.81	3 3	172		
537361067	armadillo repeat-containing protein 8 isoform 5 [Homo sapiens]	1.17	7	1	1	1	1.009	1		1.291	1		19.79	1.17	1 1	600		
	transcription factor BTF3 isoform B [Homo sapiens]	3.70	2	1	1	3	1.009	1		4.462	1		93.58	3.70	3 3	162		
154759259	spectrin alpha chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	26.90	20	52	53	185	1.009	66	6.7	1.139			511.06		47 185			
530394656 6912238	PREDICTED: STE20-like serine/threonine-protein kinase isoform X1 peroxiredoxin-5, mitochondrial isoform a precursor [Homo sapiens]	7.23 45.79	2	10	7	16	1.009	50	9.1	1.061			663.89 775.84		16 16 29 135			
	PREDICTED: folliculin-interacting protein 2 isoform X6 [Homo sapiers]	0.58	6	10	10	133	1.008	1	7.2	2.031	1	3.7	19.45	0.58	1 1	1040		
4502511	complement component C9 precursor [Homo sapiens]	44.19	14	21	21	207	1.008	77	9.4	1.244	75 2	21.5 7	958.91		57 207			
4503571	alpha-enolase isoform 1 [Homo sapiens]	78.34	14	25	30	1155	1.008	357	7.1	1.181	354 1		282.38	78.34	87 1155			
	PREDICTED: pro-cathepsin H isoform X2 [Homo sapiens]	3.70	2	1	1	3	1.008	1		1.122	1		114.83	3.70	3 3	297		
56682959	ferritin heavy chain [Homo sapiens]	73.22	1	9	9	71	1.008	27	9.3	1.044			360.94	73.22	26 71			
4885375 47132589	histone H1.2 [Homo sapiens] serine/threonine-protein kinase N1 isoform 2 [Homo sapiens]	56.81 1.59	33	6	19	336	1.008	14	3.6	1.061	14	6.8 14	857.95 80.61	56.81 1.59	52 336	942		
	pre-mRNA-processing-splicing factor 8 [Homo sapiens]	1.67	1	3	3	7	1.008	3	3.2	1.191	3	3.8	395.69	1.67	7	2335		
	protein-arginine deiminase type-2 [Homo sapiens]	22.41	1	10	11	41	1.008	11	5.2	1.184			764.60	22.41	30 41			
	perilipin-3 isoform 3 [Homo sapiens]	34.12	3	8	8	25	1.008	9	5.2	1.156			380.94	34.12	21 25			
530410617	PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]	59.17	2	15	18	178	1.008	37	7.5	1.152	37	7.5 6	883.28		53 178			
110611226 23943880	protein unc-13 homolog B [Homo sapiens] methylthloribose-1-phosphate isomerase isoform 2 [Homo sapiens]	0.31 2.48	2	1	1	3	1.008	1 4	3.9	2.274	1 2	27.6	41.63 46.35	0.31	3 3	1591		
	SAA2-SAA2 protein precursor [Homo saplens]	40.38	3	5	9	101	1.008	24	5.0	1.180			886.73		25 101			
530398067	PREDICTED: apolipoprotein A-I isoform X1 [Homo sapiens]	86.14	61	32	35	1250	1.008	460	8.2	1.247			665.02		04 1250			
578813931	PREDICTED: protein CASP isoform X8 [Homo sapiens]	0.47	6	1	1	5	1.008	2	0.3	1.473		24.0	95.94	0.47	3 5	1494	163.1	5.81
530362835	PREDICTED: suppressor of tumorigenicity 7 protein-like isoform X3	1.77	5	1	1	1	1.008	1		1.273	1		29.89	1.77	1 1	453		7.15
578821106 4503303	PREDICTED: EH domain-containing protein 1 isoform X1 [Homo sa	35.58 5.15	4	14	14	51	1.008	20	6.3	1.207	18 2	25.4 2	223.25	35.58 5.15	39 51	534		
	neutrophil defensin 4 preproprotein [Homo sapiens] adenosylhomocysteinase isoform 1 [Homo sapiens]	38.89	1 0	16	16	66	1.008	22	5.5	1.199	22	4.8 2	920.80	38.89	1 1	432		
	apoptosis-associated speck-like protein containing a CARD isoform	61.36	3	9	9	58	1.008	20	5.5	1.157			357.18	61.36	26 58			
543583725	prostaglandin E synthase 3 isoform f [Homo sapiens]	18.35	8	2	2	7	1.007	3	6.9	1.287	3 2	21.6	433.31	18.35	5 7	109	12.7	
5031749	non-histone chromosomal protein HMG-17 [Homo sapiens]	42.22	1	4	4	23	1.007	11	6.9	1.130	11 1		982.83	42.22	9 23			
	PREDICTED: protein dpy-30 homolog isoform X5 [Homo sapiens] BRISC and BRCA1-A complex member 1 isoform 2 [Homo sapiens]	20.20	2	1	1	3	1.007	1	3.5	1.193 0.978	1		204.21 471.18	20.20	3 3	254		
528078313	neutrophil cytosol factor 1 [Homo sapiens]	59.74	3	21	21	190	1.007	71	6.8	1.185			791.64		58 190			
	talin-1 [Homo sapiens]	46.32	10	78	78	418	1.007	154	7.1	1.166			142.13		24 418			
532164704	cleft lip and palate transmembrane protein 1 isoform 3 [Homo sapi	1.37	1	1	1	1	1.007	1		0.963	1		30.29	1.37	1 1	655		6.64
530421543	PREDICTED: ubiquitin-like modifier-activating enzyme 1 isoform X3	40.83	3	31	32	191	1.007	68	7.0	1.141			720.01	40.83	88 191			
115298678 530398338	complement C3 precursor [Homo saplens] PREDICTED: alpha-tectorin isoform X1 [Homo saplens]	87.61 0.47	1	149	151	4844	1.007	1739	8.2 8.8	1.264		24.6 230	94.16	87.61 4 0.47	33 4844	1663		
	60S acidic ribosomal protein P1 isoform 1 [Homo sapiens]	14.04	1	1	1	3	1.007	1	8.8	1.170	3 1	10.2	94.16 165.18	14.04	3 3	2150		
38455402	neutrophil gelatinase-associated lipocalin precursor [Homo sapiens]	71.21	1	16	16	443	1.007	159	8.8	1.188	155 1	18.9 16	980.65	71.21	48 443			
	staphylococcal nuclease domain-containing protein 1 [Homo sapier	10.66	1	7	7	20	1.007	7	5.7	1.139			792.44		20 20			
5174447	guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sa		1	6	6	21	1.007	8	6.8	1.099			506.72		16 21			
73858566 302318952	heparin cofactor 2 precursor [Homo sapiens]  PML-RARA-regulated adapter molecule 1 [Homo sapiens]	48.10 22.99	2	21	21	173	1.007	61	4.4 5.4	1.238			991.11 180.35	10110	55 173 26 37			
	ras GTPase-activating-like protein IQGAP1 [Homo sapiens]	51.30	3	59	62	309	1.007	106	7.7	1.070			210.01		75 309			
	PREDICTED: TFIIH basal transcription factor complex helicase XPB	1.67	2	1	1	4	1.007	2	12.8	1.835	2 19	95.1	47.34	1.67	1 4	718	81.9	
	PREDICTED: src kinase-associated phosphoprotein 2 isoform X1 [H	17.83	1	6	6	27	1.007	11	5.2	1.279	11 2	9.0	764.60	17.83	16 27			
530382085	PREDICTED: ribosyldihydronicotinamide dehydrogenase [quinone]	46.32	2	8	8	35	1.007	13	7.7	1.060			537.29		22 35			
530398960 19923106	PREDICTED: dynamin-1-like protein isoform X2 [Homo sapiens]	4.26	8	2	2	4	1.007	2	4.6	1.301			306.61 558.35	4.26 44.23	4 4	587		
19923106 459642365	serum paraoxonase/arylesterase 1 precursor [Homo sapiens] dynein heavy chain 11, axonemai [Homo sapiens]	44.23 0.22	42	10	10	79	1.006 1.006	27	6.7 9.2	1.304			558.35 186.73	0.22	6 22			
	ezrin [Homo sapiens]	39.42	31	14	27	226	1.006	30	6.1	1.105			927.74		79 226			
327315343	sortilin isoform 2 [Homo sapiens]	1.73	4	1	2	7	1.006	2	0.6	1.158	2	5.5	93.00	1.73	5 7	694	77.3	5.39
	complement component C8 beta chain isoform 3 [Homo sapiens]	31.57	5	14	14	81	1.006	28	7.6	1.212			185.37		42 81			
5729804	diphosphoinositol polyphosphate phosphohydrolase 1 [Homo saple	18.02	2	2	2	9	1.006	3	0.2	1.325			485.83	18.02	6	173		
	heat shock 70 kDa protein 4 [Homo sapiens] PREDICTED: vasodilator-stimulated phosphoprotein isoform X1 [Homo sapiens]	23.45	1	15	15	46	1.006	17	3.1	1.175			082.74 475.96	23.45	41 46			
	transgelin-2 isoform b [Homo saplens]	74.37	2	13	13	83	1.006	29	8.2	1.149			153.81	74.37	38 83			
	PREDICTED: immunoglobulin J chain isoform X1 [Homo sapiens]	37.11	1	5	5	56	1.006	21	5.7	1.308		21.1 2	077.48	37.11	14 56	159	18.1	5.24
530386606	PREDICTED: tyrosine-protein kinase BAZ1B isoform X1 [Homo sapi	0.85	2	1	1	1	1.006	1		1.210	1		32.47	0.85	1 1	1053		
5031985	nuclear transport factor 2 [Homo saplens]	29.92	3	3	3	11	1.006	4	4.5	1.104		6.3	585.21	29.92	9 11	127		
	zinc finger protein 280A [Homo sapiens]	1.29 67.40	1	1 31	1 52	488	1.006 1.006	4 85	11.2 7.3	1.077		8.1  5.1 22	50.76 431.50	1.29 67.40 1	1 4	542		
12025678 301129290	alpha-actinin-4 [Homo sapiens] serine/threonine-protein phosphatase 2A activator isoform e [Homo	67.40 18.06	5	31	52	488 12	1.006	85	7.3	1.172			431.50 551.06	67.40 1 18.06	48 48E 9 12			
73760401	thymopoletin isoform gamma [Homo sapiens]	19.42	5	5	5	25	1.006	9	4.6	1.184			255.89		15 25			
4507775	ubiquitin-conjugating enzyme E2 D2 isoform 1 [Homo saplens]	12.24	7	2	2	7	1.006	3	5.2	0.962			209.15	12.24	5 7	147	16.7	7.83
	PREDICTED: histone-lysine N-methyltransferase 2D isoform X4 [Ho	0.25	12	1	2	7	1.006	1		1.045	1		69.87	0.25	5 7	5536		
	protein disulfide-isomerase A3 precursor [Homo sapiens] ras-related protein Rab-7a [Homo sapiens]	52.67 57.00	1	22	23	116	1.006	40 34	5.3 5.6	1.113			750.08 524.31		56 116 33 100			
	ras-related protein Rab-7a [Homo saplens] PREDICTED: mannose-1-phosphate guanyltransferase alpha isofon	9.05	1	11	11	9	1.006	34	5.6	1.139			341.05	9.05	9 0	420		
47519798	neutrophil cytosol factor 4 isoform 1 [Homo sapiens]	59.00	4	16	17	90	1.006	32	5.5	1.223	-		168.25	59.00	45 90			
21071030	alpha-1B-glycoprotein precursor [Homo sapiens]	51.72	1	16	17	388	1.006	146	6.2	1.223			529.88	51.72	48 388	495	54.2	5.86
578819756	PREDICTED: xaa-Pro aminopeptidase 1 isoform X4 [Homo sapiens]	2.90	6	1	1	2	1.006	1		1.118	1		62.46	2.90	2 2	552	62.1	5.73
	procollagen C-endopeptidase enhancer 1 precursor [Homo sapiens	4.68	1	2	2	6	1.006	2	11.2	1.124			275.48	4.68	6 6	449		
189163532 33457316	alpha-1-antitrypsin precursor [Homo sapiens] pleckstrin homology domain-containing family O member 2 isoform	72.73 7.55	2	41	42	2801	1.006 1.006	1053	8.8 1.4	1.166		3.1	640.07 398.65	72.73 1 7.55	22 2801	418		
167857790	alpha-1-acid qlycoprotein 1 precursor [Homo sapiens]	49.75	1	3	12	1304	1.006	408	6.8	1.267			962.95		36 1304			
	phospholipase B-like 1 precursor [Homo sapiens]	29.48	1	13	13	62	1.006	24	3.6	1.188			995.26		37 62			9.06
							4 001						210.05	04.04				5.60
217330598	glyoxalase domain-containing protein 4 [Homo sapiens]	21.81	2	7	7	23	1.006	8	6.6	1.170			060.35		20 23			
217330598 261399877	glyoxalase domain-containing protein 4 [Homo sapiens] T-complex protein 1 subunit eta isoform d [Homo sapiens] epidermal growth factor receptor substrate 15 isoform B [Homo sa	19.84	2	7	8	33	1.005	12	6.6 12.1	1.170 1.167 1.107			176.78 205.78		20 23		54.8	7.68

\$30405396 PPEE 47157325 prote 4557325 apoil 4557325 apoil 4557326 call 47157320 call 47157300 call 471573 actin 471573 actin 471573 actin 471573 actin 4715731 best 471573 actin 471	Description  or vault protein isoform   Homo sapiens  DIOCTED. Provisine-protein kinase: CSK koform XI (Homo sapiens) DIOCTED. Provisine-protein kinase: CSK koform XI (Homo sapien) dispoprotein E precursor (Homo sapiens) dispoprotein E precursor (Homo sapiens) disto (Homo sapiens) disto (Homo sapiens) disto (Homo sapiens) rickosomal protein 1.17, mitochondrial (Homo sapiens) natiolizae (Homo sapiens) distalina (Homo sapiens) distalina (Homo sapiens) GCTBsse-ectivating protein 25 isoform (Homo sapiens) GCTBsse-ectivating protein 25 isoform (Homo sapiens) exessione subunit alpha type-2 (Homo sapiens) diseasome subunit alpha type-2 (Homo sapiens) disciplina (Homo sapiens) DIOCTED protein kinase C and cassin kinase substrate in neuro DIOCTED. protein kinase C and cassin kinase substrate in neuro DIOCTED. protein kinase C and cassin kinase substrate in neuro DIOCTED. protein kinase C and cassin kinase substrate in neuro	2Coverage 36.95 11.56 6.71 48.26 71.73 0.45 58.99 4.57 58.16 30.61 1.67 14.24 74.40	3 1 14 2 11 3 1 1 2 11 2 11 4	Σ# Unique Peptides  22  3  4  13  36  2  17  1  266	22 3 5 13 36 2 2 17 1	94 94 12 110 478 2	A8: 115/114 1.005 1.005 1.005 1.005 1.005	32 3 4 3 3	A8: 115/114 Variability [%] 7: 5: 0: 4:	8 1.087 2 1.206 7 1.103 2 1.500	30 3 4 36	: 117/116 Variability [96] 14.7 28.2 14.5 19.3	4154.85 364.88 315.90	36.95 11.56 6.71 48.26	# Peptides A(3,6,7) 6- 1: 31	4 94 9 9 2 12 8 110	893 450 671 317	99. 50. 76. 36.	3 5.48 7 7.06 8 7.01 1 5.73
\$3005396 PREE 47157322 prote 47157325 apple 4557325 apple 4557325 apple 4557014 catal 45727401 sacs 4757900 cale 11596559 395 5803187 tran 4885165 cysts 277208833 5-tyst 478506181 prote 5031573 actin 478506181 prote 5031573 beginned 5031573 beginned 5031573 actin 5031	CIDICED. Proxine-protein kinase CSK noform X1 [Homo sapiens in kinase C beta live beform [Homo sapiens] aligoprotine in grecursor [Homo sapiens] aligoprotine in grecursor [Homo sapiens] and the control of the control	11.56 6.71 48.26 71.73 0.45 58.99 4.57 58.16 30.61 1.67	3 1 14 2 2 1 1 3 1 1 2 1	22 3 4 13 36 2 177 1 1 26	22 3 5 13 36 2 17	478 2	1.005 1.005 1.005	37	0.	2 1.206 7 1.103 2 1.500	30 3 4 36	14.5 19.3	364.88 315.90 5407.15	11.56 6.71 48.26	1:		671	50. 76.i 36.	7 7.06 8 7.01 1 5.73
47157322 prote 4557325 apoll 4557325 apoll 4557014 catal 471274011 sacsis 4757900 caire 11596859 335' 5803187 trans 4885165 cysts 267206833 5-ty 2613599090 into 6531573 actin 52031673 b Lesi 53031674 prote 53031674 prote 53031674 prote 53031674 prote 53032444 prote 53030393500 prote 5303039500 prote 5303000 prote 53030	Iteln kinase C beta type koform   Nomo sapiens  Injeprotein E preuncy (Homo sapiens) Islase (Homo sapiens)	6.71 48.26 71.73 0.45 58.99 4.57 58.16 30.61 1.67	1 14 2 1 3 1 1 2	3 4 133 36 2 17 1 1	3 5 13 36 2 2	478 2	1.005 1.005 1.005	37	0.	7 1.103 2 1.500	3 4 36	14.5 19.3	315.90 5407.15	6.71 48.26	1:		671	76. 36.	8 7.01 1 5.73
4557325 apoli 4557014 catal 47127401 sacsid 471277900 cafer 4757900 cafer 5803187 trans 5803187 trans 580318 trans 5803187 trans 580318 trans 5803	ilipoprotier B precursor (Homo sapieno) issies (Homo sapieno) issi Isoform 2 (Homo sapieno) issi Isoform 2 (Homo sapieno) it ilibosomi protein L17, mitschondrial (Homo sapieno) in Bosomia protein L17, mitschondrial (Homo sapieno) isatilir A (Homo sapie	48.26 71.73 0.45 58.99 4.57 58.16 30.61 1.67	14 2 1 3 1 1 2	4 13 36 2 17 1 26	13 36 2 17	478 2	1.005	37	4.:	2 1.500	36	19.3	5407.15	48.26	31		317	36.	1 5.73
4557014 catal 4912274011 sacsis 4757900 calre 11596859 39S 5803187 trans 4885165 cysts 297208833 5-by 521399990 rho to 5031573 actin 4506181 proto 520419493 PREE 530392494 PREE 5303935500 PREE	alsee [Homo sapiens] eticulin precursor [Homo sapiens] eticulin precursor [Homo sapiens] eticulin precursor [Homo sapiens] sin bosoma [10] sapiens] statin-A [Homo sapiens] statin-A [Homo sapiens] statin-A [Homo sapiens] GFBsss-schading protein 2 is fordrom ([Homo sapiens] GFBsss-schading protein 2 is fordrom ([Homo sapiens] n-related protein 3 is fordrom 1 [Homo sapiens] steatome suburul alipha type-2 [Homo sapiens] steatome suburul alipha type-2 [Homo sapiens] steatome suburul alipha type-2 [Homo sapiens] steatome suburul sinks c and scassin kinuse substrate in neuro GDFGED. protein kinuse c and scassin kinuse substrate in neuro	71.73 0.45 58.99 4.57 58.16 30.61 1.67	1 3 1 1 2 1	13 36 2 17 1 26	13 36 2 17	478 2	1.005				36				Si				1 5.73
491227401 sacsi 4757900 calere 11596859 395: 5803187 trans 4885165 cysts 297206833 5-hys 261399909 rho to 5031573 actin 4506181 proto 53031973 PREE 530419493 PREE 5303197494 PREE	sin Isoform 2 (Homo saplens) etidulin percurse (Homo saplens) i ribosomali protein L17, mitochondrial (Homo saplens) statidases (Homo saplens) latilir A (Homo saplens) datilir A (Homo saplens) datilir A (Homo saplens) Gribse-schwisting protein 2 isoform of (Homo saplens) Gribse-schwisting protein 2 isoform (Homo saplens) re-related protein 3 isoform 1 (Homo saplens) stectome suburut alight bype-2 (Homo saplens) stecting precursor (Homo saplens) stecting precursor (Homo saplens) flocting precursor (Homo saplens)	0.45 58.99 4.57 58.16 30.61 1.67	3 1 1 2 1	2 17 1 26	2 17	2		1/3		6 1.099	172								
4757900 calre 11596859 395. 5803187 trans 4885165 cysts 297208833 5-tyyst 29720833 5-tyyst 29720833 a-clin 4885165 cysts 29720833 5-tyyst 4806181 proto 262206315 L-sel 530419493 PREE 5303939500 PREE 530393500 PREE	ellculin procursor (Humon sapiens) infosomal protein 177, mitochondria (Homo sapiens) salabiose (Homo sapiens) salabi-A (Homo sapiens) salabi-A (Homo sapiens) salabi-A (Homo sapiens) GFBess-eschading protein 25 isoform of (Homo sapiens) GFBess-eschading protein 25 isoform of (Homo sapiens) neclated protein 3 isoform of (Homo sapiens) leasonne subunit alipha type-2 (Homo sapiens) leason processor (Homo sapiens)	58.99 4.57 58.16 30.61 1.67 14.24	1 1 2 2 1 1	17 1 26	17	105			4.3		172	20.2	33.77	71.73 0.45	10.	3 4/6	4432		
11596859 39S 5803187 trans 4885165 cysts 297206833 5-hy 261399909 rho 0 5031573 actin 4506181 protot 262206315 L-sel 530419493 PREE 53039494 PREE 530393500 PREE	ri fibosomal protein 1.17, mitochondrial [Homo sapiens] stadidase [Homo sapiens] tatih A [Homo sapiens] tatih A [Homo sapiens] tatih A [Homo sapiens] Giffses-eichwainig protein 25 isoform ( [Homo sapiens) Giffses-eichwainig protein 25 isoform ( [Homo sapiens) eicheling frotein 3 isoform 1 [Homo sapiens] technome suburul shall pape 2 [Homo sapiens] teiching procursor [Homo sapiens] Dietling frocursor [Homo sapiens]	4.57 58.16 30.61 1.67 14.24	1 2 1	1 26	1		1.005				41	12.2		58.99	4	4 105			
5803187 trans 4885165 cysts 297206833 5-hy 26139909 rho o 5031573 actin 4506181 prote 262206315 L-sei 530419493 PREE 530393500 PREE	nsaldolase (Homo saplens)  attin A (Homo saplens)  G1Psas-ectivating protein 25 isoform d (Homo saplens)  G1Psas-ectivating protein 25 isoform c (Homo saplens)  n-related protein 3 isoform 1 (Homo saplens)  teated protein 3 isoform 1 (Homo saplens)  teatesome subunit alpha type-2 (Homo saplens)  leictin precursor (Homo saplens)  leictin precursor (Homo saplens)	58.16 30.61 1.67 14.24	2	26		103	1.005		2.1		91	10.7	50.88	4.57	4	3 /	175		
4885165 cystz 297206833 5-hy 26139909 rho 0 5031573 actin 4506181 prote 262206315 L-sel 53041942 PREE 530392494 PREE 530393500 PREE	Istain-A (Homo sapiens) ydroxytryptamine receptor 4 isoform d (Homo sapiens) GTPase-activating protein 25 isoform c (Homo sapiens) n-related protein 3 isoform 1 (Homo sapiens) n-related protein 3 isoform 1 (Homo sapiens) selsom subunit albah type-2 (Homo sapiens) selsofin procursor (Homo sapiens) DIDITED: protein kinase C and cassini kinase substrate in neuro	30.61 1.67 14.24	1		26	335	1.005				130	13.5		58.16	7	1 335			
297206833 5-hy 261399909 rho 0 5031573 actin 4506811 prote 262206315 L-sel 530419493 PREE 530392494 PREE 530393500 PREE	ydroxytryptamine receptor 4 isoform d [Homo sapiens] GPrase-activating protein 25 isoform c [Homo sapiens] n-related protein 3 isoform 1 [Homo sapiens] teasome subunit alpha type-2 [Homo sapiens] electin precursor [Homo sapiens] DICTED: protein kinase C and casein kinase substrate in neuro	1.67 14.24	- 4	2	2	9	1.005				3	7.2	634.19	30.61		6	98		
26139909 rho 0 5031573 actin 4506181 prote 262206315 L-sel 530419493 PREI 530392494 PREI 530393500 PREI	GTPase-activating protein 25 isoform c [Homo sapiens] n-related protein 3 isoform 1 [Homo sapiens] teasome subunit alipha type-2 [Homo sapiens] slectin precursor [Homo sapiens] EDICTED: protein kinase C and casein kinase substrate in neuro	14.24		1	1	2	1.005		10.	1.126	1	7.2	28.67	1.67		2	360		
5031573 actin 4506181 prote 262206315 L-sel 530419493 PREE 530392494 PREE 530393500 PREE	n-related protein 3 isoform 1 [Homo sapiens] teasome subunit alpha type-2 [Homo sapiens] electin precursor [Homo sapiens] DICTED: protein kinase C and caseln kinase substrate in neuro		6		8	26	1.005		4.		10	10.9	923.91	14.24	2	1 26			
4506181 prote 262206315 L-sel 530419493 PREI 530392494 PREI 530393500 PREI	teasome subunit alpha type-2 [Homo sapiens] electin precursor [Homo sapiens] EDICTED: protein kinase C and casein kinase substrate in neuro		11	22	22	264	1.005		6.	7 1.140	96	15.6	11733.98	74.40	6	5 264			
262206315 L-sel 530419493 PREI 530392494 PREI 530393500 PREI	electin precursor (Homo sapiens) DICTED: protein kinase C and casein kinase substrate in neuro	41.03	1	6	6	33	1.005		6.3		12	19.2	1724.79	41.03	1	7 33			
530392494 PREE 530393500 PREE		4.16	1	2	2	7	1.005	3	0.1	1 1.193	3	3.6	180.04	4.16		5 7	385	43.	6 7.15
530393500 PREE	DICTED: protein FAM107B isoform X3 [Homo sapiens]	14.61	4	6	6	26	1.005	5	8.	4 1.096	9	13.8	938.68	14.61	11	B 26	445	51.	3 5.39
		32.06	2	5	5	20	1.005	8	10.	5 1.212	8	15.2	568.85	32.06	11	3 20	131	15.	5 8.29
22091452 apoli	DICTED: hexokinase-1 isoform X3 [Homo sapiens]	7.65	6	5	7	24	1.005	5 5	1.3	2 1.276	5	19.9	960.08	7.65	11	9 24	889	99.	
	lipoprotein M isoform 1 [Homo sapiens]	42.55	3	5	5	29	1.005		5.		10	22.2		42.55	11	-			
	tathione S-transferase omega-1 isoform 1 [Homo sapiens]	71.78	3	16		168	1.005				63	6.7	5488.62	71.78	4				
	exin A4 [Homo sapiens]	63.24	2	18	20	140	1.005				45	12.2		63.24	5	5 140			
	IH basal transcription factor complex helicase XPD subunit isofo	1.73	3	1	1	2	1.005		6.3		2	10.3		1.73		1 2	405		
	sphatidylcholine-sterol acyltransferase precursor [Homo saplent	3.18	1	1	1	3	1.004			1.027	1		177.20	3.18		3 3	440		
	osine-protein phosphatase non-receptor type 6 isoform 1 [Homo		4	20	20	102	1.004		6.0		37	15.0		40.34	51				
	DICTED: mitogen-activated protein kinase 14 isoform X1 [Hom		47	6	6	21	1.004		2.		5	23.5	709.51	27.92	10	5 21			
	ngation factor 2 [Homo sapiens]	38.11	1	27	27	137	1.004		4.9		51 611	11.8	5258.73 75900.62	38.11	7:				
	inogen beta chain isoform 1 preproprotein [Homo sapiens]	78.00 47.77	2	39	39	1692 51	1.004				611	20.8		78.00 47.77	100	5 51			
	ineurin-like phosphoesterase domain-containing protein 1 isofo endonuclease 1 [Homo sapiens]	47.77	2	12	12	51	1.004		5.:		18	14.6	2412.85 211.45	47.77	3	51	314		
	ne-binding protein 2 [Homo sapiens]	30.73	1	2	2	26	1.004		4.1		10	8.4 17.8		30.73		4 26			
	cylolycerol kinase eta isoform 2 [Homo sapiens]	0.66	1	1	1	20	1.004		0	1.503	10	17.0	29.89	0.66		20	1220		
	22 domain family protein 4 [Homo sapiens]	7.09	1	1	1	2	1.004			1.143	1		344.38	7.09		3	395		
	imethylaminobutyraldehyde dehydrogenase [Homo sapiens]	6.56	1	3	3	7	1.004		3.1		3	1.4	315.31	6.56		7	518		
	eptor-type tyrosine-protein phosphatase C isoform 2 precursor [	16.24		14	14	36	1.004				14	9.8		16.24	3	3 36			
	DICTED: MOB kinase activator 1B isoform X2 [Homo sapiens]	13.22	5	2	2	6	1.004		10.:		2	23.6	225.93	13.22		5 6	174		
	one H2A type 2-B [Homo sapiens]	22.31	2	1	4	28	1.004		0.		2	14.1	587.90	22.31	1	1 28			
530386907 PREI	DICTED: GTPase IMAP family member 8 isoform X2 [Homo sap	2.85	2	2	2	7	1.004	4	4.:	2 1.167	4	11.7	83.24	2.85		5 7	456	51.	3 8.18
117320537 1-ph	hosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma	5.06	1	4	4	10	1.004	4	2.0	0 1.153	4	10.2	426.26	5.06	10	10	1265	147.	8 6.64
	atin, type II cytoskeletal 5 [Homo sapiens]	17.12	12	2	13	68	1.004	4	3.	5 1.115	4	4.5	2041.37	17.12	3-	4 68	590	62.	3 7.74
530369318 PREE	DICTED: ras-related protein Ral-B isoform X4 [Homo sapiens]	6.80	2	1	1	3	1.004	1		1.191	1		241.57	6.80		3 3	206	23.	4 6.62
4503117 cysta	tatin-B [Homo sapiens]	59.18	1	5	5	35	1.004	13			13	8.0	1099.76	59.18	11	5 35			
	cetylmuramoyl-L-alanine amidase precursor [Homo sapiens]	30.56	2	9	9	54	1.004		7.		18	17.7		30.56	2	7 54			
	luronan-binding protein 2 isoform 2 [Homo sapiens]	8.43	2	4	4	9	1.003		5.0		4	14.7	219.92	8.43		8	534		
	ancer of rudimentary homolog [Homo sapiens]	16.35	1	2	2	8	1.003		1.1		3	4.4		16.35		5 8	104		
	midine phosphorylase isoform 1 proprotein [Homo sapiens]	38.38	2	14			1.003				21	12.3		38.38	31	-			
	exin A3 [Homo sapiens]	81.42	7	31			1.003				159	13.9		81.42	9:				
19913428 V-typ	pe proton ATPase subunit B, brain isoform [Homo sapiens]	30.53	3	10	10	48	1.003				16	26.4		30.53	21	8 48			
	hepsin Z preproprotein [Homo sapiens]	12.87	1	3	3	9	1.003		0.:		3	13.8	359.37	12.87		9 9	303		
23110925 prote 530391028 PREI	teasome subunit beta type-6 isoform 1 proprotein [Homo saple	6.69	1	2	2	742	1.003		2.0		264	4.9 16.8	325.59 34337.25	6.69	100	4 10 2 742			
	DICTED: gelsolin isoform X6 [Homo sapiens]	62.24 39.90	10	35	35	742 177	1.003		8.4		63	16.8	34337.25 6900.79	62.24 39.90	10:	2 742			
	min precursor [Homo saplens] :DICTED: hepatocyte growth factor-like protein isoform X4 [Hor		2	19	19	1//	1.003		8.:		63	16.4		2.89	51	1//	519		
	EDICTED: hepatocyte growth factor-like protein isolomi x4 [nor EDICTED: lysM and putative peptidoglycan-binding domain-cont	1.63	12	1	1	4	1.003		0	1.104	2	5.1	23.24	1.63		1 1	306		
	DICTED: anoctamin-6 isoform X3 [Homo saplens]	1.23	10		2	4	1.003			1.154	1		43.71	1.23		2 /	812		
	tathione peroxidase 3 precursor [Homo sapiens]	28.32	10	- 6	. 6	23	1.003		8.		0	10.5	613.89	28.32	1	5 23			
	zyme C precursor [Homo sapiens]	70.27	1	11	11		1.003				147	16.2		70.27	3				
	ate synthase, mitochondrial precursor [Homo sapiens]	5.79	1	2	2	6	1.003		4.9		2	0.9		5.79		5 6	466		
	DICTED: leukocyte elastase inhibitor isoform X1 [Homo sapien:	52.24	3	17	18	155	1.003	55	7.9	9 1.070	55	7.5	6803.54	52.24	5:	2 155	379	42.	7 6.28
	DICTED: thrombospondin type-1 domain-containing protein 7A		5	1	1	6	1.003	6	4.	3 1.601	6	17.7	107.44	0.92		1 6	1516	169.	
	DICTED: aminopeptidase N isoform X1 [Homo sapiens]	4.45	1	4	4	12	1.003		9.0		4	3.7	498.95	4.45	11	2 12			
4506191 prote	teasome subunit beta type-10 precursor [Homo sapiens]	15.75	1	3	3	14	1.003	5	8.1	8 1.159	5	5.8	951.79	15.75		9 14	273	28.	9 7.81
29826282 prote	tein phosphatase 1G [Homo sapiens]	4.58	1	1	1	3	1.003	1		3.331	1		138.22	4.58		3 3	546	59.:	2 4.36
578811290 PREI	DICTED: PDZ and LIM domain protein 7 isoform X5 [Homo sap	6.38	6	1	1	6	1.003	3 2	7.:	2 1.336	2	0.2		6.38		3 6	188		
	DICTED: centlein isoform X2 [Homo saplens]	0.52	3	1	1	1	1.003	1		1.104	1		27.52	0.52		1 1	1343	155.	
	inoembryonic antigen-related cell adhesion molecule 8 precurs		11	4	4	14	1.002		8.		6	3.9	338.89	15.47		B 14			
	min K-dependent protein S preproprotein [Homo sapiens]	29.14	2	16	16	110	1.002		6.		39	25.2		29.14	4	5 110			
	DICTED: UPF0378 protein KIAA0100 isoform X2 [Homo sapien:	0.43	3	1	1	6	1.002		3.1		1		99.42	0.43		3 6	2092		
	-like protein 6 isoform 1 [Homo sapiens]	1.51	2	1	1	3	1.002			1.393	1		100.58	1.51		3 3	729		
	thymosin alpha isoform 2 [Homo sapiens]	23.64	4	4	4	27	1.002		18.9		9	1.7		23.64	1	2 27			
	DICTED: SH2 domain-containing adapter protein E isoform X1	1.36	2	1	1	78	1.002		81	1.283	1 15	24.1	30.85	1.36 42.17	21	1 1	440		
- 100000	dic leucine-rich nuclear phosphoprotein 32 family member A (Ho		4	5	10	78					15				21				
530363148 PREE 38016947 comp	DICTED: splicing factor, proline- and glutamine-rich isoform X5	12.41 42.30	2	5	6	19 297	1.002		5.1		6	16.1 19.7	739.67 10868.37	12.41 42.30	14	5 297			
	nplement C5 preproprotein [Homo saplens] :DICTED: septin-9 isoform X3 [Homo saplens]	42.30 14.03	4	49	50	297	1.002		5.9		99	19.7	10868.37 929.34	42.30 14.03	14	1 17			
	:DICTED: septin-9 isoform x3 [Homo sapiens] :DICTED: syntaxin-binding protein 2 isoform X1 [Homo sapiens]	18.02	8	4	- 4	22	1.002		6.1		0	16.3	1078.54	18.02	2				
	lipoprotein D precursor [Homo sapiens]	34.39	1	7	7	97	1.002				37	26.4		34.39	2				
	nfilin-2 [Homo sapiens]	31.23	1	7	7	34	1.002				12	17.9		31.23		9 34			
	bitol dehydrogenase [Homo sapiens]	5.60	4	,	2	0	1.002		0.9		2	28.0		5.60		5	357		
	trix metalloproteinase-9 preproprotein [Homo sapiens]	63.51	1	40	40	539	1.002				194	20.9		63.51	11	7 539			
	one H1.0 [Homo sapiens]	28.87	1	6	6	37	1.002				13	16.0		28.87	11				
	DICTED: DENN domain-containing protein 5B isoform X5 [Hom	0.61	5	1	1	1	1.002			1.615	1		23.01	0.61		1 1	1156		
	na-synuclein isoform NACP112 [Homo sapiens]	19.64	4	2	2	6	1.002	2 2	7.	4 1.065	2	2.8	395.09	19.64		5 6	112	11.	4 8.29
530421239 PREI	DICTED: spermine synthase isoform X2 [Homo sapiens]	2.91	4	1	1	- 1	1.002	2 1		1.297	1		28.32	2.91		1 1	275	31.	1 4.93
	DICTED: protein kinase C delta type isoform X2 [Homo sapiens	5.92	14	3	4	14	1.002	2 4	1.9	9 1.090	4	4.3	573.28	5.92	1	1 14	676	77.	5 7.75
578815670 PREE	DICTED: V-type proton ATPase subunit H isoform X1 [Homo sa	2.37	2	1	1	3	1.002	2 1		1.350	1		80.17	2.37		3 3	465	54.	1 6.48
4557741 plate	elet-activating factor acetylhydrolase IB subunit alpha [Homo s		1	3	4	15	1.002	2 3	2.0		3	8.4	471.73	10.24	1:	2 15	410	46.	
	tein S100-A9 [Homo sapiens]	91.23	1	16	16	4917	1.002	1792			1787	18.4	183128.22	91.23	4				2 6.13
	ment epithelium-derived factor precursor [Homo sapiens]	46.89	1	14	14	119	1.002	2 45	8.1	8 1.212	45	17.3	5610.40	46.89	4:	2 119	418	46.	
	A polymerase epsilon catalytic subunit A [Homo sapiens]	0.52	23	2	2	5	1.002			0.919	1		75.77	0.52		5 5	2286		
	1 complex subunit beta-1 isoform b [Homo sapiens]	8.84	4	3	7	19	1.002		1.1		3	0.1	691.47	8.84	1	7 19			
	exin A11 isoform 2 [Homo sapiens]	35.81	4	16	17	98	1.001				34	10.5		35.81	51				
	in isoform E [Homo sapiens]	7.54	6	3	3	10	1.001		2.:		4	29.3	293.35	7.54		8 10			
578809862 PREI	DICTED: serine/threonine-protein kinase NIM1 isoform X2 [Hor	2.56	6	2	2	2	1.001			1.395	1		27.92	2.56		2 2	312		
195927020 calcii	cium-binding protein 39 [Homo sapiens]	21.99	2	7	7	33	1.001	11	2.1	8 1.094	11	10.7	1072.24	21.99	2	1 33	341	39.	8 6.89

540344580 4557871 578813718 14916455 299829294 5031815	Description  Description  Liactate dehydrogenase B chain (Homo sapiens)  Liactate dehydrogenase B chain (Homo sapiens)  probable guanine nucleotide exchange factor MCF2L2 (Homo sapie serotransferrin precursor (Homo sapiens)	ΣCoverage 60.12 51.50	Σ# Proteins 8	Σ# Unique Peptides	Σ# Peptides	94	A8: 115/114 1.001	A8: 115/114 Count 35	A8: 115/114 Variability [%] 5.6	A8: 117/116 5 1.187	A8: 117/116 Count A8: 117/116 Variabilit	ty [%] 9.8	Score A(3,6,7) C 2931.58	60.12 # Peptides A(3,6,7)	36 # PSM A(3,6,7) 36 9	# AAs 4 173		calc. pl
291575128 540344580 4557871 578813718 14916455 299829294 5031815	L-lactate dehydrogenase B chain [Homo sapiens] probable guanine nucleotide exchange factor MCF2L2 [Homo sapie	51.50	4	15	13	74	1.001	33			33							
540344580 4557871 578813718 14916455 299829294 5031815	probable guanine nucleotide exchange factor MCF2L2 [Homo saple				17	132	1.001	36	7.4	4 1.136	35	9.7	4713.24	51.50	50 13:	2 334	4 36.6	
578813718 14916455 299829294 5031815	serotransferrin precursor [Homo sapiens]	0.72	1	1	1	5	1.001	5	4.5		5	7.0	48.77	0.72	1	5 1114		
14916455 299829294 5031815		81.38	43	66	68	3182	1.001	1163	8.5	1.270	1149	23.8	135782.65	81.38	197 318:			
299829294 5031815	PREDICTED: septin-7 isoform X5 [Homo sapiens]	17.10	18	5	6	26	1.001	7	2.6		7	7.7	1025.33	17.10	18 2			
5031815	serine/threonine-protein kinase H2 [Homo sapiens]	2.34	1	1	1	- 1	1.001	1 23	5.6	0.603 5 1.167	1 23	13.2	28.83 2614.88	2.34	1 6	1 385		
	neutrophil cytosol factor 2 isoform 2 [Homo sapiens] lysinetRNA ligase isoform 2 [Homo sapiens]	38.46 4.86	2	2	2	12	1.001	4	10.2		4	9.2	697.31	38.46 4.86	6 1			
UAU 1 1020J	Golgin subfamily A member 5 [Homo sapiens]	0.82	1	1	1	11	1.001	6	23.4		6	36.2	125.22	0.82	2 1			
70906437	fibrinogen gamma chain isoform gamma-A precursor [Homo sapler	82.84	4	35	36	1801	1.001	686	11.3	2 1.235	678	23.4	62867.08	82.84	104 180	1 437	7 49.5	6.09
	PREDICTED: piezo-type mechanosensitive ion channel component	0.32	3	1	1	1	1.001	1		0.982	1		21.05	0.32	1	1 2497		
	ras-related protein Rab-8B [Homo sapiens]	27.05	21	2	5	37	1.001	6	7.1	1 1.245	6	9.6	1674.26 0.00	27.05	14 3			
	PREDICTED: protein asunder homolog isoform X4 [Homo sapiens] PREDICTED: ninjurin-2 isoform X2 [Homo sapiens]	1.11 5.66	2	1	1	3	1.001 1.001	1		1.189	1		44.92	5.66	3	1 63		6.62
	angiotensinogen preproprotein [Homo sapiens]	49.48	1	13	13	144	1.000	53	7.3		50	25.4	6889.06	49.48	37 14			
	chloride intracellular channel protein 1 [Homo sapiens]	82.99	8	16	16	162	1.000	60	9.1		58	20.0	5687.64	82.99	46 16			
	PREDICTED: COMM domain-containing protein 6 isoform X1 [Home	9.00	1	1	1	3	1.000	2	2.7		2	4.5	53.04	9.00	3	3 100		
	dual specificity tyrosine-phosphorylation-regulated kinase 4 isoform	2.15	1	1	1	46	1.000	17	4.1		17	12.9	545.41	2.15	3 4			
	fibronectin isoform 3 preproprotein [Homo sapiens] KH domain-containing, RNA-binding, signal transduction-associated	49.21 3.61	28	83	83	704	1.000	255	7.9	9 1.181	253	17.6	32288.19 87.87	49.21 3.61	240 70	4 2355 3 443		
	apolipoprotein(a) precursor [Homo sapiens]	4.41	10	1	1	3	1.000	1		1.076	1		118.34	4.41	3	3 2040		
	fetuin-B precursor [Homo sapiens]	10.73	3	3	3	8	1.000	3	4.5		3	12.7	327.67	10.73	8	8 382		
4503987	gamma-glutamyl hydrolase precursor [Homo sapiens]	33.96	1	8	8	40	1.000	14	4.5	1.282	14	17.1	1645.45	33.96	23 4			
21735621	malate dehydrogenase, mitochondrial isoform 1 precursor [Homo s	23.96	3	6	6	23	1.000	8	5.1		8	6.7	1187.57	23.96	17 2			
189083844 42822872	dipeptidyl peptidase 1 isoform a preproprotein [Homo sapiens] ribonuclease inhibitor [Homo sapiens]	18.36 50.11	3	6	6	26 93	1.000	9 34	8.6		9 33	9.7	1141.09 5325.98	18.36 50.11	18 2 42 9			
	DNA damage-binding protein 1 [Homo sapiens]	3.68	1	14	14	93	1.000	34	5.0		33	12.6	5325.98	3.68	42 9	9 1140		
	SH3 domain-binding glutamic acid-rich-like protein [Homo sapiens]	91.23	1	10	10	68	1.000	27	6.9		27	17.8	2753.48	91.23	28 6			
153266841	beta-2-glycoprotein 1 precursor [Homo sapiens]	58.84	1	16	16	251	1.000	100	9.6	5 1.121	98	19.7	8799.46	58.84	47 25	1 345	5 38.3	7.97
	PREDICTED: complement C1q subcomponent subunit B isoform X1	43.08	3	9	9	94	1.000	36	7.1		35	30.7	3780.59	43.08	25 9			
	inter-alpha-trypsin inhibitor heavy chain H2 precursor (Homo saple	32.66	1	23		209	1.000	78	7.2		77	15.4	8888.92	32.66	67 20			
	UTPglucose-1-phosphate uridylyltransferase isoform a [Homo sar coronin-1A [Homo sapiens]	53.94 62.91	14	24		139 375	1.000	52 140	9.3		52 134	13.5	6625.94 13055.07	53.94 62.91	63 13 <sup>3</sup> 89 37 <sup>3</sup>			
	BH3-interacting domain death agonist isoform 2 [Homo sapiens]	19.49	14	30	31	24	1.000	140	5.0			18.6	1492.76	19.49	7 2			
4506671	60S acidic ribosomal protein P2 [Homo sapiens]	40.87	1	3	3	10	1.000	4	7.3	3 1.104	4	11.1	602.09	40.87	8 1	115	5 11.7	4.54
559098411	uncharacterized protein KIAA1958 isoform c [Homo sapiens]	1.56	3	1	1	1	1.000	1		1.362	1		31.58	1.56	1	1 448		
	actin-related protein 2 isoform b [Homo sapiens]	56.09	28	15		177	0.999	52	5.5		50	21.5	7240.21	56.09	48 17			
88853069 170016081	vitronectin precursor [Homo sapiens] protein XRP2 [Homo sapiens]	35.36 8.00	1	10	11	110	0.999	41	6.4		41	19.3 15.8	4440.69 419.08	35.36 8.00	30 11			
	PREDICTED: C4b-binding protein alpha chain isoform X2 [Homo sa	47.07	1	25	25	261	0.999	101	5.4		101	15.5	9294.63	47.07	71 26			
	actin-related protein 2/3 complex subunit 3 isoform 2 [Homo saple	40.11	2	8	8	55	0.999	20	7.3		20	9.3	1680.17	40.11	24 5			
635172849	beta-hexosaminidase subunit beta isoform 2 [Homo sapiens]	11.48	2	3	3	9	0.999	3	0.2	2 1.093	3	10.5	456.76	11.48	9	9 33		
	protein ANKUB1 [Homo sapiens]	0.92	1	1	1	1	0.999	1		1.173	1		25.94	0.92	1	1 544		
	serine/threonine-protein kinase PAK 2 [Homo sapiens]	15.27	7	43	43	19 418	0.999	162	10.0		6 158	22.8 25.3	777.12	15.27	14 11	9 524 B 764		
	complement factor B preproprotein [Homo sapiens] eukarvotic translation initiation factor 4 gamma 2 isoform 2 [Homo	1.73	33	43	43	418	0.999	162	8.	1.277	158	25.3	15867.40 142.81	1.73	6	6 869		
108773793	glucose-6-phosphate 1-dehydrogenase isoform b [Homo sapiens]	64.08	8	33	33	296	0.999	109	6.3		108	18.5	12253.40	64.08	95 29			
578812604	PREDICTED: nesprin-1 isoform X19 [Homo sapiens]	0.13	20	1	1	6	0.999	2	7.3	3 1.019	2	0.2	158.35	0.13	3	6 872	1 1002.8	5.52
68509926	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DH	3.90	1	3	3	10	0.999	5	2.0			2.7	492.73	3.90	9 1			
	PREDICTED: N-myc-interactor isoform X1 [Homo sapiens]	32.57	1		8	27 50	0.999	11	4.8 9.3		11	30.5 7.6	1102.05	32.57	19 2 24 5			
4507149	1,4-alpha-glucan-branching enzyme [Homo sapiens] superoxide dismutase [Cu-Zn] [Homo sapiens]	16.38 64.29	1	8	8	36	0.999	17	9.0		17	10.4	2670.93 2658.11	16.38 64.29	17 3			
	bcl-2-like protein 15 [Homo sapiens]	8.59	1	1	1	2	0.999	1	***	1.480	1	10.4	49.75	8.59	2	2 163		
	adiponectin precursor [Homo sapiens]	6.15	1	1	1	3	0.999	1		0.972	1		142.42	6.15	3	3 244		
	alcohol dehydrogenase class-3 [Homo sapiens]	5.08	1	3	3	6	0.999	3	2.1		3	5.2	103.69	5.08	6	6 374		
	zinc-alpha-2-glycoprotein precursor [Homo sapiens] PREDICTED: solute carrier family 25 member 48 isoform X6 [Homo	59.40 2.57	1	20	20	213	0.999	77	6.0		77	17.9 16.7	8594.26 38.54	59.40 2.57	58 21	3 298		
	clathrin interactor 1 isoform 3 [Homo sapiens]	5.92	3	3	3	11	0.998	4	7.3		4	20.4	387.27	5.92	8 1			
	coagulation factor XII precursor [Homo sapiens]	19.35	1	- 8	8	36	0.998	13	5.9		13	4.1	1499.12	19.35	21 3			
	endoplasmin precursor [Homo sapiens]	17.68	23	12	14	52	0.998	16	8.2	2 1.095	16	6.4	2428.22	17.68	38 5.	2 803	3 92.4	4.84
52353252	olfactory receptor 52E4 [Homo sapiens]	3.21	1	1	1	1	0.998	1		0.908	1		20.06	3.21	1	1 312		
	SH3 domain-binding protein 1 [Homo sapiens]	1.28	1	1	1	3	0.998	1		1.076	1		164.23	1.28	3	3 701		
48255891 62912466	glucosidase 2 subunit beta isoform 2 precursor [Homo sapiens] C4b-binding protein beta chain isoform 2 precursor [Homo sapiens	11.62 27.89	6	6	6	26	0.998	9	5.9		9	12.4	987.06 672.85	11.62 27.89	18 2 16 2			
34365783	visual system homeobox 2 [Homo sapiens]	2.49	1	1	1	6	0.998	3	1.7		3	8.4	83.42	2.49	2	6 361		7.55
578811759	PREDICTED: UHRF1-binding protein 1 isoform X3 [Homo sapiens]	0.40	17	1	1	6	0.998	2	4.5	7 1.130	2	0.3	53.73	0.40	3	6 1240	137.4	6.30
41393602	complement C1s subcomponent precursor [Homo sapiens]	36.19	1	18	18	103	0.998	38	9.3		36	18.7	3477.19	36.19	48 10			
	phosphoglucomutase-1 isoform 1 [Homo sapiens]	54.80	3	19	19	126	0.998	45	5.7		41	27.1	6311.32	54.80	57 12			
	apoptotic protease-activating factor 1 isoform d [Homo sapiens] PREDICTED: tropomyosin beta chain isoform X4 [Homo sapiens]	2.07 33.45	5	2	2	106	0.998	2	17.5 7.5		2	4.8 18.8	276.98 3511.87	2.07 33.45	43 10	5 1205 6 284		
	mediator of RNA polymerase II transcription subunit 15 isoform e [	1.62	5	1	1/	3	0.998	3	7.5		3	24.4	41.81	1.62	1	3 67		
	myotrophin [Homo sapiens]	66.10	32	7	8	52	0.998	19	7.6		19	11.5	2154.14	66.10	23 5:			
4506005	serine/threonine-protein phosphatase PP1-beta catalytic subunit is:	28.13	4	2	7	50	0.998	5	4.3		5	7.6	1674.72	28.13	19 5	327		6.19
55956899	keratin, type I cytoskeletal 9 [Homo sapiens]	17.50	2	5	6	30	0.998	8	6.4		8	8.0	1529.83	17.50	18 3			
	transferrin receptor protein 1 [Homo sapiens]	3.03	1	2	2	6	0.998	2	0.6		2	36.7	248.26	3.03	6	6 760		
4826762 4557581	haptoglobin isoform 1 preproprotein [Homo sapiens] fatty acid-binding protein, epidermal [Homo sapiens]	74.14 62.22	17	20	36	4278 65	0.998	929 24	11.1		862 24	36.0 10.9	154609.73 2321.01	74.14 62.22	105 427 22 6			
	rho GTPase-activating protein 1 [Homo sapiens]	27.79	17	8	8	34	0.997	12	6.9		12	15.9	1389.80	27.79	23 3			
312176435	stromal membrane-associated protein 2 isoform 4 [Homo sapiens]	2.29	5	1	1	2	0.997	1	-	1.327	1		70.92	2.29	2	2 349	9 37.7	9.11
530387555	PREDICTED: proline synthase co-transcribed bacterial homolog pro	8.23	2	1	1	3	0.997	1		1.154	1		137.77	8.23	3	3 158		
	olfactory receptor 51G1 [Homo sapiens]	2.49	1	1	1	2	0.997	1	7.3	1.514	1	19.3	33.78	2.49	2	321		
	cAMP-dependent protein kinase type I-alpha regulatory subunit iso purine nucleoside phosphorylase [Homo sapiens]	28.61 60.21	2	7	7	131	0.997	12 50	7.2		12 50	19.3	1487.09 5117.50	28.61 60.21	17 3 42 13			
	PREDICTED: polyadenylate-binding protein 1 isoform X1 [Homo sa	6.29	5	15	4	11	0.997	4	5.0			3.4	469.57	6.29	11 1			
	U6 snRNA-associated Sm-like protein LSm1 [Homo saplens]	5.26	1	1	1	2	0.997	1	5.0	1.029	1	5.4	40.27	5.26	2	2 133		
530405775	PREDICTED: pro-interleukin-16 isoform X5 [Homo sapiens]	6.97	7	4	4	9	0.997	4	1.1			5.4	377.50	6.97	9	9 63	1 66.6	5.97
157276599	bactericidal permeability-increasing protein precursor [Homo sapler	47.23	7	19		178	0.997	65	7.5		59	23.4	7630.54	47.23	54 17			
530405979	PREDICTED: pyruvate kinase PKM isoform X3 [Homo sapiens]	82.11 69.91	38	4	49	946	0.997	38 516	8.8		38 507	16.6	42482.76 51441.96	82.11 69.91	139 94 87 131			
530395269 11863154	PREDICTED: hemopexin isoform X1 [Homo sapiens] coatomer subunit delta isoform 1 [Homo sapiens]	13.70	5	30	30	1318 31	0.997	516	7.3		507	24.8 13.3	51441.96 1371.29	69.91 13.70	20 3			
	protein S100-A8 [Homo sapiens]	100.00	8	22	23	3965	0.997	1499	8.8		1481	20.8	155887.78	100.00	67 396			
20357599	histone H2A.V isoform 2 [Homo sapiens]	48.25	7	2	4	31	0.997	4	11.4	4 0.951	3	40.3	969.66	48.25	12 3	1 114	4 12.1	10.46
	colled-coll domain-containing protein 25 [Homo sapiens]	4.33	1	1	1	1	0.997	1		1.037	1		29.14	4.33	1	1 208		
6005764	gamma-aminobutyric acid receptor-associated protein [Homo sapic	19.66	3	2	2	8	0.997	4	6.9	9 1.054	4	11.4	203.00	19.66	5	8 117	7 13.9	8.79

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Accession 520975489	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]		A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)		,7) # Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pl
520975489 217035154	ran-specific GTPase-activating protein isoform 4 [Homo sapiens]	22.67	6		2 2	9	0.997	3	1.4	1.150 2 1.080	3	3 1.i 4 5.!	532.36 1165.10	22.67 23.32		5	9 150 5 416		
530360793	capZ-interacting protein [Homo sapiens] PREDICTED: serine/arginine repetitive matrix protein 1 isoform X6	0.68	2		, ,	35	0.996	14	4.		14	1 24.:		0.68	20	3	1 888		
	ceruloplasmin precursor [Homo sapiens]	74.93	,		2 63	839	0.996	12	4.		10	2 12.		74.93	178	839			
5174449	histone H1x [Homo sapiens]	28.17	1		7 7	35	0.996	13	6.		13			28.17	19	35			
33457348	UPF0556 protein C19orf10 precursor [Homo sapiens]	5.20	1	1	1 1	3	0.996	1		1.193	1	1	130.28	5.20	1	3	3 173	3 18.8	8 6.68
578800866	PREDICTED: gamma-interferon-inducible protein 16 isoform X2 [H	3.69	4		2 2	5	0.996	2	1.3	B 1.467	2	2 49.6		3.69	5		677	7 76.3	
	PREDICTED: THO complex subunit 4 isoform X1 [Homo sapiens]	19.39	2	3	3	13	0.996		4.		5	5 11.4		19.39	3	1:			
	protein \$100-A4 [Homo sapiens]	69.31	1		6 6	122	0.996	44	8.		43			69.31	18	122			
	dynactin subunit 1 isoform 4 [Homo sapiens]	3.78	6		3 3	9	0.996		4.9		3			3.78	9	9	9 1139		
4505227 578813467	myeloid cell nuclear differentiation antigen [Homo sapiens]	77.89 c 38.66	59	36	6 37		0.996	194	7		194			77.89 38.66	107				
4503635	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isof prothrombin preproprotein [Homo sapiens]	56.59	11	27			0.996	32	7.9		32			38.66 56.59	77				
	bcl-2-binding component 3 isoform 2 [Homo sapiens]	5.34	2	2.1	1 1	222	0.996	. 1		1.271	1	1 17	27.87	5.34		222	2 131		
	rho GDP-dissociation inhibitor 1 isoform a [Homo sapiens]	46.08	2		9 10	73	0.995	26	6.		26	14.		46.08	26	7:			
4885379	histone H1.4 [Homo sapiens]	47.03	3	3	3 15	336	0.995	14	3.0		14			47.03	44	336			
5454052	14-3-3 protein sigma [Homo sapiens]	53.23	1	6	6 12	136	0.995	10	8.1	1.086	10	9.:	4063.89	53.23	34	136	6 248	8 27.8	8 4.74
4826898	profilin-1 [Homo sapiens]	75.00	4	12	2 12	738	0.995	270	8.1	1.139	268	14.3	33099.23	75.00	35	738	8 140	15.0	0 8.27
50592994	thioredoxin isoform 1 [Homo sapiens]	63.81	3		6 6	89	0.995		8.3		34			63.81	18	89			
	PREDICTED: interleukin-1 receptor antagonist protein isoform X1	18.18	4		2 2	7	0.995		4.		3	5.		18.18	4	1	7 143		
	PREDICTED: nucleosome assembly protein 1-like 1 isoform X18 [H		6		1 1	3	0.995	1		0.952			103.28	3.35	-		3 328		
	UV excision repair protein RAD23 homolog B isoform 1 [Homo sap	19.80	41		6 8	26	0.995	7	7.0	5 1.223 1.006	7	7 8.:	979.35 195.92	19.80 6.21	23	3 20	6 409 3 145		
209969703	40S ribosomal protein S19 [Homo sapiens] protein RCC2 [Homo sapiens]	4.98	1		1 1	3	0.995	1	4.9		1	3		4.98	-	3	B 522		
	phosphoglycolate phosphatase [Homo saplens]	4.05	- 1		1 1	3	0.995	1	4.	1.245	1	1	184.22	4.75		3	3 321		
4503471	elongation factor 1-alpha 1 [Homo sapiens]	56.71	2	18	8 18	170	0.995	61	5.		61	15.1		56.71	51	170			
	PREDICTED: forkhead box protein O3 isoform X1 [Homo sapiens]	1.45	1	1	1 1	3	0.995	3	0.1		3	12.		1.45			3 484		
63162572	T-complex protein 1 subunit gamma isoform a [Homo sapiens]	21.83	2	10	0 10	30	0.995	11	4.1	B 1.148	11	1 9.:	1193.88	21.83	21	7 30	545	5 60.5	5 6.49
50845386	annexin A2 isoform 2 [Homo sapiens]	70.50	2	23	3 24	105	0.995	38	3.9		37	7 8.3		70.50	66	105			
	RNA-binding motif protein, X-linked-like-3 [Homo sapiens]	2.16	2	1	1 2	7	0.995	1		1.359	1	1	325.53	2.16	4	1	7 1067		
	structural maintenance of chromosomes protein 3 [Homo sapiens]	1.81	1		2 2	10	0.995	4	6.		4	25.		1.81		10			
	cystelne-rich secretory protein 3 isoform 1 precursor [Homo sapier		2	13	7 7	40	0.995	15	6.1		15			36.43	19				
	carbonic anhydrase 1 isoform a [Homo sapiens] PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform	82.76	16	13	3 13	449	0.995		10.		160	-		82.76 3.05	39	449	9 261 5 393		
578814219 4506179		3.05	16	1	1 1		0.995	2 24	0.:		24			3.05 52.85	33	5			
4826772	proteasome subunit alpha type-1 isoform 2 [Homo saplens] insulin-like growth factor-binding protein complex acid labile subur		3	12	7 12	2 58	0.995		4.1		24			13.72	20				
	hexokinase-3 [Homo saplens]	45.72	1	27	7 29	161	0.995	53	4.9		51			45.72	86	16			
4503165	cullin-3 isoform 1 [Homo saplens]	1.04	3	-	1 1	2	0.995	1		1.129	1	1	56.43	1.04		2	2 768		
345197264	tumor protein D54 isoform h [Homo sapiens]	14.72	10	:	2 2	6	0.995	2	2.0	5 1.133	2	2 3.4		14.72		5	6 163		
296179386	clathrin light chain A isoform e [Homo sapiens]	10.12	6		2 2	2 8	0.995	3	3.		3	3 0.5		10.12		i 1	8 168		
431822408	heat shock protein HSP 90-beta isoform c [Homo sapiens]	44.12	15	13	3 29	228	0.994	24	3.		24	1 13.4		44.12	81	228			
	complement C2 isoform 5 [Homo sapiens]	29.18	6	17	7 17	78	0.994	30	6.		29			29.18	50	78			
187607300	versican core protein isoform 2 precursor [Homo sapiens]	6.26	4	3	3	12	0.994	4	2.		4	4.		6.26	9	1:			
11067747 4505047	cell division cycle 5-like protein [Homo sapiens]	1.75	12	13	1 2	2 4	0.994	1 34	5.:	1.113 3 1.157	34	1 6.	63.93 2 3778.36	1.75		9	4 802 4 338		
	Iumican precursor [Homo sapiens]   GDP-L-fucose synthase [Homo sapiens]	16.20	1	12	3 13	1 11	0.994		5.		39	1 10.5		43.20 16.20	11				
	ferritin light chain [Homo sapiens]	49 71	1		R 5	3 40	0.774		9.		15			49 71	21				
156523970	alpha-2-HS-glycoprotein preproprotein [Homo sapiens]	41.69	1	11	1 11	327	0.994		8.		125			41.69	31				
	PREDICTED: dynein heavy chain 8, axonemal isoform X1 [Homo s	0.25	27	1	1 2	18	0.994			1.200	1	1	155.95	0.25		1 18	8 4707		
315075311	cathepsin S isoform 2 preproprotein [Homo sapiens]	25.98	2	7	7 7	23	0.994	8	2.:	3 1.144	8	8.6	1032.39	25.98	20	2	3 281		
	V-type proton ATPase catalytic subunit A [Homo sapiens]	29.34	1	15	5 15	71	0.994	27	7.0		27	7 22.0		29.34	44				
578838337	PREDICTED: bromodomain and WD repeat-containing protein 3 is	0.86	8	1	1 2	10	0.994	1		1.004	1	1	165.02	0.86	4	1 10			
4502027	serum albumin preproprotein [Homo sapiens]	94.25	13	101	1 101	26879	0.994	10343	8.		10216			94.25	291	26879			
11056044 52632383	inorganic pyrophosphatase [Homo sapiens]	23.18	1	4	4 4	16	0.994	6	2.1		6	5 13.5		23.18 27.50	11	2 38	6 289 8 589		
	heterogeneous nuclear ribonucleoprotein L isoform a [Homo saple janus kinase and microtubule-interacting protein 2 isoform 4 [Hom		6		8 8	38	0.994	16	13.:		15	18.0		27.50	22	2 38	9 778		
4506363	ras-related protein Rab-13 isoform 1 [Homo sapiens]	7.88	4		2 2	15	0.994	4	7.	1.244	- 4	1 5.1	831.91	7.88		1	5 203		
	hydroxyacylglutathione hydrolase, mitochondrial isoform 2 [Homo	1 3.85	2		1 1	3	0.994	1		1.010		1	124.19	3.85		1	3 260		
262263314	cystatin-F precursor [Homo sapiens]	4.83	1	-	1 1	9	0.77-		3			3 9,		4.83			9 145		
530412093	PREDICTED: interferon-induced 35 kDa protein isoform X1 [Homo	22.73	2	1	7 7	21	0.994	8	4.1	8 1.217	8	3 25.	704.69	22.73	18	2	1 286	16 31.5	5 6.09
11641247	Golgi-associated plant pathogenesis-related protein 1 isoform a [H	x 31.82	5	4	4 4	23	0.994	8	4.	3 1.183	8	3 22.	1442.67	31.82	12	2 2:	3 154	17.2	2 9.41
530418509	PREDICTED: eukaryotic translation initiation factor 2 subunit 2 isot	f 17.20	2	4	4 4	12	0.994	4	8.		4	1 7.4		17.20	12	1:			
	pterin-4-alpha-carbinolamine dehydratase isoform 3 [Homo saplen	29.09	2	1	1 1	3	0.994	1		0.964	1	1	132.87	29.09	3	3	3 55		
11559929	coatomer subunit gamma-1 [Homo saplens]	1.26	1	1	1 1	2	0.994			0.908	1		106.80	1.26		2 :	2 874		
5902072	serpin B3 (Homo sapiens)	22.31	2	3	8	27	0.994	10	7.		10	4.0		22.31	23				
4758112 150170699	spliceosome RNA helicase DDX39B [Homo sapiens] kinesin-like protein KIF26A [Homo sapiens]	17.52 0.74	3		7	37	0.994	13	6.:		13	3 14.5 3 21		17.52 0.74	19	31	7 428 B 1882		
	galectin-1 [Homo sapiens]	35.56	1		5 5	26	0.993	3	9.1		3	9 4.		35.56	1/	1 26			
	synaptic vesicle membrane protein VAT-1 homolog [Homo sapiens		1	13	3 13	109	0.993	41	8.		38	26.5		57.00	39	109			
4557759	myeloperoxidase precursor [Homo sapiens]	57.45	2	43			0.993		7.		249			57.45	125				8 8.97
4505621	phosphatidylethanolamine-binding protein 1 preproprotein [Homo	72.19	1	9	9 9	48	0.993	18	9.1	8 1.193	18	11.5	1956.53	72.19	25			7 21.0	0 7.53
4505881	plasminogen isoform 1 precursor [Homo sapiens]	59.01	6	41	1 41	381	0.993		6.1		137	7 16.4		59.01	110	38			
566006166	doublecortin domain-containing protein 2C [Homo sapiens]	1.37	3	1	1 1	- 1	0.993			1.371	1	1	32.65	1.37			1 364		
	PREDICTED: proline-rich protein PRCC isoform X2 [Homo sapiens]	1.96	3	1	1 1	- 1	0.993			1.089	1		28.83	1.96			1 459		
33239451 9845511	proliferating cell nuclear antigen [Homo sapiens]	2.68	1	1	1 1	3 45	0.993		3.	1.208	1	1 04	120.99	2.68	3	3 3	3 261		
9845511 54607120	ras-related C3 botulinum toxin substrate 1 isoform Rac1 [Homo sa lactotransferrin isoform 1 precursor [Homo sapiens]	43.23 86.90	8	60	2 7		0.993		3.4		961	, 0.	2027.27	43.23 86.90	180				
344179112	scavenger receptor cysteine-rich type 1 protein M130 isoform b pr		26	01	1 1	20/0	0.993	9/2	8	1.167	961	15.9	62.65	0.71	180	2676	3 1121		
38202255	threoninetRNA ligase, cytoplasmic isoform 1 [Homo sapiens]	4.15	2		2 2	6	0.993	2	6.:		2	2 1.		4.15		5	6 723		
578812358	PREDICTED: activating signal cointegrator 1 complex subunit 3 iso		2	1	1 1	101	0.993	38	3.		38	13.1		0.27		10	1 1866	6 213.1	
578838657	PREDICTED: septin-6 isoform X3 [Homo sapiens]	14.05	18	4	4 5	21	0.993	5	6.		5	3.3		14.05	15	2	1 427	7 48.8	8 6.81
	poly [ADP-ribose] polymerase 4 [Homo sapiens]	0.75	1	1	1 2	10	0.993			0.892	1	1	127.28	0.75	5	10			
530380590	PREDICTED: prefoldin subunit 1 isoform X1 [Homo sapiens]	9.57	2	1	1 1	3	0.993			1.338	1	1	123.90	9.57	3	3	3 115		
162287326	tyrosine-protein kinase Lyn isoform B [Homo sapiens]	14.46	99	4	4 7	31	0.993		4.:		5	13.5		14.46	21	3			
195539395	26S protease regulatory subunit 10B [Homo sapiens]	3.47	1	1	1 1	3	0.993			0.979	1		188.83	3.47	1	3	3 403		
7657532	protein S100-A6 [Homo sapiens] transforming protein RhoA precursor [Homo sapiens]	61.11 73.06	1	11	9 9	83	0.993		10.0		36			61.11 73.06	24				
10025040			3	11			0.992		11.8		25			73.06 29.36	28				
10835049					- 10	, 36												00.5	
530375762	PREDICTED: carboxypeptidase N subunit 2 isoform X1 [Homo sapi		3		7 10	120	0 00:	13		5 1 103	13		5527.77	54.90	29	120	1 284	5 32.0	7 5.85
	PREDICTED: carboxypeptidase N subunit 2 isoform X1 [Homo sapi F-actin-capping protein subunit alpha-2 [Homo sapiens]	29.36 54.90 46.34	3	20	7 10	120	0.992		10.4		13			54.90 46.34	51				
530375762 5453599 50659080 7657315	PREDICTED: carboxypeptidase N subunit 2 isoform X1 [Homo sapi F-actin-capping protein subunit alpha-2 [Homo sapiens] alpha-1-antichymotrypsin precursor [Homo sapiens] U6 snRNA-associated Sm-like protein LSm3 [Homo sapiens]	54.90 46.34 19.61	3 6	1	7 10 0 20 2 2		0.992		6.	5 1.109 5 1.231		8.3	7394.43	46.34 19.61			7 423 B 102	3 47.6 12 11.8	6 5.52 8 4.70
530375762 5453599 50659080 7657315 14591909	PREDICTED: carboxypeptidase N subunit 2 isoform X1 [Homo sapi F-actin-capping protein subunit alpha-2 [Homo sapiens] alpha-1-antichymotrypsin precursor [Homo sapiens] U6 snRNA-associated Sm-like protein LSm3 [Homo sapiens] 60S ribosomal protein L5 [Homo sapiens]	54.90 46.34 19.61 16.84	3 6 1	1	7 10 0 20 2 2 4 4		0.992 0.992 0.992	61 3 4	6.0 3.0 3.0	5 1.109 5 1.231 5 1.290		8.3 3 10.4 4 21.4	7394.43 329.11 4 269.00	46.34 19.61 16.84		7 16: 5 8	7 423 B 102 1 297	3 47.6 12 11.8 17 34.3	6 5.52 8 4.70 3 9.72
530375762 5453599 50659080 7657315 14591909	PREDICTED: carboxypeptidase N subunit 2 isoform X1 [Homo sapi F-actin-capping protein subunit alpha-2 [Homo sapiens] alpha-1-antichymotrypsin precursor [Homo sapiens] U6 snRNA-associated Sm-like protein LSm3 [Homo sapiens]	54.90 46.34 19.61	3 6 1 1	1	7 10 0 20 2 2 4 4 2 3		0.992	61 3 4 3	6.	5 1.109 5 1.231 5 1.290 1 1.160		8.3	7394.43 329.11 4 269.00 6 668.70	46.34 19.61			7 423 8 102 1 297 4 4646	13 47.6 12 11.8 17 34.3 16 532.1	6 5.52 8 4.70 3 9.72 1 6.40

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Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Count	A8: 115/114 Variability [%]		A8: 117/116 Count A8: 11	17/116 Variability [%]	Score A(3,6,7) C		7) # Peptides A(3,6,7)	# PSM A(3,6,7)			calc. pl
7661862	protein phosphatase 1F [Homo sapiens]	2.64	1	1	1 1	15	0.992	5	2.3	3 1.094	5	9.3	623.72	2.64	3	15	454		5.10
195976754 578813682	dysferlin isoform 9 [Homo sapiens]	0.73	16		1 1	6	0.992	2	1.:	2 1.043	2	21.8	266.34 33.71	0.73	3	6	2066		
578813682 578846043	PREDICTED: caspase recruitment domain-containing protein 11 iso	7.52	4		1 1	202	0.992	1	3.	9 1.356	0	7.8		7.52	2	202			
	PREDICTED: uncharacterized protein LOC102725101 [Homo sapier LIM and SH3 domain protein 1 isoform a [Homo sapiens]	7.52 32.95	2	1	1 3	40	0.992	9	3.º 4.		9	7.8	5642.45 1230.88	7.52 32.95	9	202			8.47
	voltage-gated potassium channel subunit beta-2 isoform 4 [Homo:	30.33	12	,	7 7	20	0.992	17	4.9		17	7.0	627.20	30.33	20	20			
	complement factor H isoform a precursor [Homo sapiens]	57.51	- 12	54	4 60	853	0.992	291	8.3		289	18.5	34483.01	57.51	171				
	phosphatidylinositol 3.4.5-trisphosphate 5-phosphatase 1 isoform b	5.30	2	4	4 4	11	0.992	4	5.1		4	13.4	440.71	5.30	11				
13129110	methylosome protein 50 [Homo sapiens]	4 39	1	1	1 1	3	0.772	1	0.0	1 198	1	10.4	186 44	4.39	3	3	342		
	PREDICTED: core histone macro-H2A.1 isoform X3 [Homo sapiens]	36.96	6	11	1 11	75	0.991	27	7 :		27	21.5	3605.72	36.96	32	75			
45580688	complement component C7 precursor [Homo sapiens]	46.62	1	25		143	0.991	52	7.		52	26.6	6566.60	46.62	74				
	PREDICTED: neuroblast differentiation-associated protein AHNAK is	7.41	9	7	7 7	17	0.991	6	5.		6	10.0	552.69	7.41	15				
45243507	eosinophil cationic protein precursor [Homo sapiens]	46.25	1	8	8 8	80	0.991	31	4.		31	12.2	3181.19	46.25	23				
578808568	PREDICTED: NEDD4-binding protein 2 isoform X2 [Homo sapiens]	0.65	14	2	2 2	22	0.991	9	5.9	9 1.331	9	24.3	287.90	0.65	6	22	1690	0 189.7	5.25
89191868	von Willebrand factor preproprotein [Homo sapiens]	1.74	1	3	3 4	14	0.991	4	3.	1 1.073	3	3.6	370.95	1.74	11	14	2813	3 309.1	5.49
4506663	60S ribosomal protein L8 [Homo sapiens]	4.28	1	1	1 1	3	0.991	1		1.053	1		104.16	4.28	3	3	257	7 28.0	11.03
	apolipoprotein C-III precursor [Homo sapiens]	34.34	1	3	3	26	0.991	9	2.	1 1.261	9	17.5	1531.35	34.34	9	26			5.41
	PREDICTED: solute carrier family 35 member F5 isoform X2 [Homo	0.97	3	1	1 1	9	0.991	3	1.0	5 1.179	3	17.7	145.14	0.97	3	9	515	5 58.1	
	eukaryotic initiation factor 4A-I isoform 1 [Homo sapiens]	22.91	5	9	9 10	43	0.991	14	2.	1.091	14	8.2	1378.23	22.91	28	43			
	PREDICTED: docking protein 3 isoform X5 [Homo sapiens]	8.18	5	2	2 2	6	0.991	2	1.0		2	15.7	319.82	8.18	6	6	330		
	heterogeneous nuclear ribonucleoprotein F [Homo sapiens]	21.45	3	4	4 6	29	0.991	7	3.0		7	15.5	1116.37	21.45	16	29			
25777615	26S proteasome non-ATPase regulatory subunit 7 [Homo sapiens]	7.41	1	1	1 1	6	0.991	2	17.		2	2.2	548.66	7.41	3	6	324		
	kininogen-1 isoform 1 precursor [Homo saplens]	38.82	1	3	3 30	337	0.991	5	2.0		5	20.1	14965.49	38.82	82	337			
	60S ribosomal protein L10a [Homo sapiens]	10.14	1	2	2 2	6	0.991	2	3.5		2	39.0	146.92	10.14	6	6	217		
	SWI/SNF-related matrix-associated actin-dependent regulator of ch	2.43	1	1	1 1	2	0.991	1		1.232	1		85.19	2.43	2	2	411		
578828247 98986457	PREDICTED: SUMO-conjugating enzyme UBC9 isoform X4 [Homo s	6.96 0.54	2	2	2 2	7	0.991	3	0.		3	3.3	253.50	6.96	4	7	158		
	host cell factor 1 [Homo sapiens] protein \$100-P [Homo sapiens]	0.54 86.32	4	1	1 1	130	0.991	1	10.	1.211	1	22.4	111.19 8587.20	0.54 86.32	3 22	130	2035		
5174663 4885381	protein S100-P [Homo sapiens] histone H1.5 [Homo sapiens]	86.32 43.81	1	8	1 1	130	0.990	48	10.		46 76	22.4 15.1	8587.20 12374.37	86.32 43.81	22	130			
	calicin [Homo sapiens]	1.36	1	11	. 10	294 A	0.990	75	9.1		75	44.4	76.03	1.36	4/	294	588		
	bridging integrator 2 isoform 2 [Homo sapiens]	21.71	6	9	B 8	4	0.990	16	6.9		16	15.5	2055.32	21.71	23	46			
158138507	mitogen-activated protein kinase 3 isoform 3 [Homo sapiens]	17.01	21	1	1 4	14	0.990	1	0.	1.352	1	10.5	574.71	17.01	9	14			
	PREDICTED: tetranectin isoform X1 [Homo sapiens]	41.88	2	5	5 5	16	0.990	6	4.:		6	11.8	887.96	41.88	13	16			
	26S proteasome non-ATPase regulatory subunit 13 isoform 1 [Hon	2.13	2	1	1 1	3	0.990	1		1.021	1		90.93	2.13	3	3	376		
289547631	leukocyte immunoglobulin-like receptor subfamily A member 3 isof	24.37	78	7	7 7	35	0.990	- 11	5.	1 1.155	11	45.6	1457.34	24.37	20	35	439	9 47.4	8.09
	poly(rC)-binding protein 2 isoform g [Homo sapiens]	11.95	11	1	1 4	15	0.990	1		1.231	1		263.44	11.95	9	15	318	8 33.5	8.24
	PREDICTED: ras GTPase-activating protein-binding protein 1 isofor	4.94	1	1	1 1	3	0.990	2	4.	7 1.090	2	23.1	177.31	4.94	2	3	466	6 52.1	5.52
530426780	PREDICTED: TNF receptor-associated factor 2 isoform X2 [Homo s	2.81	3	2	2 2	11	0.990	4	3.0	1.082	4	5.4	175.70	2.81	6	11	533	3 59.1	
578819493	PREDICTED: antigen KI-67 isoform X1 [Homo sapiens]	0.29	3	1	1 1	2	0.990	1		1.388	1		31.07	0.29	2	2	2406	6 264.8	9.38
19482158	desert hedgehog protein preproprotein [Homo sapiens]	1.26	1	1	1 1	2	0.990	2	11.8		2	9.8	16.49	1.26	1	2	396		
530402464	PREDICTED: M-phase phosphoprotein 8 isoform X2 [Homo saplens	1.01	3	1	1 1	3	0.990	1		1.127	1		83.64	1.01	3	3	597		
	caspase-14 precursor [Homo sapiens]	12.81	1	3	3	9	0.990	3	16.		3	1.0	383.10	12.81	9	9	242		
5729850	guanine nucleotide-binding protein G(k) subunit alpha [Homo sapid	13.28	13	1	1 4	20	0.990	1		0.978	1		904.43	13.28	12	20			
530389385	PREDICTED: copine-3 isoform X1 [Homo sapiens]	44.69	17	15	5 16	97	0.990	28	5.:		28	21.2	4296.38	44.69	41	97			
	serpin B10 [Homo sapiens]	63.73	1	20			0.990	37	5.1		37	19.2	4399.44	63.73	56	103			
	plasma protease C1 inhibitor precursor [Homo sapiens]	40.60	5	20	0 20		0.990	103	5.1		101	18.8	10921.85	40.60	58				
	vasorin precursor [Homo sapiens]	2.38	1	1	1 1	3	0.990	1	21	0.952	1	78 7	240.79	2.38	3	23			
	PREDICTED: zinc finger protein 319 isoform X1 [Homo sapiens]	1.03	1	10	1 1	23	0.990	9			8	78.7 15.5	237.82	1.03 34.32	28				
	corticosteroid-binding globulin precursor [Homo sapiens]	19.28	1	11		57	0.990	21	7.9		21	15.5	2610.70 1262.82	19.28	28				
	heterogeneous nuclear ribonucleoprotein U-like protein 2 [Homo sa	6.61	7	- '	4 5	10	0.990	10	3.1		10	13.9	392.22	6.61	30	10			
	PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protein ADP-sugar pyrophosphatase [Homo sapiens]	4.11	,	- 4	4 0	10	0.989	4	3.	1.008	4	13.9	129.49	4.11	10	10	219		
	tigger transposable element-derived protein 1 [Homo sapiens]	0.85	1		1 1	1	0.989	1		1.274	1		24.60	0.85	1	1	591		
	glutaredoxin-1 [Homo sapiens]	74.53	3		5 5	55	0.989	20	13.:		19	12.4	3201.17	74.53	15	55			
	high mobility group protein HMG-I/HMG-Y isoform b [Homo sapien	37.50	1	1	1 3	10	0.989	2	12		2	9.8	163.15	37.50	7	10			
	RRP12-like protein isoform 3 [Homo sapiens]	0.58	3		1 1	118	0.989	62	7.0		61	31.6	1147.47	0.58	3	118			
	kinesin-like protein KIF14 [Homo sapiens]	0.55	- 1	1	1 1	6	0.989	2	3.3	3 1.809	2	24.5	95.05	0.55	3	6	1648		
161169015	neuron navigator 2 isoform 3 [Homo sapiens]	0.30	7	1	1 1	1	0.989	1		1.200	1		22.26	0.30	1	1	2365	5 254.8	8.94
395132436	60S ribosomal protein L18 isoform 2 [Homo sapiens]	8.18	2	1	1 1	2	0.989	1		1.261	1		137.33	8.18	2	2	159	9 18.1	11.84
324021743	vitamin D-binding protein isoform 1 precursor [Homo sapiens]	79.75	5	35	5 37	705	0.989	249	8.	3 1.214	248	20.4	28821.92	79.75	106	705	474	4 52.9	5.45
224028248	non-POU domain-containing octamer-binding protein isoform 2 [Hc	11.78	2	2	2 3	17	0.989	5	5.9		5	8.7	925.38	11.78	8	17			
4503143	cathepsin D preproprotein [Homo sapiens]	20.63	1	7	7 7	31	0.989	12	9.		12	13.7	1345.00	20.63	17	31			
495528154	collagen alpha-1(V) chain isoform 2 preproprotein [Homo sapiens]	1.74	2	2	2 2	5	0.989	2	11.0		2	13.8	337.33	1.74	5	5	1838		
13569962	ras-related protein Rab-1B [Homo sapiens]	45.77	23	5	5 8	54	0.989	13	11.9		13	11.5	2664.36	45.77	24				5.73
4504489	histidine-rich glycoprotein precursor [Homo sapiens]	35.05	7	15	5 16	198	0.989	73	7.		72	17.4	6920.55	35.05	47	198			
	PREDICTED: glia maturation factor gamma isoform X1 [Homo sapi	60.40	6	3	3 5	59	0.989	14	6.		14	8.9	2258.87	60.40	15	59			
221316614 530356822	extracellular matrix protein 1 isoform 1 precursor [Homo sapiens]	10.74 3.24	3	4	4 4	15	0.988	5	1.		4	16.1	687.27 118.07	10.74 3.24	12	15			
	PREDICTED: uncharacterized protein LOC101929393 [Homo sapier	3.24 6.41	2	1	1 1		0.988	7	11.5		6	60.8	118.07 366.05	3.24 6.41	2	13			
	CD177 antigen precursor [Homo sapiens] splicing factor 3B subunit 3 [Homo sapiens]	6.41 3.70	1	3	4 4	14	0.988	5	2.1		5	18.5	366.05 478.23	6.41 3.70	8	14			
	SAM domain-containing protein SAMSN-1 isoform 3 [Homo sapiens	5.26	1	4	1 4	11	0.988	4	8	1.206	1	22.0	134.86	5.26	11	11	304		
4504349	hemoglobin subunit beta [Homo sapiens]	95.26	,	10	n 17	4519	0.988	904	10		904	8.6	134.86 224584 70	95.26	51	4519			
	hemoglobin subunit beta [Homo sapiens]  L-xylulose reductase isoform 2 [Homo sapiens]	95.24 4.96	1	10	1 17	4519	0.988	904	10.		904	8.6 7.3	224584.70 270.45	95.24 4.96	51	4519	147		
	far upstream element-binding protein 2 [Homo sapiens]	1.27	2	-	1	3	0.988	1	0.9	1.157	1	7.3	95.26	1.90	3	3	711		
	D-3-phosphoglycerate dehydrogenase [Homo sapiens]	3.75	1		2 2	6	0.988	2	3.1		2	9.3	161.53	3.75	6		533		
527317371	structural maintenance of chromosomes protein 1A isoform 2 [Horn	5.86	2	6	6 6	18	0.988	6	4.		6	7.8	695.88	5.86	15	18			
	translin-associated protein X [Homo saplens]	32.07	1	6	6 6	19	0.988	7	8.1		7	8.9	1185.20	32.07	16	19			
	programmed cell death 6-interacting protein isoform 1 [Homo sapic	24.31	3	14	4 14	50	0.988	18	6.		18	18.3	2335.46	24.31	40	50			
530410036	PREDICTED: eukaryotic translation initiation factor 5A-1 isoform X5	59.09	4	7	7 7	35	0.988	13	6.		13	11.8	1507.44	59.09	20	35		4 16.8	5.24
530415994	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin isoform X1 [Hc	4.38	2	1	1 1	3	0.988	1		1.204	1		109.01	4.38	3	3	320	0 33.7	10.18
21624607	coactosin-like protein [Homo sapiens]	69.01	1	10	0 10	56	0.988	22	5.1	B 1.245	22	12.0	1738.03	69.01	27	56	142	2 15.9	5.67
4557367	bleomycin hydrolase [Homo sapiens]	9.89	1	3	3 3	14	0.988	5	1.0		5	3.4	518.93	9.89	9	14			
578834138	PREDICTED: serine/threonine-protein phosphatase 6 regulatory su	2.39	2	1	1 1	2	0.987	1		1.046	1		69.51	2.39	2	2	754	4 82.2	4.55
	elongation factor Tu GTP-binding domain-containing protein 1 isofo	1.07	1	1	1 1	3	0.987	1		1.348	1		86.94	1.07	3	3	1120		
	cell division control protein 42 homolog isoform 1 precursor [Homo	52.88	6	6	6 7	70	0.987	19	8.		19	23.1	3210.55	52.88	21	70			
	serine/threonine-protein phosphatase 2A 65 kDa regulatory subuni	19.86	10	g	9 9	29	0.987	11	4.1		11	22.1	1260.56	19.86	24	29			
	WW domain-binding protein 2 [Homo sapiens]	7.66	1	2	2 2	6	0.987	2	3.:		2	16.2	160.11	7.66	6	6	261		
5454016	oxygen-regulated protein 1 [Homo sapiens]	0.56	1	1	1 2	7	0.987	1		1.167	1		110.91	0.56	3	7	2156		
	kinesin-like protein KIF21B isoform 2 [Homo sapiens]	0.92	17	2	2 3	144	0.987	53	4.1		53	8.2	1776.78	0.92	6	144			
83716024		19.10	1	1	1 1	2	0.987	1		1.221	1		73.34	19.10	2	2	89	9 9.9	
83716024 83582815	cornifin-B (Homo sapiens)																		
83716024 83582815 66347875	complement C1r subcomponent precursor [Homo sapiens]	42.84	1	22	2 23	162	0.987	55	8.		54	18.5	6906.61	42.84	69	162			
83716024 83582815 66347875 544063449			3	22	2 23 9 9	162 34 130	0.987 0.987 0.987	55 13 52	5.1 5.1	5 1.181	54 13	18.5 5.1 27.7	6906.61 852.64 2350.83	42.84 18.30 24.80	69 26 22	34	519	9 59.7	6.80

	1																		
Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/11	A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116	A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs		
4502053	arachidonate 12-lipoxygenase, 12R-type [Homo sapiens]	0.71	4		1 1	1	0.9		1	1.127	1		32.89	0.71		1	701	80.3	3 7.64
451172106 578837685	coronin-1C isoform b [Homo sapiens] PREDICTED: plexin-B2 isoform X5 [Homo sapiens]	23.42 0.54	1	10	) 11	44	0.9		14 3	7 1.147 0.962	14	5.5	1549.48 32.83	23.42 0.54	28	44	474 1838		
197927454	protein DEK isoform 2 [Homo sapiens]	12.32	2			21	0.9		9 3		1	19.6		12.32	10	21	341		
530361160	PREDICTED: filamin-binding LIM protein 1 isoform X1 [Homo saple	3.21	1			1	0.9		1	1.371	7	17.0	0.00	3.21	10	1	374		
219842236	tyrosine-protein kinase Fes/Fps isoform 4 [Homo sapiens]	4.61	4		2 2	6	0.9		2 8		2	1.2		4.61		6	694		
530379292	PREDICTED: transportin-1 isoform X2 [Homo sapiens]	1.39	12		2 2	12			1	1.444	1		130.66	1.39	5	12			
32189394	ATP synthase subunit beta, mitochondrial precursor [Homo sapiens	10.59	1	4	1 4	18	0.9	86	6 3	7 1.274	6	5.0	1263.63	10.59	12	18	529	56.5	5 5.40
20357559	galectin-10 [Homo sapiens]	43.66	3	6	5 6	69	0.9	86	26 8	1 1.089	26	9.5	2123.75	43.66	16	69	142	16.4	4 7.37
14149680	extended synaptotagmin-1 isoform 2 [Homo sapiens]	2.54	2		2 2	6	0.9	86	2 4	5 1.138	2	5.9	314.19	2.54		6	1104	122.8	8 5.83
5031569	alpha-centractin [Homo sapiens]	33.78	3	4	1 8	44			6 3		6	22.0		33.78	23	44			
530375309	PREDICTED: polyhomeotic-like protein 3 isoform X3 [Homo sapiens	0.56	6	1	1 1	3	0.9		1	1.262	1		54.98	0.56	3	3	897		
578833911	PREDICTED: tubulin-folding cofactor B isoform X1 [Homo sapiens]		2	1	1 1	3	0.9		1	1.442	1		208.33	9.33	3	3	193		
7669492	glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Homo sapi		3	3	3 27				34 10		34	31.7		90.45	79	1785	335		
4504351	hemoglobin subunit delta [Homo sapiens]	92.52	1		3 15	2318	0.9		79 8		79	7.3		92.52	43		147		
110624781	myosin-13 [Homo sapiens]	0.98	36	1	1 3	23			1	1.406	1		476.32	0.98	8	23			
126362971	serine/threonine-protein kinase 10 [Homo sapiens]	10.85	1		7 8	23			7 7		7	22.8		10.85	23	23			
19923231	ras-related protein Rab-6A isoform a [Homo sapiens]	14.90	21	-	2 3	9	0.9		2 2		2	3.9		14.90	9	9	208		
4506597 530420952	60S ribosomal protein L12 [Homo sapiens] PREDICTED: male-specific lethal 3 homolog isoform X2 [Homo sap	14.55			2 2		0.9		2 0		2	14.4		14.55		6	165 355		
578806818	PREDICTED: male-specific retrial 3 homolog isolorm x2 (nomo sap PREDICTED: TPR and ankyrin repeat-containing protein 1 isoform.)	1.69	- 1		1	1	0.9		1	0.806	- '		69.83 24.08	1.69 0.30		2	2969		
		26.77	1			28			9 3	3 1 219	0	13.2		26.77	20	28			
4507909	BTB/POZ domain-containing protein KCTD12 [Homo sapiens] wiskott-Aldrich syndrome protein [Homo sapiens]	11.95	4		4 4	17	-		6 14		4	16.8		11.95	12				
4506017	serine/threonine-protein phosphatase 2A catalytic subunit alpha isc	12.94	2		1 4	17			6 3			12.0		12.94	la C	17			
	PREDICTED: DNA polymerase zeta catalytic subunit isoform X4 [Ho		4		1 1	1	0.9		1	1.244	1	12.0	15.58	0.19		1	2679		
52487191	endoplasmic reticulum resident protein 44 precursor [Homo saplen	7.88	1		2 3	14			3 0		3	11.5		7.88		14			
578814066	PREDICTED: filamin-C isoform X1 [Homo sapiens]	2.39	3	1	1 9	64	0.9		6 9		6	2.2		2.39	25	64			
13399298	immunoglobulin lambda-like polypeptide 1 isoform a precursor [Ho		1		2 2	34	0.9		12 7		11	12.0		14.08		34	213		
530369689	PREDICTED: striated muscle preferentially expressed protein kinas	0.21	23		1 1	5	0.9		3 3		3	5.6	34.37	0.21		5	2418		4 8.09
5453678	epididymal secretory protein E1 precursor [Homo sapiens]	31.79	2	1	3 3	11	0.9		5 10		5	3.3		31.79		11	151		
295986608	immunoglobulin lambda-like polypeptide 5 isoform 1 [Homo sapien	47.66	2	ç	9	1880		184 6	78 9	5 1.271	670	24.6	79472.07	47.66	21	1880	214	23.0	
578839125	PREDICTED: putative V-set and immunoglobulin domain-containing	21.29	1		2 4	190			38 5		38	21.2	10249.28	21.29	12				
530412286	PREDICTED: ATP-citrate synthase isoform X3 [Homo sapiens]	28.34	21	23	3 24	119			12 5		42	14.1		28.34	71	119			
530379158	PREDICTED: centrosomal protein POC5 isoform X2 [Homo sapiens]	1.28	4	1	1 1	1	0.9		1	0.956	1		29.02	1.28		1	547		
345441817	kinesin-like protein KIF2A isoform 3 [Homo sapiens]	1.60	4	1	1 1	3	0.9		1	1.244	1		206.66	1.60	1	3	686		
556695469	mRNA-capping enzyme isoform b [Homo sapiens]	1.22	2	1	1 1	1	0.9		1	1.136	1		15.16	1.22		1	574		
4557587	fumarylacetoacetase [Homo sapiens]	4.77	1		2 2	5	0.9		2 0		2	18.7		4.77		5	419		
44890052	stathmin isoform a [Homo sapiens]	33.56	5	6	5 6	26			9 1		9	7.2		33.56	17	26	149		
4504041	guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 1 [	43.10	21		3 12	52			2 5		12	17.8		43.10	33	52			
583966148	isocitrate dehydrogenase [NADP], mitochondrial isoform 2 [Homo s	25.75	3	9	10	35			2		12	13.7		25.75	25	35	400	45.2	
10835240 578810775	high mobility group nucleosome-binding domain-containing protein	26.67 22.15	1	-	2 2	7	0.9		3 5 9 3		3	2.1	181.18 892.48	26.67 22.15		7	289	9.5	5 10.48 6 6.92
578828075	PREDICTED: glucosamine-6-phosphate isomerase 1 isoform X2 [Ho PREDICTED: pyrin isoform X1 [Homo sapiens]	3.33	1			24	0.9		2 9		9	22.0		3.33	10	24	780		
578819639	PREDICTED: pyrin isoform X1 [Homo sapiens] PREDICTED: tudor domain-containing protein 1 isoform X3 [Homo	0.72	2		2 2		0.9		3 11		2	25.0		0.72		5	1104		
6912396	glyoxylate reductase/hydroxypyruvate reductase [Homo sapiens]	23.17	3		1 1	12			4 8		3	20.9		23.17	12	12			
530390795	PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]		23			15			5 3			25.9		8.35	15				
32130518	apolipoprotein C-II precursor [Homo sapiens]	34.65	1		2 2	10	-		4 14		4	28.8		34.65		10			
58761500	obg-like ATPase 1 isoform 1 [Homo sapiens]	10.61	2		2 2	7	0.5		3 7		3	0.4		10.61		7	396		
	PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sap		3		7 7	23	-		8 8		8	14.8		14.24	20	23			
578812388	PREDICTED: collagen alpha-1(XII) chain isoform X1 [Homo sapiens	0.81	2		2 2	6	0.9		2 4		2	6.6		0.81	-	6	2972		
648216372	aspartatetRNA ligase, cytoplasmic isoform 2 [Homo sapiens]	9.23	2	3	3 3	9	0.9		3 2		3	2.5		9.23		9	401		
325652048	transcription elongation factor B polypeptide 1 isoform b [Homo sa		2		2 2	4	0.9	82	2 4		2	11.3		21.88	4	4	96		
62198235	drebrin-like protein isoform b [Homo sapiens]	25.81	5	10	10	52	0.9	82	19 7	2 1.172	19	14.4	2282.30	25.81	27	52	430	48.2	2 5.05
545688902	regulator of telomere elongation helicase 1 isoform 4 [Homo sapier	0.80	4	1	1 1	1	0.9	82	1	5.569	1		22.49	0.80		1	996		
578812959	PREDICTED: utrophin isoform X8 [Homo sapiens]	0.32	6	:	2 2	28	0.9		10 10		10	5.8		0.32		28	2499		
38504669	serpin B8 isoform a [Homo sapiens]	9.89	6	:	2 3	14	0.9	82	2 1		2	9.4		9.89	8	14	374	42.7	
539845980	protein phosphatase 1 regulatory subunit 7 isoform 6 [Homo saple	12.96	7	1	3	20	0.9	82	7 5		7	9.9	1034.23	12.96	9	20			
578834355	PREDICTED: glutamate receptor ionotropic, kainate 5 isoform X5 [I		4	1	1 1	2	0.9		1	1.072	1		32.02	1.10		2	912		
32483377	thioredoxin-dependent peroxide reductase, mitochondrial isoform b		2	4	1 4	12			4 3		4	5.2		17.23	12				
5803076	chromobox protein homolog 1 [Homo saplens]	19.46	1		2 3	8	-		2 1		2	14.7		19.46	8	8			
4504067	aspartate aminotransferase, cytoplasmic [Homo sapiens]	20.10	56	6	5 7	25			8 9		8	10.2		20.10	19				
	PREDICTED: A-kinase anchor protein 9 isoform X3 [Homo sapiens]		66	3	5	18			3 4		3	9.0		0.91	11	18			
387527974	dynactin subunit 2 isoform 3 [Homo sapiens]	12.72	3		3 3	7	0.9		3 11		2	6.8		12.72		7	401		
11386147	prosaposin isoform a preproprotein [Homo sapiens]	25.95	3	12	12	106			10 6		39	12.4		25.95	35	106			
18375644 17149836	tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Hom-	2.39 82.41	4		1	2	0.9		1 9	1.078 3 1.201	1	22.3	112.29 4030.17	2.39 82.41	21	2	460 108		
17149836 195222722	peptidyl-prolyl cis-trans isomerase FKBP1A isoform a [Homo sapien U6 snRNA-associated Sm-like protein LSm5 isoform b [Homo sapien		4		, 9	84	0.9		1	3 1.201 1.422	30	22.3	4030.17 96.80	82.41 37.10	25	84	108		
27477041	AP-2 complex subunit alpha-2 isoform 2 [Homo sapiens]	1.17	2 A	1		3	0.9		1	0.987	1		72.06	1.17	-	3	939		
578810605	PREDICTED: calpastatin isoform X17 [Homo sapiens]	17.74	24		3 8	37	0.9		14 5		14	10.0		17.74	21	37	654		
5032057	protein \$100-A11 [Homo sapiens]	88.57	1		9 9	145			56 7		56	15.6		88.57	21	145			
4758442	glia maturation factor beta [Homo sapiens]	33.10	2	1	1 3	22			1	1.250	1		973.81	33.10		22			
4507065	antileukoproteinase precursor [Homo sapiens]	9.09	1	1	1 1	3	0.9		1	1.203	1		103.07	9.09		3	132		
530408197	PREDICTED: alpha-hemoglobin-stabilizing protein isoform X2 [Hom		1	1	1 1	6	0.9		2 7		2	4.5		12.75		6	102		
578836536	PREDICTED: integrin beta-2 isoform X1 [Homo sapiens]	6.29	7	4	1 4	10	0.9	80	4 9	1 0.996	4	1.5		6.29	10	10	700		
170932494	syntaxin-7 [Homo sapiens]	19.92	1		1 4	14			5 5		5	3.2		19.92	11	14			
578818366	PREDICTED: ankyrin repeat domain-containing protein 26 isoform	0.48	9	1	1 1	3	0.9		1	1.825	1		40.15	0.48	3	3	1677		
530368297	PREDICTED: quinone oxidoreductase PIG3 isoform X1 [Homo sapie	6.58	2	1	2 2	5	0.9		2 3		2	8.8		6.58	5	5	243	26.8	
304555610	EF-hand calcium-binding domain-containing protein 13 isoform A [I	0.92	1	1	1 1	2	0.9		1	1.170	1		29.95	0.92	1	2	973		
23110939	proteasome subunit alpha type-3 isoform 2 [Homo sapiens]	37.50	21	9	9	48	0.9		15 5		15	10.9		37.50	26	48	248		
6912618	glutaminyl-peptide cyclotransferase precursor [Homo sapiens]	13.57	1		2 2	7	0.9		3 6		3	32.3		13.57	5	7	361		
118150660	zinc finger CCCH domain-containing protein 15 [Homo sapiens]	1.41	1	1	1 1	24	0.9		10		10	63.4		1.41	1	24	426		
299758394	dynamin-2 isoform 5 [Homo sapiens]	17.49	23	13	3 13	35	0.9		14 4		13	17.0		17.49	33	35			
5453539	multifunctional protein ADE2 isoform 2 [Homo sapiens]	7.29	3		3	8	0.9		3 7		3	17.8		7.29	8	8	425		
	rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha [Ho		1		1 1	8	0		3 3		3	7.1		0.58		8	860		
578800886 4504957	PREDICTED: involucrin isoform X1 [Homo sapiens]	9.40	1	4	1 4	18			6 9		6	1.7		9.40 7.07	12	18			
4504957 573014819	lysosome-associated membrane glycoprotein 2 isoform A precursor	7.07	20	13	3	12	-		4 3		18	5.3		7.07 25.04		12			
573014819 578807840	X-ray repair cross-complementing protein 6 isoform 3 [Homo sapie PREDICTED: E3 ubiquitin-protein ligase CBL-B isoform X4 [Homo s	25.04 3.39	36	12	12	54	0.9		2 8		18	9.9		25.04 3.39	35	54	914		
	CD5 antigen-like precursor [Homo saplens]	38.90	36	11	3 12	73			27 6		2	17.5		38.90	24	73	347		
			13	12	1 1	/3	0.9		1	1.180	2/	19.6	3753.99 154.56	15.89	36	73	107		
5174411		15.80							The second secon										
5174411 545688677	transport and Golgi organization protein 2 homolog isoform h [Hon	15.89	13		1 1	2		179	2 17	8 1 240	2	5.2				2			3 9.42
5174411 545688677 256419001	transport and Golgi organization protein 2 homolog isoform h [Hon double-stranded RNA-binding protein Staufen homolog 2 isoform d	2.01	13	1	1 1	2	0.9		2 17		2	5.2	40.01	2.01		2	398	43.3	
5174411 545688677	transport and Golgi organization protein 2 homolog isoform h [Hon		13 11 4	1	1 1	2 3		79	2 17 1 9 2	1.153	2 1 9	5.2	40.01 147.06		11	2 3 25	398 462	3 43.3 2 53.1	1 9.60

Accession 28302131	Description hemoglobin subunit gamma-1 [Homo saplens]	ΣCoverage 65.99	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs A8	0.979	A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116 1.028	A8: 117/116 Count	%] Scon	6619.35	Coverage A(3,6,7) 65.99	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pl
	cathepsin G preproprotein [Homo sapiens]	47.06	1	1/	4 14	175	0.979	4	6.8		4 65	12.6	6837.08	47.06	24	175	255	28.8	11.19
293332611	tyrosine-protein kinase SYK isoform Syk(S) [Homo sapiens]	8.50	8	5	5 5	16	0.978	6	3.1	1.094	5	4.6	502.70	8.50	14	16	612	69.5	7.56
	N-alpha-acetyltransferase 20 isoform c [Homo sapiens]	6.31	3	1	1 1	20	0.978	12	5.3		12	13.4	177.96	6.31	2	20	111	12.7	4.67
	histidine triad nucleotide-binding protein 1 [Homo sapiens]	39.68	1	4	4 4	14	0.978	5	3.6	1.126	5	5.2	507.65	39.68	11	14	126	13.8	6.95
319918857	coronin-7 isoform 3 [Homo sapiens]	6.19	4	5	5 5	17	0.978	6	10.9	1.143	6	39.2	556.34	6.19	14	17	840	91.6	6.14
	glutathione reductase, mitochondrial isoform 2 precursor [Homo sa	44.22	4	15	5 15	88	0.978	32	4.9		32	13.9	4392.00	44.22	44	88	493	53.0	8.84
	class E basic helix-loop-helix protein 40 [Homo sapiens]	1.21	1	1	1 1	2	0.978	2	16.1		2	0.3	26.29	1.21	1	2	412		8.10
31652249	lipopolysaccharide-binding protein precursor [Homo sapiens]	9.98	1	4	4 4	26	0.978	9	6.7			17.9	1507.61	9.98	12		481	53.3	6.70
	pregnancy zone protein precursor [Homo sapiens]	25.44 17.37	1	18	8 27	554	0.978	25	6.4 5.9				35163.24	25.44 17.37	76	554	1482 190		
32171249 291575165	prostaglandin-H2 D-isomerase precursor [Homo sapiens]		1	2	2 2	18	0.978	2	5.9		2	9.1	273.42 760.85	17.37	6	6		21.0 40.1	7.80
	monocyte differentiation antigen CD14 precursor [Homo sapiens] glutamate-rich protein 6B [Homo sapiens]	20.00	1		5 5	18	0.978	7	4.5		7	23.2	48.10	1.01	14	18	375 696	81.6	6.23 4.75
25121972	copine-8 [Homo sapiens]	2.48	18		1 2	25	0.978	1	4.0	1.112	1	23.2	610.86	2.48	4	25	564	63.1	5.96
	prenylated Rab acceptor protein 1 [Homo sapiens]	4.32	1	1	1 1	2	0.978	. 2	3.0	14.549	2 1	145.1	31.25	4.32	1	2	185	20.6	7.34
	PREDICTED: serine/arginine-rich splicing factor 7 isoform X2 [Hom		5	2	2 2	3	0.978	2	22.8			22.0	57.94	13.00	3	3	223	25.6	11.80
	filaggrin [Homo sapiens]	6.45	1	8	8 8	41	0.978	15	7.9	1.037	15	8.5	1793.99	6.45	21	41	4061	434.9	9.25
15431310	keratin, type I cytoskeletal 14 [Homo sapiens]	44.49	18	8	8 21	95	0.978	10	6.7	1.094	10	4.0	3343.80	44.49	59	95	472	51.6	5.16
	bisphosphoglycerate mutase [Homo sapiens]	29.34	1	5	5 5	25	0.978	9	10.0		9	6.2	945.92	29.34	14		259	30.0	6.54
29789445	desmoglein-4 isoform 2 preproprotein [Homo sapiens]	0.96	5	1	1 2	27	0.977	1		1.375	1		353.21	0.96	5	27	1040	113.8	4.56
	PREDICTED: FYVE, RhoGEF and PH domain-containing protein 2 is		2	1	1 1	1	0.977	1					31.03	0.97	1	1	620		7.30
	PREDICTED: ribosomal protein S6 kinase alpha-3 isoform X5 [Hom	2.96	18		2 2	8	0.977	3	1.1			12.9	329.73	2.96	5	8	710	80.6	8.28
	triosephosphate isomerase isoform 1 [Homo sapiens]	78.71 1.06	3	14	4 14	208	0.977	75	6.7	1.136 0.948	75	11.3	10311.34	78.71	42	208	249 1225		6.90 7.77
	NHS-like protein 2 [Homo sapiens] THAP domain-containing protein 5 isoform 3 [Homo sapiens]	3.00	2		1 1	3	0.977	1		1.065	1		129.96 80.12	1.06 3.00	3	3	233	133.2 26.5	4.92
	NADPHcytochrome P450 reductase [Homo sapiens]	6.76	3	1	3 3	8	0.977	1	9.0	1.102	3	7.9	461.43	6.76	3	3	233 680	77.0	5.58
	protein AMBP preproprotein [Homo sapiens]	46.88	2	14	4 14	140	0.977	52	9.0		51	12.8	5420.14	46.88	38	140	352	39.0	6.25
	prolow-density lipoprotein receptor-related protein 1 precursor [Ho	0.11	1	1	1 1	7	0.977	3	8.4	1.375		26.7	68.27	0.11	3	7	4544	504.3	5.39
530389740	PREDICTED: uncharacterized protein KIAA2026 isoform X1 [Homo		58	1	1 2	14	0.977	2	1.8	1.169	2	3.3	232.37	0.58	4	14	2073	224.4	9.09
530399942	PREDICTED: R3H domain-containing protein 2 isoform X15 [Homo	0.61	16	1	1 1	30	0.976	11	4.0		11	17.4	298.01	0.61	3	30	976	106.9	8.85
	PREDICTED: peptidase inhibitor 16 isoform X3 [Homo sapiens]	3.70	2	1	1 1	3	0.976	1		1.018	1		158.53	3.70	3	3	270	29.7	5.71
	serine/threonine-protein kinase pim-1 isoform 2 [Homo sapiens]	1.60	14	1	1 1	3	0.976	1		0.956	1		70.90	1.60	3	3	313	35.7	6.11
	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	3.75	7	2	2 2	6	0.976	2	5.1	1.397	2	17.7	166.08	3.75	6	6	534	59.5	7.91
	insulin-like growth factor-binding protein 3 isoform b precursor [Ho	11.68	57	3	3 4	23	0.976	4	2.5		4	4.2	473.25	11.68	11		291	31.7	8.69
	plectin isoform 1d [Homo sapiens]	2.99 1.98	21	- 11	11 11	33	0.976 0.976	13	8.6		13	8.5 18.1	926.07 78.02	2.99	29	33	4515 353	512.3 41.0	5.77 6.40
24308273	tyrosine-protein phosphatase non-receptor type 2 isoform 3 [Homo costars family protein ABRACL [Homo saplens]	1.98 54.32	8	1	1 1	24	0.976	4	3.8			13.2	984.57	1.98 54.32	2	26	353	9.1	6.40
	TBC1 domain family member 8 [Homo sapiens]	1.05	7	3	1 2	20	0.975	10	0.4	1.215	1	13.2	39.52	1.05	3	20	1140		5.52
	collagen alpha-3(VI) chain isoform 4 precursor [Homo sapiens]	7.70	8	14	4 14	59	0.975	21	7.3	1.122	21	12.9	2813.56	7.70	40	59	2570	278.0	8.15
	signal recognition particle receptor subunit alpha isoform 2 [Homo	3.93	2	1	1 2	5	0.975	1		0.944	1		114.83	3.93	5	5	610	66.5	9.04
	C-1-tetrahydrofolate synthase, cytoplasmic [Homo sapiens]	8.66	1	8	8 8	20	0.975	8	8.7	1.072	8	21.7	566.86	8.66	20	20	935	101.5	7.30
4757804	copper transport protein ATOX1 [Homo sapiens]	20.59	8	2	2 2	11	0.975	4	2.5		4	4.7	142.12	20.59	5	11	68	7.4	7.24
228008398	heterogeneous nuclear ribonucleoprotein Q isoform 3 [Homo sapie	14.04	9	5	5 7	25	0.975	5	2.0		5	7.6	951.53	14.04	19	25	527	58.7	7.56
	probable aminopeptidase NPEPL1 isoform 3 [Homo sapiens]	2.53	3	1	1 1	3	0.974	1		1.102	1		100.48	2.53	3	3	475	50.5	6.52
	core-binding factor subunit beta isoform 2 [Homo sapiens]	7.69	4	2	2 2	6	0.974	2	3.0		2	8.3	108.17	7.69	6	6	182	21.5	6.60
	ras-related protein Rab-18 isoform 4 [Homo sapiens]	7.69	4	1	1 1	2	0.974	1		1.353	1		68.10	7.69	2	2	182	20.4	5.00
	carbonic anhydrase 2 isoform 1 [Homo sapiens]	55.00 1.41	2	- 11	1 11	131	0.974	46	8.5 2.6		46	6.8 5.7	6862.67 49.97	55.00	32	131	260 426	29.2 46.1	7.40 8.21
4826952	testicular acid phosphatase precursor [Homo saplens] 26S proteasome non-ATPase regulatory subunit 5 isoform 1 [Homc	5.95	2		2 2	6	0.974	2	6.1		2	13.9	356.71	5.95		- Z	504	56.2	5.48
	F-box only protein 11 isoform 1 [Homo sapiens]	1.07	5	1	1 1	5	0.974	2	5.7			15.6	76.40	1.07	2	5	843	94.0	6.84
	zinc finger protein 605 isoform 1 [Homo sapiens]	2.65	36	2	2 3	9	0.974	3	0.5		3	3.0	113.46	2.65	7	9	641	74.3	9.11
	ATPase ASNA1 [Homo sapiens]	5.46	1	2	2 2	6	0.974	2	6.4		2	10.1	162.16	5.46	6	6	348	38.8	4.91
	uncharacterized protein C19orf71 [Homo sapiens]	3.83	4	1	1 1	4	0.974	1		2.065	1		35.14	3.83	2	4	209	24.2	8.95
	prolyl endopeptidase [Homo sapiens]	6.06	2	3	3 3	16	0.974	6	4.5		6	9.5	885.53	6.06	7	16	710	80.6	5.86
	AP-2 complex subunit alpha-1 isoform 2 [Homo sapiens]	1.57	2	1	1 1	3	0.974	1		1.247	1		187.23	1.57	3	3	955	105.3	7.66
	PREDICTED: uncharacterized protein LOC100293211 [Homo sapier	25.93	2	6	6 8	318	0.974	50	5.7	1.312	50	19.2	9597.86	25.93	24	318	270		8.59
	trophoblast glycoprotein-like precursor [Homo sapiens]	2.36	1		1 1	1	0.974	1	6.5	1.310	46	18.1	28.83	2.36	1	1	382	40.4	8.27
	adenine phosphoribosyltransferase isoform a [Homo sapiens]	45.56 15.34	2		6	44 22	0.974	15	6.5			10.1	1690.71	45.56 15.34	18		180 352	19.6 39.6	6.02 5.19
	PREDICTED: tropomodulin-3 isoform X1 [Homo saplens]	8 61	2		5 5	18	0.974	8	11.2			15.8	747.03	8 61	14	18	352 488	39.6 54.7	
	coagulation factor X preproprotein [Homo sapiens] cystatin-C precursor [Homo sapiens]	19.18	3	3	2 2	10	0.973	2	8.0		2	4.7	382.90	19 18	6	10	146	15.8	8.75
	titin isoform N2-A [Homo sapiens]	0.11	33	4	4 7	23	0.973	3	0.7		1	4.7	247.65	0.11	15	23	33423		
	PREDICTED: nesprin-2 isoform X7 [Homo sapiens]	0.16	46	1	1 2	3	0.973	1	0.7	1.174	1		35.56	0.16	3	3	6883	795.9	5.39
	protein bicaudal D homolog 2 isoform 2 [Homo sapiens]	0.97	2	1	1 1	2	0.973	1		1.465	1		26.39	0.97	2	2	824	93.5	5.44
45580723	haptoglobin-related protein precursor [Homo sapiens]	50.00	2	5	5 21	1913	0.973	13	2.8	1.192		12.3	67245.04	50.00	61	1913	348	39.0	7.09
334724455	acetyl-coenzyme A synthetase, cytoplasmic isoform 3 [Homo sapiei	1.82	9	1	1 2	32	0.973	2	2.7			54.0	482.66	1.82	5	32	606	67.6	6.15
	60S ribosomal protein L30 [Homo sapiens]	13.91	1	1	1 1	6	0.973	2	0.6	1.154	2	20.4	316.51	13.91	3	6	115	12.8	9.63
	glycogen (starch) synthase, muscle isoform 2 [Homo sapiens]	1.19	2	1	1 1	3	0.973	1		1.187	1		92.70 29.58	1.19	3	3	673 441	76.4 49.9	6.54 7.08
	zinc finger and BTB domain-containing protein 26 [Homo sapiens] complement factor H-related protein 3 isoform 2 precursor [Homo	12.64	1	1	1 1	16	0.973	1	18.0		1	30.3	29.58 430.26	12.64	1	1 15	441 269	49.9 30.7	7.08
	ras-related protein Rab-21 [Homo saplens]	12.64	- 1	2	3 2	12	0.972	4	18.0			14.3	487.39	12.64	8	15	269	24.3	7.78
	WASH complex subunit FAM21C isoform 3 [Homo sapiens]	0.88	10	3	1 1	1	0.972	1	4.2	1.040	1	. 4.0	35.45	0.88	1	12	1245		4.74
	neutrophil defensin 1 precursor [Homo sapiens]	67.02	.0	q	9 9	198	0.972	88	6.6		85	24.3	3321.93	67.02	22	198	94		
	PREDICTED: neutrophil elastase isoform X1 [Homo sapiens]	52.43	1	10	0 10	185	0.972	69	10.1			19.6	9997.96	52.43	26	185	267	28.5	9.35
4827036	peptidoglycan recognition protein 1 precursor [Homo sapiens]	53.06	1	6	6 6	78	0.972	28	5.5			32.8	4363.24	53.06	17	78	196	21.7	8.59
206597515	arf-GAP with Rho-GAP domain, ANK repeat and PH domain-contain	1.94	3	2	2 2	5	0.972	2	6.6		2	16.5	202.73	1.94	5	5	1133		6.14
225543094	interstitial collagenase isoform 2 [Homo sapiens]	4.47	2	2	2 2	5	0.972	2	1.9		2	5.6	188.35	4.47	5	5	403	46.2	6.77
	kallistatin isoform 2 precursor [Homo sapiens]	2.11	2	1	1 1	3	0.972	1		1.166	1		129.40	2.11	3	3	427	48.5	7.75
	vacuolar protein sorting-associated protein 35 [Homo sapiens]	10.93	2	8	8 8	41	0.972	14	3.4			17.3	1478.53	10.93	24	41	796	91.6	5.49
	carboxypeptidase D isoform 1 precursor [Homo sapiens]	1.38	1	1	1 1	6	0.972	3	0.6	1.277 2.276	3	10.9	83.62 29.92	1.38	2	6	1380 295	152.8 32.7	6.05 7.02
	glycine N-methyltransferase [Homo saplens] complement component C8 gamma chain precursor [Homo saplens	2.37 52.48	1	1	7 7	43	0.971	1	7.7	1.287	15	14.7	29.92	2.37 52.48	10	1 43	295	32.7 22.3	7.02 8.31
	PREDICTED: protein TFG isoform X2 [Homo sapiens]	4.55	2	2	2 2	43	0.971	10	2.1			26.1	155.08	4.55	10	43	396	43.0	5.17
	adenylate kinase 2, mitochondrial isoform b [Homo sapiens]	11.21	3	2	2 2	7	0.971	3	11.7			36.3	229.61	11.21	5	7	232		7.88
	ERO1-like protein alpha precursor [Homo sapiens]	5.34	1	2	2 2	6	0.971	2	2.7		2	3.8	316.80	5.34	6	6	468		5.68
567316250	ribokinase isoform 2 [Homo sapiens]	7.45	2	2	2 2	4	0.971	2	0.1	1.155	2	12.9	91.01	7.45	4	4	255	27.1	4.73
145275185	UPF0160 protein MYG1, mitochondrial precursor [Homo sapiens]	2.66	1	1	1 1	2	0.971	1		0.873	1		80.21	2.66	2	2	376	42.4	6.67
530395488	PREDICTED: lysosomal acid phosphatase isoform X4 [Homo sapien	2.12	7	1	1 1	1	0.971	1		1.263	1		26.27	2.12	1	1	236	26.6	5.38
56550081	mitotic checkpoint protein BUB3 isoform b [Homo sapiens]	4.60	2	2	2 2	5	0.971	2	8.0	1.120		17.8	81.25	4.60	5	5	326	36.9	6.84
	PREDICTED: cathepsin B isoform X1 [Homo saplens]	17.99	1	5	5 5	32	0.971	12	7.2		12	6.9	1071.82	17.99	12	32	339	37.8	6.30
4506209 530371375	26S protease regulatory subunit 7 isoform 1 [Homo sapiens] PREDICTED: espin-like protein isoform X2 [Homo sapiens]	6.00 1.10	2	2	2 2	11	0.971	4	1.3	1.121 1.227	4	9.0	390.99 55.89	6.00 1.10	6	11	433 637	48.6 69.1	5.95 6.15
	FREDICTED. espiri-like protein isolorni Az [nonio sapiens]		2	1	1	194	0.970	71	7.1	1.227	71	13.5	9717.57	53.39	2	194			9.50
		53 30	1																
11342670	azurocidin preproprotein [Homo sapiens] U6 snRNA-associated Sm-like protein LSm6 [Homo sapiens]	53.39 13.75	1	9	9 9	194	0.970	- 1	7.1	1.156	1	13.5	118.50	13.75	27	194	251 80	26.9 9.1	

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Accession	Description		Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs		A8: 115/114 Variability [%]		A8: 117/116 Count	A8: 117/116 Variability [%]			# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs MV	V [kDa]	calc. pl
530381903	PREDICTED: high mobility group protein HMG-I/HMG-Y isoform X3	35.51	1	1	3	8	0.9	1	1.292		1	219.62	35.51	7	8	107	11.7	10.32
52317237	olfactory receptor 4C6 [Homo sapiens]	2.27	1	1	1	2	0.9	2 4.4	1.619		2 50.6	33.08	2.27	1	2	309	34.5	8.13
5902102	small nuclear ribonucleoprotein Sm D1 isoform 1 [Homo sapiens]	36.97	2	3	3	26	0.9	9 5.9	1.131		9 13.6	981.97	36.97	9	26	119	13.3	11.56
578799295	PREDICTED: formin-binding protein 1-like isoform X1 [Homo sapler	1.13	4	1	1	15	0.9	7 7.3	1.315		7 14.7	156.56	1.13	3	15	533	61.8	5.94
4502419	flavin reductase (NADPH) [Homo sapiens]	59.71	1	8	8	74	0.9	7 8.9	1.034	2	7 5.5	3541.53	59.71	23	74	206	22.1	7.65
	protein farnesyltransferase/geranylgeranyltransferase type-1 subur	3.69	1	2	2	6	0.9	2 0.4	1.208		2 9.0	95.56	3.69	6	6	379	44.4	5.08
	pyruvate kinase PKM isoform b [Homo sapiens]	76.65	36	2	47	853	0.9	4 9.4	1.337		4 23.6	37814.24	76.65	133	853		58.0	7.71
	ubiquitin-conjugating enzyme E2 variant 1 isoform g [Homo sapien	48.57	31	6	7	23	0.9	7 2.3	1.040		7 9.2	651.46	48.57	18	23		12.0	9.72
22550104	ubiquitin carboxyl-terminal hydrolase 32 [Homo sapiens]	0.37	1	1	1	2	0.9	1	0.769		1	33.94	0.37	2	2	1604	181.5	6.44
	PREDICTED: putative bifunctional UDP-N-acetylglucosamine transfe		11	1	1	1	0.9	1	1.046		1	22.82	1.53	1	1	652	71.4	6.79
34147630	elongation factor Tu, mitochondrial precursor [Homo sapiens]	3.74	1	1	1	6	0.9	2 3.8	1.032		2 14.4	291.94	3.74	3	6	455	49.8	7.61
	protein disulfide-isomerase A6 isoform e precursor [Homo sapiens]	16.25	8	6	6	21	0.9	8 3.7	1.101		8 16.3	1081.34	16.25	17	21		47.8	5.08
82880645	ubiquitin carboxyl-terminal hydrolase 14 isoform b [Homo sapiens]	10.68	2	4	1 4	21	0.9	8 9.0	1.054		8 7.8	894.84	10.68	12	21	459	52.4	5.78
	non-secretory ribonuclease precursor [Homo sapiens]	19.88	1	3	3	24	0.9	8 8.9	1.244		8 19.5	1021.40	19.88	9	24	161	18.3	8.73
	ribose-phosphate pyrophosphokinase 1 isoform 1 [Homo sapiens]	18.24	5	4	1 4	17	0.9	5 8.7	1.115		5 12.0	811.31	18.24	11	17	318	34.8	6.98
	60S ribosomal protein L11 isoform 2 [Homo saplens]	10.73	2	1	1 2	8	0.9	1	1.266		1	156.44	10.73	6	8	177	20.1	9.60
578802657	PREDICTED: SET and MYND domain-containing protein 5 isoform )	1.91	4	1	1	2	0.9	1	1.256		1	33.42	1.91	2	2	366	41.7	4.83
	transmembrane protein 17 [Homo sapiens]	4.55	1	1	1	1	0.9	1				28.32	4.55	1	1	198	23.0	6.79
	collagen alpha-2(VI) chain isoform 2C2 precursor [Homo sapiens]	2.16	3	2	2 2	5	0.9	2 5.8	1.054		2 10.8	128.77	2.16	5		1019	108.5	6.21
	PREDICTED: mediator of RNA polymerase II transcription subunit	0.67	4	1	1	1	0.9	1	1.156		1	28.83	0.67	1	1	1338	148.5	8.60
	PREDICTED: leucine-rich repeat and WD repeat-containing protein	2.22	3	1	1	1	0.9	1	1.519		1	35.72	2.22	1	1	495	53.7	6.93
	40S ribosomal protein S6 [Homo sapiens]	6.83	32	1	2	6	0.9	1	1.442		1	148.00	6.83	6	6	249	28.7	10.84
	PREDICTED: importin-5 isoform X2 [Homo sapiens]	3.59	1	2	2	6	0.9	2 1.4	1.234		2 18.5	392.39	3.59	6	6	1115	125.5	4.92
336391093	ras-related protein Rab-2A isoform b [Homo sapiens]	19.15	4	3	3	9	0.9	3 3.5	1.099		3 9.1	486.74	19.15	9	ç	188	20.8	6.11
4503513	eukaryotic translation initiation factor 3 subunit I [Homo sapiens]	2.77	1	1	1	3	0.9	1	0.930		1	96.14	2.77	3	3	325	36.5	5.64
	crk-like protein [Homo sapiens]	9.57	1	2	2	6	0.9	2 1.5	1.293		2 14.1	265.31	9.57	6	6	303	33.8	6.74
	PREDICTED: inactive serine/threonine-protein kinase VRK3 isoform	1.46	3	1	1	2	0.9	2 1.9	1.145		2 4.9	24.55	1.46	1	- 2	412	45.9	9.09
126032350	DNA-dependent protein kinase catalytic subunit isoform 2 [Homo s	2.56	25	9	9	34	0.9	0 5.2	1.169	1	0 13.7	737.69	2.56	24	34	4097	465.2	7.17
578796778	PREDICTED: putative UPF0607 protein ENSP00000383144 [Homo:	1.92	2	1	1	2	0.9	1	1.120		1	25.48	1.92	2	- 2	416	46.1	10.65
301171475	ATP-dependent RNA helicase DDX3X isoform 3 [Homo sapiens]	3.87	6	1	2	6	0.9	1	1.096		1	320.34	3.87	6	6	646	71.3	6.62
	myosin-11 isoform SM2A [Homo sapiens]	9.03	17	1	19	165	0.9	1	0.911		1	6515.52	9.03	53	165	1938	223.4	5.53
	poly(rC)-binding protein 1 [Homo sapiens]	19.38	1	3	5	14	0.9	4 2.0	1.134		4 5.5	476.74	19.38	11	14	356	37.5	7.09
	PREDICTED: bis(5'-adenosyl)-triphosphatase isoform X4 [Homo saj	6.12	2	1	1	3	0.9	1	1.120		1	110.06	6.12	3	3	147	16.8	7.08
324120908	doublecortin domain-containing protein 5 [Homo sapiens]	0.67	1	1	1	2	0.9	1	1.090		1	28.34	0.67	2	- 2	890	100.3	8.95
4506221	26S proteasome non-ATPase regulatory subunit 12 isoform 1 [Hor	12.06	2	4	4	14	0.9	5 5.2	1.438		5 17.3	664.56	12.06	11	14		52.9	7.65
530391261	PREDICTED: TBC1 domain family member 13 isoform X1 [Homo sa	2.47	1	1	1	4	0.9	2 13.8	1.160		2 6.0	55.43	2.47	2	4	324	37.7	4.97
237649049	small nuclear ribonucleoprotein Sm D2 isoform 2 [Homo sapiens]	43.52	2	4	1 4	16	0.9	6 0.4	1.240		6 7.5	535.03	43.52	11	16	108	12.4	9.89
	dedicator of cytokinesis protein 2 [Homo sapiens]	2.19	7	4	4	10	0.9	4 0.8	1.221		4 33.7	274.60	2.19	10	10		211.8	6.87
4507231	single-stranded DNA-binding protein, mitochondrial precursor [Hon	4.05	2	1	1	2	0.9	1	1.193		1	27.48	4.05	2	2	148	17.2	9.60
7657015	tRNA-splicing ligase RtcB homolog [Homo saplens]	1.98	1	1	1	4	0.9	2 4.9	1.143		2 8.7	102.01	1.98	3	4	505	55.2	7.23
578823733	PREDICTED: matrix metalloproteinase-19 isoform X1 [Homo sapier	3.58	4	1	2	10	0.9	2 3.8	1.127		2 16.9	164.61	3.58	6	10	279	31.7	7.94
530374793	PREDICTED: DCN1-like protein 1 isoform X1 [Homo sapiens]	9.84	2	2	2 2	7	0.9	3 9.8	1.220		3 18.8	315.42	9.84	5	7	244	28.3	4.98
530392249	PREDICTED: FERM domain-containing protein 4A isoform X7 [Hom	0.86	13	1	1	1	0.9	1	1.143		1	0.00	0.86	1	1	701	76.9	8.94
4507467	transforming growth factor-beta-induced protein ig-h3 precursor [F	35.87	1	16	17	102	0.9	5 7.3	1.177	3	4 17.9	4142.41	35.87	47	102		74.6	7.71
	PREDICTED: zinc finger MYM-type protein 4 isoform X4 [Homo sap	1.06	6	2	2 2	2	0.9	1	2.168		1	19.93	1.06	2	2	1224	136.2	8.13
	collagen alpha-2(I) chain precursor [Homo sapiens]	1.83	1	2	2 2	6	0.9	2 2.1	1.179		2 3.1	382.56	1.83	6	6	1366	129.2	8.95
42794779	unconventional myosin-XVIIIa isoform b [Homo sapiens]	1.86	5	3	3	7	0.9	3 4.5	1.110		3 14.0	387.95	1.86	7	7	2039	231.1	6.20
14141159	heterogeneous nuclear ribonucleoprotein H3 isoform b [Homo sapi	7.55	4	1	2	6	0.9	1	1.174		1	346.74	7.55	6	6	331	35.2	6.87
118918435	von Willebrand factor A domain-containing protein 3B [Homo saple	0.54	3	1	1	4	0.9	2 20.0	1.188		2 19.4	105.97	0.54	2	4	1294	145.7	7.33
149999611	signal recognition particle 14 kDa protein [Homo sapiens]	25.74	1	4	4	14	0.9	5 13.1	1.117		5 10.2	646.37	25.74	11	14	136	14.6	10.04
4557795	merlin isoform 1 [Homo sapiens]	2.02	25	1	2	9	0.9	3 1.1	1.041		3 7.6	87.25	2.02	5	ç	595	69.6	6.47
7705753	complement C1q subcomponent subunit A precursor [Homo sapien	17.55	1	3	3	26	0.9	9 2.4	1.264		8 5.1	1105.73	17.55	9	26	245	26.0	9.11
19913408	DNA topoisomerase 2-beta [Homo sapiens]	0.68	2	1	1	2	0.9	1	1.190		1	62.09	0.68	2	2	1621	182.5	8.06
530414090	PREDICTED: alpha-protein kinase 2 isoform X1 [Homo sapiens]	0.53	2	1	1	8	0.9	2 20.9	1.132		2 6.6	122.14	0.53	3	8	1501	163.7	5.44
578811811	PREDICTED: transcriptional-regulating factor 1 isoform X8 [Homo s	1.08	7	1	1	1	0.9	1	1.347		1	28.58	1.08	1	1	741	80.8	6.51
	colled-coll domain-containing protein 51 isoform 2 [Homo sapiens]	2.32	2	1	1	2	0.9	1	1.215		1	42.34	2.32	2	2	302	33.6	6.96
	PREDICTED: myb-related transcription factor, partner of profilin-lik	1.61	6	1	1	1	0.9	1	1.075		1	29.57	1.61	1	1	311	33.9	12.12
	60S ribosomal protein L13 isoform 2 [Homo sapiens]	5.73	2	1	1	3	0.9	1	1.095		1	186.15	5.73	3	3	192	22.2	11.65
257900451	plezo-type mechanosensitive ion channel component 2 [Homo sapi	0.18	1	1	1	2	0.9	2 3.6	1.633		2 80.4	28.95	0.18	1	2	2752	317.9	6.15
578816096	PREDICTED: zinc finger protein ZFAT isoform X1 [Homo sapiens]	0.83	5	1	1	1	0.9	1	1.228		1	29.24	0.83	1	1	845	94.3	7.53
	PREDICTED: rho guanine nucleotide exchange factor 2 isoform X9	1.22	11	1	1	3	0.9	1	1.082		1	123.10	1.22	3		817	92.8	5.71
	26S proteasome non-ATPase regulatory subunit 14 [Homo sapiens	20.32	1	3	3	17	0.9	7 10.5	1.283		6 34.5	672.14	20.32	7	17	310	34.6	6.52
	PREDICTED: hedgehog-interacting protein isoform X1 [Homo sapie	1.03	3	1	1	2	0.9	1	1.553		1	27.88	1.03	2	- 2	682	76.8	8.02
	PREDICTED: microtubule-associated serine/threonine-protein kinas	0.26	11	1	1	2	0.9	1	1.483			25.60	0.26	2	- 2	2275	247.6	8.54
27754778 46094009	ficolin-3 isoform 2 precursor [Homo sapiens]	7.99 1.53	2	2	2	11	0.9	4 0.9 3 3.2	1.257		4 14.0 3 25.8	302.20 112.44	7.99 1.53	6	11	288	31.7 74.0	6.84 4.34
	melanoma inhibitory activity protein 2 precursor [Homo sapiens] cytoplasmic FMR1-interacting protein 2 isoform b [Homo sapiens]	1.53 3.83	1	1		7	0.9	3 3.2 7 8.6	1.834		7 6.8	903.06	1.53 3.83	3		1227	74.0 142.5	4.34 7.17
619328949 10645195	cytoplasmic FMR1-interacting protein 2 isoform b [Homo sapiens] histone H2A type 1-B/E [Homo sapiens]	3.83	5	4	4	20	0.9	7 8.6	1.103		6.8	903.06 834.17	3.83	12	20	1227	142.5	7.17
10645195 530394084	histone H2A type 1-B/E [Homo sapiens] PREDICTED: pleckstrin homology domain-containing family A mem	37.69 1.50	5	1	5	37	0.9	1	1.118		1	834.17 22.84	37.69 1.50	14	37	130	14.1 38.1	11.05 8.97
	PREDICTED: pieckstrin nomology domain-containing family A mem PREDICTED: fatty-acid amide hydrolase 2 isoform X6 [Homo saplei	2.35					0.9	1	1.436		1	27.15	2.35	1		334	37.1	9.10
	IgGFc-binding protein precursor [Homo sapiens]	1.17		1	1	1	0.9	3 3.0	1.056		3 6.5	533.37	1.17	1		5405	571.6	5.34
	PHD finger protein 12 isoform 2 [Homo sapiens]	0.99	1	3	. 3	9	0.9	3.0	1.120		5 6.5	22 94	0.99	9		704	76.9	7.68
		7.28	5	1	1	1 12		4 39	1.140		4 62	750.71	7.28	1	1		76.9 61.2	7.68 6.48
5729770 11386157	tripeptidyl-peptidase 1 preproprotein [Homo sapiens] cytidine deaminase [Homo sapiens]	7.28	1	2	. 2	12	0.9	4 3.9 5 3.6	1.151	1		750.71 1811.19	7.28	6	12	146	16.2	6.48
	cytidine deaminase [Homo sapiens] 26S proteasome non-ATPase regulatory subunit 8 [Homo sapiens]	71.92 2.57	1	6	, 6	41	0.9	3.6	1.054	1	10.0	1811.19	71.92 2.57	18	41	146	16.2 39.6	6.92 9.70
			1			2	0.9	1			1			2		116		
	PREDICTED: uncharacterized protein LOC102723902 [Homo sapier 60S ribosomal protein L18a [Homo sapiens]	6.90 7.39	1	1	1	1	0.9	1	1.099		1	29.67 157.81	6.90 7.39	1		116	12.5 20.7	11.81 10.71
11415026 530384161	60S ribosomal protein L18a [Homo sapiens] PREDICTED: sorting nexin-3 isoform X2 [Homo sapiens]	7.39 5.71	1	1	1	3	0.9	1	0.879		1	157.81 58.73	7.39 5.71	3		176	20.7 16.3	10.71
	MAP kinase-activated protein kinase 3 [Homo sapiens]	2.88	2			3	0.9	1	1.117		1	184.38	2.88	3		382	43.0	7.28
	ras suppressor protein 1 isoform 1 [Homo sapiens]	53.43	2	1	1	25	0.9	9 12.8	1.148		9 13.1	184.38	53.43	3	25	277	31.5	8.65
	echinoderm microtubule-associated protein-like 1 isoform a [Homo	1.08	3	9	9	25	0.9	12.8	1.136		1 13.1	35.34	1.08	25	25	834	91.9	7.43
	proteasome subunit beta type-2 isoform 1 [Homo sapiens]	27.86	2	1		28	0.9	0 9.9	1.469	10	0 17.1	35.34 1024.55	27.86	15	28		22.8	7.43
	ras-related GTP-binding protein A [Homo sapiens]	6.71	3	1	2	42	0.9	1	1.156		17.1	618.59	6.71	15	42		36.5	7.02
	properdin precursor [Homo sapiens]	21.32	32		3	36	0.9	4 3.7	1.136	1-	4 19.1	1608.98	21.32	30	42	469	51.2	7.72
62530391		21.32	1	8	. 8	36	0.9	4 3.7 3 8.9	1.275	1	3 2.2	166.22	21.32	20	38	469	43.2	7.90
	selenoprotein P isoform 1 precursor [Homo sapiens]	2.10	2	1	1	9	0.9	3 8.9	0.943		2.2	166.22 28.32	2.10	3		381	43.2	7.87
	LIM homeobox transcription factor 1-alpha [Homo sapiens] MORC family CW-type zinc finger protein 2 [Homo sapiens]	0.93	1	1		-	0.9	1	1.238		1	25.27	0.93	1		970	110.7	8.63
	cullin-4B isoform 2 [Homo sapiens]	1.90	3	1	2		0.9	1	1.238		1	173.32	1.90			895	102.2	7.94
	protein TANC1 isoform 2 [Homo sapiens]	0.58		2	2	20	0.9	6 14.1	1.555		5 52.9	480.31	0.58	4	20	1390	152.1	8.34
225543463 571026678	transcription factor E4F1 isoform 3 [Homo sapiens]	1.15	8	2	. 2	30	0.9	1 14.1	1.607		1	27.97	1.15	4	30	607	64.0	5.39
571026678	PREDICTED: ATP-binding cassette sub-family A member 1 isoform	0.42	,			1	0.9	1	2.082		1	36.80	0.42	1		1659	186.5	6.40
530390862	PREDICTED: ATP-binding cassette sub-ramily A member 1 solorini PREDICTED: signal transducer and activator of transcription 5B iso	2.82	2	1	1	2	0.9	1	1.102		1	160.13	2.82	3		497	56.8	6.37
144446030	lymphocyte antigen 75 precursor [Homo saplens]	0.29	4	1	1	1	0.9	1	1.154		1	36.55	0.29	1	1	1722	198.2	6.67
	PREDICTED: engulfment and cell motility protein 1 isoform X3 [Hor		57	2	2 2	8	0.9	2 17.9	1.516		2 9.2	310.91	5.64	8	5	727	83.8	6.28
	3			_				 										

\$3041726 PPEE  167900484 pent 167900484 pent 167900484 pent 16790286 serial 195972866 kera 175972866 kera 175972866 kera 175972866 kera 17597286 pent 175972866 kera 17597286 pent 175972866 kera 17597286 pent 17597186 pent 1759	Description  verdin reductase A precursor [Homo saplens]  EDICTED trafficking protein particle complex subunit 8 isoform  tradar-related protein PTS3 precursor [Homo saplens]  invalraginine-rich späticing factor 3 [Homo saplens]  invalraginine-rich späticing factor 3 [Homo saplens]  invalraginine-rich späticing factor 3 [Homo saplens]  sarpoit: translation initiation factor 3 subunit G [Homo saplens]  EDICTED: Supplier [Homo saplens]  EDICTED: supplier [Homo saplens]  EDICTED: supplier protein sorting-associated protein 53 homoic  finger BED domain-containing protein 1 [Homo saplens]  EDICTED: avoid protein sorting-associated protein 53 homoic  finger BED domain-containing protein 1 [Homo saplens]  sine-5-monophosphate dehydrogenase 2 [Homo saplens]  EDICTED: Annophosphate dehydrogenase 2 [Homo saplens]  bio-5-bio-10-10-10-10-10-10-10-10-10-10-10-10-10-	25.00   25.00   0.69   10.50   26.83   2.50   31.16   8.80   5.32   3.57   1.25   1.44   14.67   3.70   0.59   10.08   2.64   7.01   41.85	Σ# Proteins  1 5 1 1 1 1 1 1 15 2 3 6 4 1 1 3 2 2 15 3 3	Σ# Unique Peptides 5 1 3 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5 3 4 1 1 2 1 1 1 1 1	17 1 9 10 1 72 3 12 3 12	0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0	955 955 955 955 955 954 954 254	A8: 115/114 Variability [%] 1 1 3 1 17.2 4 4 4.2 1 1 1 1 1 1 1 1 1 1 1	1.201 1.212 1.255 1.122	A8: 117/116 Count	1.9 1.7 7.5	562.77 27.20 549.74 317.86 30.48 3690.33 97.41	25.00 0.69 10.50 26.83 2.50 31.16 8.80	# Peptides A(3,6,7)	# PSM A(3,6,7)  4 17  1 1  9 9  10 10  1 1  2 72  3 3  5 12	# AAs 296 1161 381 164 320 584 125	33.4 130.1 41.9 19.3 35.6 58.8 14.3	7.52 5.01 3 11.65 5 6.13 3 5.21
\$304.1726 PREE \$167900484 pent \$4504001 serin \$167900484 pent \$4504001 serin \$167900480 pent \$1679072866 kera \$4759224 prog \$2503821158 PREE \$5303821158 PREE \$5303821158 PREE \$53038016 pent \$2383006699 zinc \$66933016 inous \$66933016 inous \$66933016 inous \$64933016 inous	EDICTED: trafficking protein particle complex subunit 8 isoform tradni-related protein PTA3 precursor (Homo saplens) rangolet translation initiation factor 3 subunit 6 (Homo saplens) angolet translation initiation factor 3 subunit 6 (Homo saplens) garamend call death protein 5 (Homo saplens) garamend call death protein 6 (Homo saplens) EDICTED: synthain-3 isoform X6 (Homo saplens) girn alphi-M soforma 2 precursor (Homo saplens) site-5-monephrosphate dehydrogenases 2 (Homo saplens) site-5-monephrosphate dehydrogenases 2 (Homo saplens) et eceptor by pe 7 member 13 (Homo saplens) for eceptor by pe 7 member 13 (Homo saplens) refluction-18 isoform 2 proprieto (Homo saplens) tribly-CpG-binding domain protein 2 testis-specific Isoform (Homo proplex protein) subunit zeta isoform a (Homo saplens)	0.69 10.50 26.83 2.50 31.16 8.80 5.32 3.57 1.25 1.44 14.67 3.70 0.59 10.08 2.64	1 5 1 1 1 1 1 1 1 5 2 2 3 3 6 4 1 1 3 3 2 2 1 5 3 3	5 5 3 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5 5 1 3 3 4 4 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3 1 2	0. 0. 0. 0. 0. 0.	955 955 955 954 254 954	1 3 17.2 4 4.2 1	1.212 1.255 1.122 1.077	3 4 1 20	1.9	27.20 549.74 317.86 30.48 3690.33 97.41	0.69 10.50 26.83 2.50 31.16	14	1 1 2 72 3 3	381 164 320 584 125	130.1 41.9 19.3 35.6 58.8 14.3	7.52 5.01 3 11.65 5 6.13 3 5.21
167900484 penti  49478282 eukuk  49478282 eukuk  49478282 eukuk  4759224 prog  5303821158 PREE  530410472 Inlend  64672344 inlend  64672344 inlend  6472344 o-ph  118402586 lactor  118402586 lactor  177010145 mett  4507509 mete  7710145 mett  4507509 APP  17978485 vacu	Intrain-related protein PTX3 precursor (Homo sapiers) Incharginierich spicing factor 3 [binom sapiers) anayotic translation initiation factor 3 subunit 6 [Homo sapiers] surpoite translation initiation factor 3 subunit 6 [Homo sapiers] grammed cell death protein 5 [Homo sapiers] grammed cell death protein 5 [Homo sapiers] [DICTED: septin 89 isoform X [Homo sapiers] [DICTED: syntain-3 foolorm X6 [Homo sapiers] [DICTED: vacuolar protein sorting-associated protein 53 homolo (Enger 8ED domain-containing protein 11 [Homo sapiers] signif alpha-3 lisoform 2 precursor (Homo sapiers) [Signia plah-3 lisoform 2 precursor (Homo sapiers) [DICTED: chromodomain-helicase-DIAN-binding protein 3 soform quilti-conjugating engyme 2 A isoform 4 [Homo sapiers] to receptor type 2 member 13 [Homo sapiers] in receptor type 2 member 13 [Homo sapiers] helpopfortuco-2-kinassifuctose 2,6-bisphosphatase 2 isoforn b polyglutathione phase [Homo sapiers] ericular-18 lisoform 2 proprotein [Homo sapiers] included the soft of the protein sapiers [Homo sapiers] [	10.50 26.83 31.16 8.80 5.32 3.57 1.25 1.44 14.67 3.70 0.59 10.08 2.64 7.01	5 1 1 1 1 15 2 3 6 4 4 1 1 3 2 2	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 3 3 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3 1 2	0. 0. 0. 0. 0. 0.	955 955 954 2 954 2 954	4 4.2	1.255 1.122 1.077	3 4 1 20	1.7	549.74 317.86 30.48 3690.33 97.41	10.50 26.83 2.50 31.16	9 10 45	1 1 2 72 3 3	381 164 320 584 125	41.9 19.3 35.6 58.8 14.3	5.01 3 11.65 5 6.13 3 5.21
450,4901 serim 4490,2901 serim 4491,2902 euka 4491,2902 euka 1959,29866 kera 1959,2986 kera 1959,2986 kera 195	ine/arginien-rich spicing factor 3 [Homo sapiens] argivel translation initiation factor 3 subunit 6 [Homo sapiens] attin, type 1 cytoskeletal 10 [Homo sapiens] grammed cell deship protein 5 [Homo sapiens] EDICTED. serpin 80 Isoform XI [Homo sapiens] EDICTED. syntams 3 soform XI [Homo sapiens] EDICTED. vasualar protein string-associated protein 51 homote Cinggri BED domain-containing protein 1 [Homo sapiens] grim alpha-M Soform 2 precursor [Homo sapiens] grim alpha-M Soform 2 precursor [Homo sapiens] EDICTED: chromodomain-heticae-D-W-banding protein 3 Isoform quitin-conjugating enzyme 22 A Isoform 4 [Homo sapiens] EDICTED: chromodomain-heticae-D-W-banding protein 3 Isoform quitin-conjugating enzyme 22 A Isoform 4 [Homo sapiens] ericukin-18 Isoform 2 proprieto [Homo sapiens] ericukin-18 Isoform 2 proprieto [Homo sapiens] ericukin-18 Isoform 2 proprieto [Homo sapiens] tithyl-CpG-binding domain protein 2 Isoform bomplex protein 1 Subunit zela Isoform a [Homo sapiens]	26.83 2.50 31.16 8.80 5.32 3.57 1.25 1.44 14.67 3.70 0.59 10.08 2.64 7.01	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3 4 1 12 1 1 1 1 1 1 1 14	3 4 4 1 2 14 1 2 1 2 1 1 1 1 1 14	3 1 2	0. 0. 0. 0. 0.	955 955 954 2 954 954	4 4.2	1.255 1.122 1.077	4 1 20	1.7	317.86 30.48 3690.33 97.41	26.83 2.50 31.16	10	1 1 2 72 3 3	164 320 584 125	19.3 35.6 58.8 14.3	11.65 6.13 5 5.21
49472822 eukuka 195972866 kerra 4759224 prog 530382158 PREE 530382158 PREE 530382158 PREE 530382158 PREE 530382158 PREE 530382158 PREE 530382669 2inc 68501734 integ 66933016 inca 68501734 integ 66933016 inca 12965778 tasts 64702456 iacto 17701045 integ 4507509 meta 77710145 met 4507509 integ 4507509 APP 4507509 APP 4	caryotic translation initiation factor 3 subunit 6 [Homo sapiens] sim. bps e   optoceletal 10 [Homo sapiens] grammed cell death protein 6 [Homo sapiens] grammed cell death protein 6 [Homo sapiens] EDICTED: seprin 89 isoform XI [Homo sapiens] EDICTED: syntaxin-3 barolom X6 [Homo sapiens] EDICTED: vacuolar protein sorting-associated protein 53 homolc (finger 8ED domain-containing protein 11 [Homo sapiens] sigrin alpha-XI isoform 2 precursor [Homo sapiens] egrin alpha-XI isoform 2 precursor [Homo sapiens] EDICTED: chromodomain-helicase-DMA-binding protein 3 sofori quilti-conjugating enzyme 2 A isoform 4 [Homo sapiens] te receptor type 2 member 13 [Homo sapiens] te receptor type 2 member 13 [Homo sapiens] et could be a substitution of the s	2.50 31.16 8.80 5.32 3.57 1.25 1.44 14.67 3.70 0.59 10.08 2.64 7.01	1 1 15 2 2 3 3 6 4 4 1 1 3 3 2 2 15 3 3	1 12 1 1 1 1 1 1 14	1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3 1 2	0. 0. 0. 0.	955 954 954 954	1	1.122	1 20 1		30.48 3690.33 97.41	2.50 31.16	42	1 1 2 72 3 3	320 584 125	35.6 58.8 14.3	6.13 5 5.21
195972866 kerar 195972866 kerar 195972866 kerar 195972867 kerar 1959728 propies 1959728 propie	atin, type I cytoskeletal 10 (Homo sapiens) grammed cell deship protein 5 (Homo sapiens) EDICTED, serpin 80 (soform XI (Homo sapiens) EDICTED, serpin 80 (soform XI (Homo sapiens) EDICTED, variants a Josefum XI (Homo sapiens) EDICTED, variants a Josefum XI (Homo sapiens) EDICTED, variants protein serting associated protein 51 homose rights also form 2 precursor (Homo sapiens) grim alpha-M soform 2 precursor (Homo sapiens) EDICTED: chromodomian-heticase-DAV-banding protein 3 (soform EDICTED: chromodomian-heticase-DAV-banding protein 3 (soform EUICTED: chromodomian-heticase-DAV-banding protein 3 (soform Euichten) European (EUICTED) Eur	31.16 8.80 5.32 3.57 1.25 1.44 14.67 3.70 0.59 10.08 2.64 7.01	15 2 3 6 4 1 3 2 2 15	122 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3 1 2	0. 0. 0. 0.	954 2 954 954 954	10.6 1 1 1	1.077	20	7.5	3690.33 97.41	31.16	42	3 3	584 125	58.8 14.3	5.21
4759224 prog 5530382158 PREE 5303821798 PREE 5303821798 PREE 5303184718 PREE 5303184718 PREE 5303184718 Intege 569533016 incol 530409856 PREE 531990811 judiqu 12965178 taste 64762449 6-ph 118402586 iacrot 64762449 FREE 56959 mete 77710145 met 4502643 T.co. 64762449 T.co. 6476249 T.co. 6476	grammed cell death protein 5 (Homo saplens) EDICTED: serpin Bolfordm XI (Homo saplens) EDICTED: syntaxin-3 isoform Xio (Homo saplens) EDICTED: vacuolar protein sorting-associated protein 53 homoto (Eniger BED domain-containing protein 11 (Homo saplens) sgrin alpha-XI (soform 2 precursor (Homo saplens) sgrin alpha-XI (soform 2 precursor (Homo saplens) EDICTED: chromodomain-helicase-DNA-binding protein 3 storn EDICTED: chromodomain-helicase-DNA-binding protein 3 storn et receptor type 2 member 13 (Homo saplens) te receptor type 2 member 13 (Homo saplens) te receptor type 2 member 13 (Homo saplens) et receptor type 2 member 13 (Homo saplens) et call adaption and type and t	8.80 5.32 3.57 1.25 1.44 14.67 3.70 0.59 10.08 2.64 7.01	2 3 6 4 1 3 2 15	1 1 1 1 1 14	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3 1 2	0. 0. 0.	954 954	1 1 1		1		97.41			3 3	125	14.3	
\$30397196 PERE \$303197196 PERE \$30310472 PEE \$230310472 PEE \$2303104099 zinc \$88501734 integ \$69533016 integ \$69533016 integ \$69533016 integ \$69533016 integ \$69533016 integ \$604702445 e-ph \$118402586 integ \$64702445 e-ph \$118402586 integ \$64702445 e-ph \$18402586 integ \$64702445 e-ph \$18402586 integ \$64702445 e-ph \$18402586 integ \$6470245 e-ph \$18402586 e-ph \$18402	EDICTED: syntaxin-3 kofurm & [Homo sapiens] EDICTED: vacuolar protein sorting-associated protein 53 homoto fringer BED domain-containing protein 1 [Homo sapiens] egrin alpha-M losform 2 precursor [Homo sapiens] sine-5-monophosphate delydrogenses 2 [Homo sapiens] EDICTED: chromodomain-helicase-DMA-binding protein 3 sofor quiti-conjugating enzyme 2 A isoform 4 [Homo sapiens] ter ecceptor type 2 member 13 [Homo sapiens] ter ecceptor type 2 member 13 [Homo sapiens] ter color type 2 member 13 [Homo sapiens] etculari 18 losform 2 proprotein [Homo sapiens] etculari 18 losform 2 proprotein 2 testis-specific isoform [Homo complex protein 1 subunit zeta koform a [Homo sapiens]	3.57 1.25 1.44 14.67 3.70 0.59 10.08 2.64 7.01	3 6 4 1 3 2 15	1 1 1 1 14	2 1 1 1 1 1 14	3 1 2	0.	954	1							. 12	376	42.4	6.04
\$300.10472 PEREZ \$3806.699 zinc \$8501734 integ \$8501734 integ \$66933016 incisos \$53040986 PREZ \$531990811 ubiqs \$6476.2445 6-ph \$1840256 is \$6476.2445 6-ph \$7710145 meter \$7710145 meter \$7710145 \$15092 meter \$7710145 \$15092 \$1	EDICTED vacualar protein sorting-associated protein S3 homose, finger BED domain-containing protein I1 (Heno sapiens) legin alpha-M isoform 2 precursor (Homo sapiens) sine-5-monophosphate dehydrogenase 2 (Homo sapiens) DEDICTED: chromodomain-helcase—DM-banding protein 3 isofor quilin-conjugating enzyme 22 A isoform 4 (Homo sapiens) te receptor type 2 remmber 13 (Homo sapiens) hosphorfundo-2-kinase/fractores-2,6-bisphosphatase 2 isoform b toysjutatinion bysa (Homo sapiens) erieukish-18 isoform 2 proprotein (Homo sapiens) erieukish-18 isoform 2 proprotein (Homo sapiens) tithyl-CpG-binding domain protein 2 testis-specific isoform (Homo propiets protein 1 subusti zeta isoform a (Homo sapiens)	1.25 1.44 14.67 3.70 0.59 10.08 2.64 7.01	6 4 1 3 2 15 3	1 1 1 14	1 1 14	3 1 2 47	0.		1	0.897	1		472.77	5.32					
28380e699 zinc 88501734 integ 66933016 intosi 530409866 PREE 531909811 ulsiq 12965178 tasta 64762445 6-ph 118402586 lacto 342249321 inter 4807509 meta 7710145 mete 4502643 T-co 100913206 ATP 17978485 vacu	cfinger BED domain-containing protein 1 (Homo sapiens) grigin alpha-M lotoma 2 precursor (Homo sapiens) sine-5-monophosphate dehydrogenase 2 (Homo sapiens) DIOTED: chromodomain-fisicase-DNA-binding protein 3 isofor- quitin-conjugating enzyme E2 A isoform 4 (Homo sapiens) te receptor type 2 member 13 (Homo sapiens) te receptor type 2 member 13 (Homo sapiens) te receptor type 2 member 13 (Homo sapiens) totylgulatathone lysise (Homo sapiens) talioproteinase inhibitor 1 precursor (Homo sapiens) talioproteinase inhibitor 1 precursor (Homo sapiens) thyl-CyG-binding domain spotein 2 tests-specific isoform (Homo- propies protein 1 subunit zeta isoform (Homo sapiens)	1.44 14.67 3.70 0.59 10.08 2.64 7.01	4 1 3 2 15 3	1 1 14 1	1 14	1 2 47	-	953		1.140	1		109.78	3.57	1	3 3	252	28.8	5.22
283806699 zinc. 885801734 integ 66933016 insol 530409856 PREE 531990811 ublq 12965178 tasts 64762486 6-ph 118402586 lacto 342249321 inter 7710145 metel 4502643 T-co 100913206 ATP- 1197978885 vacu	cfinger BED domain-containing protein 1 (Homo sapiens) grigin alpha-M lotoma 2 precursor (Homo sapiens) sine-5-monophosphate dehydrogenase 2 (Homo sapiens) DIOTED: chromodomain-fisicase-DNA-binding protein 3 isofor- quitin-conjugating enzyme E2 A isoform 4 (Homo sapiens) te receptor type 2 member 13 (Homo sapiens) te receptor type 2 member 13 (Homo sapiens) te receptor type 2 member 13 (Homo sapiens) totylgulatathone lysise (Homo sapiens) talioproteinase inhibitor 1 precursor (Homo sapiens) talioproteinase inhibitor 1 precursor (Homo sapiens) thyl-CyG-binding domain spotein 2 tests-specific isoform (Homo- propies protein 1 subunit zeta isoform (Homo sapiens)	14.67 3.70 0.59 10.08 2.64 7.01	1 3 2 15 3	14 14	1 14	2 47	0.		1	1.110	1		30.07	1.25	1	1 1	641	72.4	7.83
69933016 Inosis 530407856 PREI 531990811 ubiq 12965178 tasts 64762445 6-ph 118402586 lacto 342349321 inter 48097599 meta 7710145 meth 4802643 T-co 100913206 ATP- 11978485 vacu	sine-5-monophosphate dehydrogenase 2 [Homo sapiens] EDICTED: chromonain-helicae-Do-holmdig protein 3 soforr quitin-conjugating enzyme E2 A isoform 4 [Homo sapiens] te receptor type 2 member 13 [Homo sapiens] te receptor type 3 member 13 [Homo sapiens] totyglutathione lysse [Homo sapiens] telligentiae-1 bis doring 2 proprotein [Homo sapiens] tallioproteinase inhibitor 1 precursor [Homo sapiens] thyl-CyG-binding domain protein 2 testis-specific isoform [Homo complex protein 1 subunt rate is forform a [Homo sapiens]	3.70 0.59 10.08 2.64 7.01	3 2 15 3	14	1 14	47		953	1	1.255	1		36.43	1.44		2 2	694		6.10
\$3040986 PREE \$319908111 ubight 12965178 taste 64762445 6-ph 118402586 lacto 342249321 inter 4507509 meta 77710145 met 4507509 total 100913206 ATP- 11978485 vaca 15305548 serin	EDICTED. chromodomain-helicase-DNA-binding protein 3 soforr quillin-conjugaling enzyme 2A isotom 4 (Homo sapiens) te receptor type 2 member 13 (Homo sapiens) hospiduruto-2-kinase/fuctose-2,6-bisphosphatase 2 soform b polygiquitathione bysac (Homo sapiens) ericuksin-18 soform 2 proprotein (Homo sapiens) ericuksin-18 soform 2 proprotein (Homo sapiens) thyli-CpG-binding domain protein 2 testis-specific soform (Homo complex protein 1 subusti rate isoform a (Homo sapiens)	0.59 10.08 2.64 7.01	2 15 3	1	1		0.	953 1	6 9.4	1.131	16	11.8	1974.80	14.67	41	1 47	1152	127.1	7.23
531990811 ubiq 12965178 taste 64762445 6-ph 118402586 lacto 342349321 inter 4507509 mete 7710145 metel 4502643 T-co 100913206 ATP- 17978485 vacu 16300548 serin	quillin-coujugating enzyme E2 A isoform 4 [Homo sapiens] te receptor type 2 member 13 [Homo sapiens] te receptor type 2 member 13 [Homo sapiens] todyglutathione lyase [Homo sapiens] retection-18 Boform 2 proprotein [Homo sapiens] talliproteinase inhibitor 1 precursor [Homo sapiens] thyl-CpG-binding domain protein 2 testis-specific isoform [Homo complex protein 1 subunit zeta isoform a [Homo sapiens]	10.08 2.64 7.01	15 3	1		2		953	1	1.797	1		129.29	3.70		2 2	514		
12965178 taste 64762445 6-ph 118402586 lactoc 342349321 inter 4507509 meta 77710145 meth 4502643 T-co 100913206 ATP-117978485 vacu 16300548 serin	te receptor type 2 member 13 (Homo saplens) bloophortus-2-5 kansal/fustores 2-6 kelphosphalase 2 isoforn b toylglutathlorie lysse (Homo saplens) erteukin-15 laoform 2 proprotein (Homo saplens) fullaproteinase inhibitor 1 precursor (Homo saplens) fiftyl-CpG-binding domain protein 2 tests-specific isoform (Homo complex protein 1 subunit zeta koform a (Homo saplens)	2.64 7.01	3		1	1		953	1	1.267	1		23.14	0.59		1 1	1185		
64762445 6-ph 118402586 lacto 342349321 inter 4507509 mete 7710145 meth 4502643 T-co 100913206 ATP- 17978485 vacu 16300548 serin	hosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 isoform b torglutathione lyase [Homo sapiens] erleukin-18 isoform 2 proprotein [Homo sapiens] talloproteinase inhibitor 1 procursor [Homo sapiens] thyl-CpG-binding domain protein 2 testis-specific isoform [Homo omplex protein 1 subunit zeta isoform a [Homo sapiens]	7.01		1	1	1		953	1	1.024	1		22.45	10.08		1 1	119		
118402586 lacto 342349321 inter 4507509 meta 7710145 metf 4502643 T-co 100913206 ATP- 17978485 vacu 16306548 serin	toylglutathione lyase [Homo sapiens] erleukin-18 isoform 2 proprotein [Homo sapiens] talignoteinase inhibitor 1 precursor [Homo sapiens] thyl-CpC-binding domain protein 2 testis-specific isoform [Homo complex protein 1 subunit zeta isoform a [Homo sapiens]		1	1	1	4		953	2 2.2		2	31.2	60.83	2.64		2 4	303		
342349321 inter 4507509 meta 7710145 metf 4502643 T-co 100913206 ATP- 17978485 vacu 16306548 serin	erleukin-18 isoform 2 proprotein [Homo sapiens] talloproteinase inhibitor 1 precursor [Homo sapiens] thyl-CpG-binding domain protein 2 testis-specific isoform [Homo complex protein 1 subunit zeta isoform a [Homo sapiens]	41.85	17	3	3	8		952	3 3.2		3	7.9	282.48	7.01	8	8	471		
4507509 meta 7710145 meth 4502643 T-co 100913206 ATP- 17978485 vacu 16306548 serin	talloproteinase inhibitor 1 precursor [Homo sapiens] thyl-CpG-binding domain protein 2 testis-specific isoform [Homo complex protein 1 subunit zeta isoform a [Homo sapiens]		1	7	7	22		952	8 6.9		8	8.4	707.51	41.85	19	9 22	184		
7710145 meth 4502643 T-co 100913206 ATP- 17978485 vacu 16306548 serin	hthyl-CpG-binding domain protein 2 testis-specific isoform [Homo complex protein 1 subunit zeta isoform a [Homo sapiens]	4.23	2	1	1	6		952	2 5.1		2	19.7	93.70	4.23	-	3 6	189		
4502643 T-co 100913206 ATP- 17978485 vacu 16306548 serin	complex protein 1 subunit zeta isoform a [Homo sapiens]	5.80	1	1	1	3		952	1	1.043	1		173.10	5.80	3	3	207		
100913206 ATP- 17978485 vacu 16306548 serin		1.99	4	12	1 12	71	0.	952	16 9.6	1.057	26	14.5	29.50 2789.40	1.99		1 71	302 531		
17978485 vacu 16306548 serin		3.15		12	12	12	-				26		380.72		34				
16306548 serin	cuolar protein sorting-associated protein 18 homolog [Homo sap	1.13	1	4	4	12		951	4 2.7	1.541	4	8.3	121.98	3.15 1.13	10	12	973		
	inetRNA ligase, cytoplasmic [Homo sapiens]	2.72	2	1	1	3		951	1	0.837	1		57.40	2.72		3 3	514		
31742501 sorti	ting nexin-27 [Homo sapiens]	1.89	2		1	3		950	1	1.245	1		125.91	1.89		3 3	528		
	ckstrin homology domain-containing family A member 2 [Homo	1.65	1		1	2		950	1	1.892	1		33.04	1.65		2 2	425		
	osine-protein phosphatase non-receptor type substrate 1 precur	7.94	4	3	3	8		950	3 3.2		3	4.0	345.37	7.94		8 8	504		
	characterized protein C9orf142 [Homo sapiens]	13.24	1	1	1	2		950	1	1.270	-		44.22	13.24		2 2	204		
	EDICTED: protein S100-A7 isoform X1 [Homo sapiens]	55.45	1	. 5	. 8	115		950 2	16 6.0	1.110	26	12.5	6266.67	55.45	24	115			
	inal dehydrogenase 1 [Homo sapiens]	7.98	2	4	4	10		950	4 3.4		4	8.0	430.77	7.98	10	10	501		
4507511 meta	talloproteinase inhibitor 2 precursor [Homo sapiens]	11.82	1	2	2 2	4		950	2 7.8	2.171	2	129.6	82.41	11.82		4 4	220		7.49
578824944 PREI	EDICTED: paraspeckle component 1 isoform X2 [Homo sapiens]	5.39	2	1	1	3		950	1	1.008	1		79.57	5.39		3 3	427		
	chidonate 5-lipoxygenase isoform 2 [Homo sapiens]	4.21	3	2	2 2	6	0.	950	2 10.5	1.094	2	15.8	348.95	4.21		5 6	642	74.6	5.63
5174613 nucle	cleosome assembly protein 1-like 4 [Homo sapiens]	2.93	1	1	1	3	0.		1	1.440	1		93.96	2.93	3	3 3	375		
530379765 PREI	EDICTED: eukaryotic peptide chain release factor subunit 1 isofc	11.88	3	3	3	6	0.		3 10.9	0.921	3	29.3	251.41	11.88		6	404		
	ydropyrimidinase-related protein 5 [Homo sapiens]	1.24	1	1	1	6		949	3 1.1		3	18.4	74.65	1.24		2 6	564		
	ell CLL/lymphoma 7 protein family member C isoform 1 [Homo:	4.55	7	1	2	6		949	1	2.577	1		80.81	4.55	ć	6	242		
	totriosidase-1 isoform 2 precursor [Homo sapiens]	9.17	3	3	3	11		949	4 9.1		4	28.5	578.85	9.17	8	B 11	447		
4505981 plate	telet basic protein preproprotein [Homo sapiens]	14.84	1	2	2 2	6		949	2 5.6		2	8.0	267.25	14.84		6	128		
578798461 PREI	EDICTED: WD repeat-containing protein 65 isoform X4 [Homo s	0.59	4	1	1	2		948	2 0.5		2	47.6	30.31	0.59		1 2	1192		
	erleukin enhancer-binding factor 2 isoform 2 [Homo sapiens]	2.84	2	1	1	- 6		948	2 3.2		2	5.0	245.41	2.84	3	3 6	352		
	S ribosomal protein S16 [Homo sapiens]	14.38	2	2	2	- 6		948	2 1.0		2	15.9	272.24 105.21	14.38		6	146		
	EDICTED: myosin regulatory light chain 10 isoform X1 [Homo sa	6.80 0.77	1	1		2		947	1	1.204	1		33.43	6.80 0.77		2 2	1165		
	nsient receptor potential cation channel subfamily M member 5 EDICTED: filamin-8 isoform X7 [Homo sapiens]	3.84	2			43			1	1.088	1		1402.01	3.84	21	5 43			
	EDICTED: histone-lysine N-methyltransferase SETD2 isoform X1	0.29	9		9	93	-		1	1.247	1		37 27	0.29	20	43	2058		
	EDICTED: historie-iysine N-metriyitransierase SETD2 isoloriii XT EDICTED: obscurin isoform X32 [Homo sapiens]	1.01	43	1		15	-		3 0.0		2	41.5	218.16	1.01		7 15	7297		
	EDICTED: COX assembly mitochondrial protein 2 homolog isofor		43	1	1	1	0.		1	1.248	1	41.5	30.11	4 97		1 1	181		
	EDICTED: cleavage and polyadenylation specificity factor subuni	6.56	. 6	1	1	3		946	1	0.813	1		156.88	6.56		3 3	381		
	-related protein Rab-5C isoform a [Homo sapiens]	16.20	4	1	3	11		945	1	1.000	1		344.58	16.20		3 11	216		
	EDICTED: amphoterin-induced protein 2 isoform X1 [Homo sapi	1.72	1	1	1	2		945	2 11.4		2	3.6	28.22	1.72		1 2	522		
	sin-1A-interacting protein 1 isoform 2 [Homo sapiens]	2.40	1	1	1	3		945	1	1.068	1		217.09	2.40	3	3 3	583		
	predoxin reductase 1, cytoplasmic isoform 5 [Homo sapiens]	14.97	9	4	5	11	0.	945	4 9.9	1.253	3	8.6	424.83	14.97	11	1 11	461	50.8	6.62
	teasome subunit beta type-3 [Homo sapiens]	31.71	1	5	5 5	21	0.	945	9 4.5	1.047	9	7.4	796.63	31.71	13	3 21	205	22.9	6.55
115334675 ubiqu	quitin thioesterase otulin [Homo sapiens]	1.99	1	1	1	2	0.	945	1	2.387	1		36.14	1.99		2 2	352	40.2	5.47
66932916 mito	ogen-activated protein kinase 1 [Homo sapiens]	24.44	19	4	7	29	0.	944	6 14.4	1.161	6	17.2	956.26	24.44	18	3 29	360	41.4	6.98
	nscription factor PU.1 isoform 2 [Homo sapiens]	3.70	2	1	1	3	0.	944	1	1.408	1		114.84	3.70		3 3	270	31.1	
38201714 ELAV	AV-like protein 1 [Homo sapiens]	3.37	1	1	1	3	0.	944	1	1.159	1		103.89	3.37		3 3	326	36.1	9.17
	F0587 protein C1orf123 [Homo sapiens]	10.63	1	1	1	1		944	1	1.121	1		25.18	10.63		1 1	160		
154240671 mae:	estro heat-like repeat-containing protein family member 2B [Ho	0.50	1	1	1	1	0.		1	1.576	1		33.71	0.50	1	1 1	1585		
530418502 PREI	EDICTED: dolichol-phosphate mannosyltransferase isoform X3 [	4.23	4	1	1	2	0.		1				19.60	4.23		2 2	189		
	ckstrin homology domain-containing family D member 1 [Homo	1.38	1	1	1	4		943	4 1.0		4	0.8	52.44	1.38		4	506		
	min-like protein 1 [Homo sapiens]	3.27	10	3	3	9		943	3 14.2		3	8.6	177.94	3.27		9	1100		
	steasome subunit beta type-5 isoform 2 [Homo sapiens]	7.50	2	1	1	3		943	1	0.986	1		128.71	7.50		3	160		
	EDICTED: actin filament-associated protein 1 isoform X3 [Homo- riostin isoform 4 precursor [Homo sapiens]	0.90 47.67	3	1	1	159		942	1	0.918	1		24.78 7396.91	0.90 47.67	7.	1 1	558 751		
	nostin isoform 4 precursor [Homo sapiens] EDICTED: lisH domain and HEAT repeat-containing protein KIAA	0.70	7	1	26	109		942	1	2,564	1		30.64	0.70	76	159	860		
	mocyte nuclear protein 1 isoform 1 [Homo sapiens]	12.44	/ A	1	2	- 2		942	3 6.5		3	13.9	227.90	12.44		3 0	225		
	osin-15 precursor [Homo sapiens]	0.41	1	3	1	2		942	1	0.834	1	10.7	31.28	0.41		2 2	1946		
	-like protein isoform 2 [Homo sapiens]	1.10	3	1	1	1	0.		1	2.367	1		28.83	1.10		1 1	638		
	EDICTED: haloacid dehalogenase-like hydrolase domain-contain	21.89	3	2	2 2	5	0.		2 16.4		2	18.4	262.60	21.89		5 5	169		
	tein FAM184B [Homo sapiens]	0.47	1	1	1	1		940	1	3.180	1		18.61	0.47		1 1	1060		
	GpppX diphosphatase [Homo sapiens]	8.61	1	3	3	11	0.	940	4 7.1	1.081	4	5.1	493.19	8.61	8	3 11	337		
	mplement component C1q receptor precursor [Homo sapiens]	1.07	1	1	1	1	0.		1	1.237	1		23.58	1.07		1 1	652		
4885583 rho-a	-associated protein kinase 1 [Homo sapiens]	2.36	1	3	3	15		940	7 9.3	0.954	7	18.6	388.87	2.36	8	B 15	1354	158.1	5.90
530387370 PREI	EDICTED: kelch repeat and BTB domain-containing protein 11 is	2.41	1	1	1	3		939	1	1.317	1		243.82	2.41	3	3 3	623	65.7	6.07
5031863 galer	ectin-3-binding protein precursor [Homo sapiens]	16.75	1	7	7	30		939 1	1 5.7		11	29.1	1495.33	16.75	19	9 30	585		
578807364 PREI	EDICTED: colled-coll domain-containing protein 37 isoform X9 [I	0.82	2	1	1	3		939	1	1.135	1		68.50	0.82	1	3 3	611		
4557469 AP-2	-2 complex subunit beta isoform b [Homo sapiens]	7.68	3	2	6	15		939	2 8.0		2	30.1	501.17	7.68	13	3 15	937		
	citatory amino acid transporter 2 isoform 2 [Homo sapiens]	1.42	5	1	1	4		939	2 3.6		2	1.5	67.82	1.42	3	3 4	565		
	EDICTED: serpin A11 isoform X1 [Homo sapiens]	4.13	1	1	1	3		938	1	1.033	1		70.72	4.13	3	3 3	218		
	63 antigen isoform D precursor [Homo sapiens]	5.13	3	1	1	2		938	1	1.069	1		53.42	5.13		2 2	156		
	onin-1B [Homo sapiens]	4.29	1	2	3	11			2 13.9		2	16.9	135.41	4.29		5 11			
	-related protein Rab-3D [Homo sapiens]	19.18	22	2	4	13			2 5.0		2	9.0	327.37	19.18	10	13			
	S proteasome non-ATPase regulatory subunit 1 isoform 2 [Homo	4.77	2	2	2 2	6			2 3.7		2	1.9	494.21	4.77		6	922		
	optosis regulator BAX isoform sigma [Homo sapiens]	7.26	4	1	1	3		937	1	1.549	1		158.83	7.26	1	3 3	179		
4507947 tyros	osinetRNA ligase, cytoplasmic [Homo sapiens]	7.77	1	4	4	12		937	5 2.7		5	24.3	312.44	7.77	10	12			
13129018 gami 90669511 guine	mma-glutamylcyclotransferase isoform 1 [Homo sapiens] none oxidoreductase-like protein 1 [Homo sapiens]	21.28 3.44	2	3	3	7		937	3 10.2		3	3.2 8.8	306.06 203.55	21.28 3.44		7	188 349		
	none oxidoreductase-like protein 1 [Homo sapiens] EDICTED: mitochondrial inner membrane protease ATP23 homo	3.44	1	1	- 1	8		936	2 9.5		3	28.5	203.55 30.29	3.44		8	349 185		
	EDICTED: mitochondrial inner membrane protease ATP23 homo lin-associated NEDD8-dissociated protein 1 [Homo sapiens]	3.78 5.93	2	1	1	2		935	2 9.5 8 11.6		7	28.5 32.0	30.29 829.43	3.78 5.93		2	185 1230		
	RCKS-related protein [Homo sapiens]	7.69	1	,	,	19		934	1	1.356	1	32.0	36.74	7.69	10	19	1230		
	S acidic ribosomal protein P0 [Homo sapiens]	3.79	1	1	1	5		934	2 9.2		2	0.9	274.28	3.79		3 5	317		

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Accession	Description	ΣCoverage	Σ# Proteins Σ# Uniqu	Peptides Σ# F	Peptides Σ# PSMs	A8: 115/11	4 A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116	A8: 117/116 Count A8: 117/116 Variabi	lity [%]	Score A(3,6,7) C	overage A(3,6,7) # Pepti	ides A(3,6,7) #	# PSM A(3,6,7)	# AAs		calc. pl
530394395	PREDICTED: WD repeat-containing protein 96 isoform X5 [Homo s	0.52	6	1	1		934	1	1.064	1		24.80	0.52	1	1	1535	176.8	
526253088 22027655	endothelial differentiation-related factor 1 isoform 4 [Homo sapiens AP-1 complex subunit sigma-2 isoform 2 [Homo sapiens]	11.81 5.73	5	1	1		934	3 7.8	8 1.145 0.929	3	37.9	270.63 44.81	11.81 5.73	3	8	127 157		
14150098	transmembrane protein 79 [Homo sapiens]	2.03	4	- 1	1		933	1	5.752	1		39.51	2.03	2	2	394		
269847098	phospholysine phosphohistidine inorqanic pyrophosphate phosphat	9.63	2	2	2		933	5 5.7		5	5.3	297.95	9.63	6	12	270		
320461689	ankyrin repeat and SOCS box protein 12 [Homo sapiens]	2.20	1	1	1		932	1	1.173	1	5.5	28.63	2.20	1	1	318		
226530313	protein-methionine sulfoxide oxidase MICAL1 isoform 2 [Homo sap	3.36	3	2	2		932	2 12.8		2	17.4	240.62	3.36	5	5	981		
578804605	PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isofor	0.71	4	1	1		931	1	1.137	1		134.56	0.71	3	3	1544		
530383030	PREDICTED: Lebercilin isoform X2 [Homo sapiens]	2.15	1	1	1	1 0.	931	1	1.064	1		25.09	2.15	1	1	697	80.5	5 7.68
7019439	ATP-sensitive inward rectifier potassium channel 14 [Homo sapiens	2.06	1	1	1	1 0.	931	1	1.255	1		21.27	2.06	1	1	436	47.8	B 5.41
375298720	gamma-tubulin complex component 2 isoform 3 [Homo sapiens]	0.78	3	1	1	1 0.	930	1	1.085	1		41.53	0.78	1	1	772	88.0	0 6.76
223278387	calmodulin-like protein 5 [Homo sapiens]	21.23	1	2	2	8 0.	930	3 5.1	7 1.149	3	4.6	681.93	21.23	5	8	146	15.9	9 4.44
578825543	PREDICTED: centrosomal protein of 128 kDa isoform X2 [Homo sa	0.47	2	1	1		930	1	1.195	1		0.00	0.47	1	1	1055		
4502315	V-type proton ATPase subunit C 1 [Homo sapiens]	6.54	1	2	2		929	2 3.9		2	29.6	292.40	6.54	4	4	382		
42544239	complement factor D preproprotein [Homo sapiens]	34.39	1	6	6		928	5 7.5		5	13.9	299.08	34.39	13	13	253		
530397411	PREDICTED: isoaspartyl peptidase/L-asparaginase isoform X3 [Hon	5.56	2	1	1		928	1	1.154	1		120.80	5.56	3	3	180		
566559963	phosphopantothenatecysteine ligase isoform c [Homo sapiens]	10.48	3	1	1		928	1	1.004	1		96.75	10.48	2	2	105		
11342680	beta-centractin [Homo sapiens]	14.36	2	1	4		928	2 0.3		2	27.6	460.45	14.36	10	14	376		
9507239	immunoglobulin iota chain precursor [Homo saplens]	3.45	2	1	1 '		927	4 6.9		4	3.4	172.71	3.45	3	10	145		
578822447 4507133	PREDICTED: centrosomal protein KIAA1731 isoform X7 [Homo sap	0.42	7	1	1		927	1	1.249	1		66.38	0.42	3	3	2382		
	small nuclear ribonucleoprotein G [Homo sapiens]	17.11	1	- 1	1		927	1	1.407	1		186.56 31.18	17.11	3	3	76 102		
4504523 530407962	10 kDa heat shock protein, mitochondrial [Homo sapiens]		2	- 1	1		927 926	1	1.077	1		31.18 24.30	6.86 0.73	1	1	102 958		
48717372	PREDICTED: zinc finger CCCH domain-containing protein 7A isofori mediator of RNA polymerase II transcription subunit 11 [Homo sap	8.55	2	- 1	1		925	5 40			64.3	92.88	8.55	- 1	1	117		
	UV excision repair protein RAD23 homolog A isoform 2 [Homo sapi		41	2	4		923	2 13.5		2	12.8	302.07	8.01	11	0	362		
313102999	diacylglycerol kinase zeta isoform 7 [Homo sapiens]	0.66	- 1	1	1		923	1	1.193	1	12.0	32.92	0.66	1	1	906		
4503727	peptidyl-prolyl cis-trans isomerase FKBP3 [Homo sapiens]	6.25	1	2	2		923	2 5.3		2	3.2	120.41	6.25	5	5	224		
523704487	ubiquitin-like-conjugating enzyme ATG3 isoform 2 [Homo sapiens]	3.22	2	1	1		923	1	1.090	1	5.2	81.52	3.22	3	3	311		
262118263	55 kDa erythrocyte membrane protein isoform 4 [Homo sapiens]	1.15	4	1	1		923	1	1.029	1		26.67	1.15	1	1	436		
530404921	PREDICTED: serine/threonine-protein kinase Nek9 isoform X2 [Hor	1.49	4	1	1		923	1	1.181	1		27.71	1.49	1	1	873		
578838069	PREDICTED: protein-cysteine N-palmitoyltransferase porcupine isol	4.33	14	1	2		922	1	1.205	1		44.57	4.33	2	2	323	36.3	3 7.99
114431246	keratin, type I cytoskeletal 28 [Homo sapiens]	3.02	15	1	2	7 0.	922	1	1.303	1		105.47	3.02	5	7	464		5 5.47
578837230	PREDICTED: 3-mercaptopyruvate sulfurtransferase isoform X2 [Ho	9.28	3	2	2		922	2 4.8		2	30.9	230.46	9.28	6	6	237		
530422114	PREDICTED: RNA-binding protein 41 isoform X4 [Homo sapiens]	2.50	7	1	1		921	3 7.6		3	21.2	38.42	2.50	1	3	240		
530414204	PREDICTED: asparaginetRNA ligase, cytoplasmic isoform X1 [Hor	1.46	2	1	1		921	1	1.272	1		42.62	1.46	2	2	547		
530384257	PREDICTED: bcl-2-associated transcription factor 1 isoform X3 [Ho		6	1	1		921	1	1.242	1		77.54	1.40	3	3	642		
578828512	PREDICTED: PDZ domain-containing protein 9 isoform X3 [Homo s	2.73	5	1	1		920	1				32.40	2.73	2	2	220		
33589861	ras-related protein Rab-31 [Homo sapiens]	9.23	3	2	2		920	2 2.0		2	17.4	108.27	9.23	5	5	195		
530399725	PREDICTED: leucine-rich repeat serine/threonine-protein kinase 2	0.75	33	1	3		919	1	1.732	1		62.74	0.75	5	5	2521		
271398277	cytosolic non-specific dipeptidase isoform 2 [Homo sapiens]	5.37	2	1	1		919	1	0.988	1		222.42	5.37	3	3	391		
51477708 530364444	heterogeneous nuclear ribonucleoprotein D0 isoform d [Homo sapi	29.27 0.41	9	1	9 :		918 918	1	1.001	1		1515.28 27.31	29.27 0.41	19	36	287 2708		
151301228	PREDICTED: protein PRRC2C isoform X16 [Homo sapiens] pre-mRNA-processing factor 40 homolog A [Homo sapiens]	0.41	18	1	1		918	1	1.133	1		123.97	0.41	1	1	930		
41281429	basic leucine zipper and W2 domain-containing protein 1 isoform 4	9.35	4	1	1		918	4 13.1		1	4.5	459.63	9.35	3	3	353		
122939149	rho GTPase-activating protein 9 isoform 3 [Homo sapiens]	6.95	4	2	2		917	2 8.5		3	1.7	299.69	6.95	0	- 11	547		
525342616	acvI-protein thioesterase 1 isoform 6 [Homo sapiens]	15.06	7	2	2		917	2 0.1		2	8.8	282.71	15.06	5	5	166		
42476083	interferon alpha-8 precursor [Homo sapiens]	4.76	1	1	1		917	1	1.348	1	0.0	28.83	4.76	1	1	189		
530409873	PREDICTED: SET and MYND domain-containing protein 4 isoform )	2.68	3	2	2		917	2 75		2	39.8	106.62	2.68	5	7	635		
	PREDICTED: uncharacterized protein C10orf118 isoform X2 [Homo	1.34	17	1	2		917	3 0.0		1	37.0	158.08	1.34	6	10	898		
4504297	histone H3.1 [Homo sapiens]	61.03	3	1	9		916	6 19.4		4	94.2	1809.12	61.03	26	73	136		
528524494	dynein light chain roadblock-type 1 isoform b [Homo sapiens]	19.05	7	1	1		916	1	1.137	1		160.14	19.05	3	3	63		
339895853	RAC-beta serine/threonine-protein kinase isoform 2 [Homo sapiens	1.91	3	1	1	1 0.	916	1	1.047	1		23.75	1.91	1	1	419		
206597509	arf-GAP domain and FG repeat-containing protein 1 isoform 4 [Hon	4.02	8	2	2	6 0.	916	2 13.4	1.348	2	8.6	225.96	4.02	6	6	522	54.1	1 8.92
14150155	vacuolar protein-sorting-associated protein 25 [Homo sapiens]	5.68	1	1	1		915	1	1.323	1		133.36	5.68	3	3	176		7 6.34
528078329	centrosomal protein of 85 kDa isoform 2 [Homo sapiens]	1.83	4	2	2		914	2 7.2		2	3.3	64.21	1.83	4	4	711		
31542319	coatomer subunit epsilon isoform a [Homo sapiens]	18.51	3	4	4		914	3 11.9		3	8.6	384.96	18.51	9	9	308		
	U4/U6.U5 tri-snRNP-associated protein 1 [Homo sapiens]	2.50	1	1	1		913	1	1.562	1		154.81	2.50	3	3	800		
214832050	dual specificity protein phosphatase 19 isoform 2 [Homo sapiens]	4.82	2	1	1		911	1	1.434	1		35.72	4.82	2	2	166		
20330805	guanine nucleotide-binding protein G(t) subunit alpha-2 [Homo sap	6.50	13	1	3		911	1	2.354	1		399.36	6.50	7	10	354		
118572606	hemicentin-1 precursor [Homo sapiens]	0.25	1	1	1		910	2 7.5		2	29.1	61.23	0.25	3	8	5635		
	PREDICTED: adenosine kinase isoform X1 [Homo sapiens]	13.27	5	2	2		910	3 0.4		3	7.5	771.38	13.27	6	9	294		
556503347	vacuolar protein sorting-associated protein VTA1 homolog isoform	3.60	3	1	1		910	3 29.3	1.240	1	0.3	49.51	3.60	2	2	222		
4505469 4503535	neurotrophin-3 isoform 2 preproprotein [Homo sapiens] eukaryotic translation initiation factor 4E isoform 1 [Homo sapiens]	2.72 14.75	2	1	1		909	3 29.3 4 4.8		3	35.8	42.63 300.47	2.72 14.75	1	3	257 217		
4503535 5174735	eukaryotic translation initiation factor 4E isoform 1 [Homo sapiens] tubulin beta-4B chain [Homo sapiens]	14.75	6	3	20 16		908	1 4.8	1.158	1	35.8	300.47 6449.98	14.75 64.27	/	161	217 445		
5174735	PREDICTED: serine/threonine-protein kinase mTOR isoform X2 [Ho	0.34	2	1	1		907	3 10.0		3	143.9	33.95	0.34	1	101	2322		
116235474	serine/threonine-protein kinase 11-interacting protein [Homo saple	0.55	1	1	1		907	1	4.975	1	143.7	33.95	0.55	2	3	1099		
14165466	polypyrimidine tract-binding protein 1 isoform c [Homo sapiens]	13.56	37	4	5		907	5 4.1		5	1.1	1250.78	13.56	15	31	531		
312433960	NLR family CARD domain-containing protein 4 [Homo sapiens]	1.07	1	1	1		906	1	0.925	1		150.11	1.07	3	3	1024		
29725624	collagen alpha-1(XXIII) chain [Homo sapiens]	1.67	5	1	1		906	1	0.994	1		21.27	1.67	1	1	540		
365192579	calcium-independent phospholipase A2-gamma isoform 3 [Homo si		3	1	2		906	1	2.123	1		52.88	2.05	3	3	682	77.0	8.98
16418355	cyclic AMP-responsive element-binding protein 3-like protein 1 [Ho		1	1	1		905	1	1.624	1		28.82	1.54	2	2	519		
269954692	inositol 1,4,5-trisphosphate receptor type 1 isoform 2 [Homo saple	0.82	13	2	2	31 0.	904	14 10.3	7 1.474	14	75.2	548.02	0.82	4	31	2695	306.6	
46049114	kinesin-like protein KIF20B isoform 2 [Homo sapiens]	0.79	2	1	2		904	5 3.2		5	10.5	86.42	0.79	4	8	1780		
22267436	protein NipSnap homolog 3A [Homo sapiens]	4.86	1	1	1		904	2 14.9		2	14.4	188.67	4.86	3	6	247		
578802647	PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Homo saple	10.66	3	1	3		903	5 8.8		5	12.5	659.11	10.66	9	19	272		
	24-hydroxycholesterol 7-alpha-hydroxylase isoform 3 [Homo sapier	3.70	5	1	2		902	1	2.027	1		65.99	3.70	5	5	297		
221316573	barrier-to-autointegration factor [Homo sapiens]	7.87	1	1	1		900	2 1.5		2	12.3	22.93	7.87	1	2	89		
530408236	PREDICTED: polycystin-1 isoform X5 [Homo sapiens]	0.24	10	1	1		900	3 0.8		3	19.0	50.88	0.24	2	5	3288		
384551649	proto-oncogene vav isoform 3 [Homo sapiens]	1.35	3	1	1		898	1	1.062	1		184.73	1.35	3	3	813		
145701025	multiple epidermal growth factor-like domains protein 8 isoform 2	0.29	2	1	1		898	1	1.112	1		25.97	0.29	1	1	2778		
4507577	tumor necrosis factor receptor superfamily member 1B precursor [i	3.69	1	1	1		897	1	1.095	1		177.56	3.69	3	3	461		
194018537	phosphoribosyl pyrophosphate synthase-associated protein 1 [Hom	3.12	12	1			897	1	1.187	1		136.22	3.12	3	3	385		
301601630 355330279	LIM and senescent cell antigen-like-containing domain protein 1 iso	4.62 3.83	12	1	1		897	1	1.404	1		116.89	4.62	3	3	325 235		
355330279 4507791	ubiquitin carboxyl-terminal hydrolase 15 isoform 3 [Homo sapiens]	3.83 6.01	b	1	1		897	1	0.893	1		120.78 96.24	3.83	3	3	235 183		
157311622	NEDD8-conjugating enzyme Ubc12 [Homo saplens] acyl-coenzyme A synthetase ACSM2B, mitochondrial [Homo saplen	1.91	2	1	1		896	1	1.068	1		96.24 26.92	1.91	3	3	183 577		
530414349	PREDICTED: colled-coll domain-containing protein 102B isoform X6	1.91	3	1	1	1 0.		1	0.818	1		32.12	1.91	1	1	331		
542133065	DNA primase large subunit isoform b [Homo saplens]	5.06	2	1	1		895	1	1.115	1		39.66	5.06	2	2	158		
	ras/Rap GTPase-activating protein SynGAP [Homo sapiens]	0.82	49	1	2		895	1	1.776	1		59.78	0.82	4	4	1343		
194248068					1		891	5 43		5	18.7	93.12	1.64	2	10	365		
194248068 530403141	PREDICTED: mirror-image polydactvly gene 1 protein isoform X2 ft	1.64	3													365		
	PREDICTED: mirror-image polydactyly gene 1 protein isoform X2 [I	1.64 0.46	3 11	2	2		890	2 6.1		2	18.7	72.25	0.46	3	5	2623		
530403141	PREDICTED: mirror-image polydactyly gene 1 protein isoform X2 [I PREDICTED: immunoglobulin superfamily member 10 isoform X1 [i pantetheinase precursor [Homo sapiens] PREDICTED: tyrosine-protein phosphatase non-receptor type 12 is	0.46 6.63	3 11 1	2	2	5 0.		2 6.7	7 1.242	2				3	5 10		290.7	7 9.13

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Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs					A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)		7) # Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs		calc. pl
115298659	spectrin alpha chain, erythrocytic 1 [Homo sapiens]	1.32	1		2 2	5	0.8		2 18.2		2	2 38.3		1.32		5	5 2419		
568384725 578807020	BRO1 domain-containing protein BROX isoform c [Homo sapiens] PREDICTED: programmed cell death protein 10 isoform X4 [Homo	7.40 4.72	,		1 1	2	0.8		1	1.354 0.648		1	64.53 72.36	7.40 4.72		2 2	2 338 3 212		
	ankyrin-1 isoform 2 [Homo sapiens]	0.47			1 1	3	2 0.8		1	1.085		3	37.67	0.47		3	2 1719		
145309300	cyclin-dependent kinase 13 isoform 2 [Homo sapiens]	0.96	03		1 2	13	2 0.8		2 8.8		-	2 70.3	222.87	0.96		12			
530436491	PREDICTED: uncharacterized protein LOC101930119 [Homo sapier	4.09	2		1 1	1	0.8		1	1.238	-	1	28.41	4.09		1	1 220		
	PREDICTED: E3 ubiquitin-protein ligase TRIM69 isoform X2 [Homo	6.08	53		1 3	8	0.8		1	1.257	7	1	43.97	6.08	4	1 8	8 296		
578824474	PREDICTED: probable ATP-dependent RNA helicase DDX23 isoform	1.00	9		1 1	2	2 0.8	32	1	1.372		1	27.35	1.00		2 2	2 602	71.4	4 9.66
287326622	tyrosine-protein kinase HCK isoform d [Homo sapiens]	11.11	102	:	2 5	18	0.8	31	2 8.6	1.167	2	2 0.3	519.92	11.11	11	18	B 504	57.2	2 6.86
4506629	60S ribosomal protein L29 [Homo sapiens]	9.43	1		1 1	3	0.8		1	1.065	7	1	185.41	9.43	1	3	3 159		7 11.66
530407865	PREDICTED: calcium-regulated heat stable protein 1 isoform X2 [H	10.88	2		1 1	2	0.8		1	1.347	7	1	52.02	10.88		2	2 147		
9951923	carbonic anhydrase-related protein 11 precursor [Homo sapiens]	1.83	1		1 1	1	0.8		1	1.355	1	1	16.88	1.83		1	1 328		
530402038	PREDICTED: NEDD4-binding protein 2-like 2 isoform X11 [Homo sa	1.23	6		1 1	1	0.8		1	0.976	1	1	29.27	1.23		1	1 568		
	PREDICTED: glutamine synthetase isoform X1 [Homo sapiens]	2.14	1		1 1	3	0.8		1	0.815	1	1	96.09	2.14	3	3	3 373		
315113860	serine/threonine-protein phosphatase 2A 56 kDa regulatory subuni	3.03	2		1 1	2	0.8		1	1.751	1	1	132.98	3.03		2 2	2 429		
66346685	plasminogen activator inhibitor 1 RNA-binding protein isoform 4 [H	7.49	4	:	2 2	4	1 0.8		2 16.0		2	2 18.4		7.49	4	1 4	4 387		
	zinc finger protein 90 [Homo sapiens]	2.00	1		1 1	1	0.8		1	1.240	1	1	24.26	2.00		1	1 601		
578821102 4506505	PREDICTED: NADP-dependent malic enzyme, mitochondrial isoforn	2.88	4		1 1	3	0.8		1	0.853		1	91.35	2.88	-	3	3 313		
	regulator of G-protein signaling 10 isoform b [Homo sapiens] FERM and PDZ domain-containing protein 4 [Homo sapiens]	7.19 0.45	2		1 1	3	0.8		1	1.323		1	165.80 34.99	7.19 0.45	-	3	3 167 2 1322		
	PREDICTED: kelch-like protein 28 isoform X3 [Homo sapiens]	1.51	3		1 1	1	0.8		1	1.097		3	42.10	1.51		2	1 332		
	116 kDa U5 small nuclear ribonucleoprotein component isoform b [	2.67	4		1 2	12			1	1.984		3	462.62	2.67		12			
	beta-actin-like protein 2 [Homo saplens]	30.85	- 1		1 14				1	1.283		1	31378.87	30.85	42				
	ganglioside GM2 activator isoform 1 precursor [Homo sapiens]	10.36	1		1 1	3773	0.8		1	0.972		1	183.40	10.36	***	3	3 193		
157266317	serine/threonine-protein kinase ATR [Homo sapiens]	0.38	7		1 2	3	3 0.8		1	0.989	,	i	47.20	0.38	-	3	3 2644		
618466461	dynein heavy chain 12, axonemal isoform 3 [Homo sapiens]	0.38	27		1 2	18	0.8		1	1.659		1	159.13	0.38		1 18			
	PREDICTED: granulins isoform X1 [Homo sapiens]	14.33	1		6 6	43			6 8.3		15	5 20.1		14.33	16	43			
530412114	PREDICTED: integrin beta-4 isoform X4 [Homo sapiens]	0.63	9		1 1	1	0.8		1	1.205	1	1	0.00	0.63		1	1 1752		
578816585	PREDICTED: DENN domain-containing protein 4C isoform X4 [Hom	0.82	5		1 1	9	0.8	59	4 12.1	1.106		4 9.6	178.79	0.82	3	3 9	9 1456		1 6.57
	putative deoxyribose-phosphate aldolase isoform 1 [Homo sapiens]	3.14	1		1 1	2	0.8	88	1	1.136	7		56.03	3.14		2 2	2 318	35.2	2 8.94
	ankyrin repeat and LEM domain-containing protein 1 isoform 2 [Ho	1.11	1		1 1	2	0.8		1	1.531	7	1	46.15	1.11		2 2	2 632		
	cadherin-5 preproprotein [Homo sapiens]	0.64	1		1 1	11	0.8		6 3.4		6	6 74.5		0.64		11			
24638446	histone H2A type 2-C [Homo saplens]	59.69	10		1 6	52			6 20.6			4 183.7		59.69	18	52			
	prospero homeobox protein 2 isoform 2 [Homo sapiens]	3.84	3		1 1	2	0.8		1	2.325	1	1	50.15	3.84		2 2	2 365		
578821054	PREDICTED: protein argonaute 12-like [Homo sapiens]	3.00	1		1 1	2	0.8		1	2.881	1	1	25.74	3.00		2 2	2 233		
	PREDICTED: 60S ribosomal protein L26 isoform X1 [Homo sapiens	9.66	3		1 1	- 6	0.8		2 7.6		2	2 9.6		9.66	3	6	6 145		
67782319	spectrin beta chain, erythrocytic isoform b [Homo sapiens]	0.66	5		1 2	4	1 0.8		1	1.607	1	1	123.17	0.66	4	1 4	4 2137		
	leucine-rich repeat-containing G-protein coupled receptor 6 isoform	1.45	5		1 1	1	0.8		1	1.255	1	1	27.26	1.45		1	1 828		
	metal regulatory transcription factor 1 [Homo sapiens]	1.20	1		1 1	1	0.8		5 17.3			4 5.1	20.27	1.20		1	1 753		
4505585 530423607	platelet-activating factor acetylhydrolase IB subunit beta isoform a	14.41	4		2 2	14	1 0.8		5 17.2		4	5.1		14.41		14	4 229 1 1372		
	PREDICTED: leucine-rich repeat-containing protein 16C isoform X1 heat shock-related 70 kDa protein 2 [Homo saplens]	0.51 18.15	,		1 1	146	0.8		1	1.542		1	28.72 6906.01	18.15	20	146			
10835085	metallothionein-1H [Homo sapiens]	13.11	-		1 10	140	0.8		1	1.042		3	92.86	13.11	21	140	3 61		
	brain-specific angiogenesis inhibitor 1-associated protein 2-like pro	1.96	1		1 1	2	2 0.8		1	1.097		1	39.33	1.96		2 2	2 511		
	PREDICTED: sperm-associated antiqen 1 isoform X2 [Homo saplen	0.57	. 2		1 1	8	3 0.8		3 33.6			3 2.4		0.57			8 884		
	PREDICTED: protein unc-45 homolog A isoform X3 [Homo sapiens]	3.13	45		1 2	11			1	0.765	-	1	216.09	3.13		11			
	CWF19-like protein 1 [Homo sapiens]	2.60	- 1		1 1	9	0.8	36	3 21.1	1.434	7	3 13.4	351.58	2.60		9	9 538	60.6	6 7.24
	PREDICTED: transmembrane protein 161A isoform X1 [Homo sapic	2.26	3		1 1	4	1 0.8		2 0.1		1	1	66.02	2.26		2 4	4 354		
7706244	protein CutA isoform 2 precursor [Homo sapiens]	8.97	3		1 1	3	0.8		1	0.987	T	1	196.28	8.97	3	3	3 156		
578824503	PREDICTED: ARF GTPase-activating protein GIT2 isoform X12 [Hor		12		1 1	2	2 0.8		1	1.018	T	1	44.16	4.70		2 2	2 596		
42822891	migration and invasion enhancer 1 [Homo sapiens]	20.00	2		1 1	3	0.8	00	1	1.736		1	131.29	20.00	1	3	3 115	12.4	4 4.37
166235186	methylthioribulose-1-phosphate dehydratase [Homo sapiens]	4.55	1		1 1	2	0.8	26	1	0.801	7	1	36.50	4.55		2	2 242	27.1	1 7.12
	PREDICTED: metastasis suppressor protein 1 isoform X15 [Homo s	1.03	13		1 1	1	0.8	19	1	1.065	1	1	19.52	1.03		1	1 677	73.7	
586798161	general vesicular transport factor p115 isoform 2 [Homo sapiens]	1.87	4		1 1	2	0.8		1	1.218	1	1	62.93	1.87		2	962		
	PREDICTED: protein FAM189A2 isoform X2 [Homo sapiens]	1.15	1		1 1	1	0.8		1	1.133	1	1	28.81	1.15		1	1 522		
	dnaJ homolog subfamily B member 1 [Homo sapiens]	2.94	1		1 1	2	2 0.8		1	1.181	1	1	49.00	2.94		2 2	2 340		
	transcription elongation regulator 1 isoform 2 [Homo sapiens]	1.49	4		2 2	2	0.8		2 21.5		1	1	31.08	1.49		2 2	2 1077		
289547636 4505501	complement C1r subcomponent-like protein isoform 1 precursor [H	10.06	1		2 3	11			2 21.8		1	1	497.75	10.06	8	3 11			
	oxidized low-density lipoprotein receptor 1 isoform 1 [Homo saplen	6.23	1		1 1	3	0.8		1	1.254	1	1	232.24	6.23	3	3	3 273		
	active regulator of SIRT1 [Homo sapiens]	4.41	1		1 1	2	0.8		1	1.439	1	1	49.56	4.41		2 2	2 136		
222144324 16933567	myosin regulatory light chain 128 [Homo sapiens]	72.09 20.29	- 50		1 12	123			1	0.976		1	5256.33 1092.19	72.09 20.29	36	123			
	ras-related protein Rab-8A (Homo sapiens) EMILIN-2 precursor (Homo sapiens)	20.29 0.66	20		1 4	22	2 0.7		1	1.713		1	1092.19 33.26	20.29 0.66	11	22	2 207		
	PREDICTED: latent-transforming growth factor beta-binding protein	0.66	11		1 1	2	3 0.7		1	1.237		1	60.05	0.66		2	3 1247		
	colled-coil domain-containing protein 154 [Homo sapiens]	0.72	1		1 1	2	2 0.7		1	1.166		1	33.74	0.72		2 2	2 667		
	cardiotrophin-1 isoform 2 [Homo sapiens]	5.50	2		1 1	1	1 0.7		1	1.160		1	23.03	5.50		1	1 200		
	POTE ankyrin domain family member I [Homo sapiens]	10.14	2		1 9	407			1	1.397		1	13212.09	10.14	26	407			
	POTE ankyrin domain family member F [Homo sapiens]	11.63	2		1 10	700	0.7	32 1	4 6.3	1.474	14	4 25.9	26363.09	11.63	30	700	1075	121.4	4 6.20
	BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 [Homo s	1.61	2		1 1	1	0.7		1				18.48	1.61	1	1	1 435		
5730075	fibroleukin precursor [Homo sapiens]	4.56	1		1 1	3	0.6		1	1.597	7	1	122.95	4.56	3	3	3 439		
	ribonucleoside-diphosphate reductase subunit M2 isoform 2 [Homo	2.06	2		1 1	1	0.6		1	1.380	1	1	29.15	2.06		1	1 389		
4506467	radixin isoform 2 [Homo saplens]	22.64	5		2 17	184			2 72.8		2	2 47.7		22.64	48	184			
	PREDICTED: PC4 and SFRS1-interacting protein isoform X4 [Homo	6.38	9		1 2	5	0.6		1	1.186	1	1	120.06	6.38	5	5 5	5 329		
530384633	PREDICTED: uncharacterized protein KIAA0895 isoform X3 [Homo		1		1 1	2	0.5		1	1.056	1	1	33.10	2.55		2 2	2 275		
	PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sa	0.48	28		2 3	23			3 8.7		3	3 4.2		0.48		23			
	zinc finger and SCAN domain-containing protein 1 [Homo sapiens]	2.45	2		1 1	1	0.4		1	1.022	1		28.83	2.45		1	1 408		
	trafficking protein particle complex subunit 3 isoform 3 [Homo sapi		4		2 2	5	0.4		1	0.863	1	1	102.51	14.18		5	5 134		
90265805	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1		2		1 1	2	0.4	10	1	13.553	1	4	37.26	0.93		2	2 756		
17986275 34734062	myosin light chain 1/3, skeletal muscle isoform isoform 3f [Homo s fibulin-1 isoform C precursor [Homo sapiens]	18.00	3		1 3	55							2710.49 407.04	18.00 10.10	18	55			
	fibulin-1 isoform C precursor [Homo sapiens] probable histidinetRNA liqase, mitochondrial isoform 2 [Homo sap	10.10 7.07	4		7	18							407.04 200.04	10.10 7.07	18				
156139155	guanine nucleotide-binding protein G(t) subunit alpha-3 [Homo sar		13		1 4	10							200.04 400.58	6.21	10	7 10			
	guanine nucleotide-binding protein G(t) subunit aipna-3 [Homo sap colled-coll domain-containing protein 12 2 [Homo sapiens]	5.42	13		1 3	10	1						400.58 28.83	5.42		10	1 166		
	PREDICTED: kinetochore-associated protein DSN1 homolog isoforn	4.82	47		1 2								53.46	4.82			6 249		
530375558	PREDICTED: kinetocnore-associated protein DSN1 normolog isotom PREDICTED: leukocyte surface antigen CD47 isoform X2 [Homo sa		4/		1 1	1	1						37.08	4.44		1	1 293		
530375556	PREDICTED: redicocyte surface artigen CD47 Isoform X2 [Homo sa PREDICTED: nucleoredoxin-like protein 2 isoform X2 [Homo sapien	4.44	1		1 1								30.13	4.44		1	1 139		
	CDK5 and ABL1 enzyme substrate 1 isoform 3 [Homo sapiens]	4.32	24		1 2	17	7						227.79	4.25		17			
	PREDICTED: BTB/POZ domain-containing protein KCTD16 isoform	3.74	7		1 3	7	7						85.83	3.74		7	7 428		
	kunitz-type protease inhibitor 2 isoform b precursor [Homo sapiens	3.59	2		1 1	1	1						23.03	3.59		1	1 195		
578826968	PREDICTED: homeobox protein Meis2 isoform X8 [Homo sapiens]	3.53	3		1 1	2	2						29.34	3.53		2	2 255		
		3.16	3		1 1	1							28.32	3.16		1	1 285		
	PREDICTED: putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform	3.10																	
	PREDICTED: putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform interleukin-17C precursor [Homo sapiens]	3.05	1		1 1	1							21.51	3.05		1	1 197	21.8	8 8.12
578804706 7019435 530388041		3.05	1		1 1	1							21.51 24.76 27.86	3.05 2.84 2.79		1 1	1 197 1 211 1 323	23.9	9 9.61

International Content   1.0	Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	A8: 115/114	A8: 115/114 Count	A8: 115/114 Variability [%]	A8: 117/116	A8: 117/116 Count	A8: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pl
Marging pages and pages	130499472	PIH1 domain-containing protein 2 isoform 2 [Homo sapiens]		2	1	1	1									1	1			6.24
Mile Mile Mile Angle in plant part of	397138098	PREDICTED: uncharacterized protein LOC100996598 [Homo sapler	2.40	2	1	1	12							118.94	2.40	3	12	208	23.2	7.93
Margin State   Margin State Langer   Margi						1	1									1	1			10.29
Margin   Process   Proce						1	15									3	15			9.77
SEASON AMERICAN ELECTRICATES AND ALTER AMERICAN						2	5													
MINISTED				-		1	1													5.10
MINISTER							1													5.17
Mile				4	1	1	1								2.01		1			11.87
Mile						1	1									1	1			7.20
Mile College   Mile	40788007	FYN-binding protein isoform 2 [Homo sapiens]	1.79	3	1	1	3							59.69	1.79	2	2 3	783	85.3	6.48
MINISTED SIGN   MINISTED SIGN property serving profession profession of the property of the profession of the professi		protein-tyrosine kinase 6 isoform 1 [Homo sapiens]		1	1	1	1							28.83		1	1		51.8	7.03
MINISTREEN   MIN							1									1	1			8.92
Section   Section content processed processe				_			1									1	1			6.83
Margin   M				-			1									1	1			5.43
Margine   Designation   Desi							1													
March   Marc							2								1100					7.74
March   Programs Symbol   Programs   Progr						1	2										2			6.46
March   Marc				2	1	1	1									1	1			9.19
Marchan   Marc	578830763		1.36	52	1	2	2							46.78	1.36	2	2 2	2 441	47.5	6.71
Section   Management in the Cap Section   1.90							1									1	1			8.00
Marchine   Professionary   P							2									2	2 2			9.36
1968-000   1969-000 person p							1									1	1			9.33
Property   Controlled by Property Pro							1									1	1			7.66
2005-2006-2006-2006-2006-2006-2006-2006-																,				6.65
Section   Sect							3													7.85
Marie   Mari						2	26									4				7.24
1977-106   Professionary   P	530424037		1.18	2	1	1	1							32.18	1.18	1	1		65.8	5.11
Separate   Miles   M		PREDICTED: unconventional myosin-Va isoform X7 [Homo sapiens]		9	1	3	23							214.34		8	23		172.8	8.48
Secretary   Market				-		1	2									1	1 2			5.12
2007/19   Application of Application Confidence of Confidence (Note Application (N						1	1									1	1	101		5.53
SAROTIVE   PREDICTED Records algoring   107   4   1   1   1   1   1   1   1   1   1						1	1									1	1			8.56
March   Marc				_		1	1													
				1	1	1	1													8.66
STREAMS    PREDICTIO Interruptional softwar New Journal Prince Segment   1-02   1   2   1   1   1   1   1   1   1				39	1	. 2	3									3	3			7.09
SPECIAL PRINCIPLE Planting protein 3040 looks   0.86   7   7   1   1   1   1   1   1   1   1					1	1	2									2				8.07
SERVICTION   Service   S	578813371	PREDICTED: NAC-alpha domain-containing protein 1 isoform X1 [H	0.96	2	1	1	1							37.59	0.96	1	1	1349	139.8	4.22
1988/2019   1988		ATM interactor isoform 1 [Homo sapiens]		1	1	1	1								0.00	1	1			5.16
SPRINGER   PREDICTED paths a transmitting protein like beform XT PRC   0.84   8   1   1   2						1	1								0.00	1	1			7.94
SPRINGER							1									1	1			6.19
SADJA-1512   PREDICTED RAA-brinding protein 10 loofwort XI [Horon suplems]   0.76   4   1   1   7   7   10.11   7.7   7.8				-			2									2	2			
PREDICTIO metamons inhibitory activity protein its bloom X2 [file 0				-			7													7.17
National Prince Figure 1 Indoorne   Homo saplems   0.71   4   1   1   3   96   110   5.5							1													6.83
Possession with the possession of the possessi							3													5.27
14558026/26   Transcription factor EZF [Horno sapiens]   0.66   4   1   1   1   98   81   1   1   1   98   81   1   1   1   1   1   1   1   1	6912446	potassium voltage-gated channel subfamily H member 4 [Homo sa	0.69	1	1	1	1							15.66	0.69	1	1	1017	111.6	8.54
## First Process of Process against an approximation of Process against Proces				3	1	1	1							27.01	0.66	1	1	911		8.16
1984/10/99   chromodomin-helicuse-DM-hidring protein 2 fortown 1 [time as a constraint of the constr							1								0.00	1	1			9.77
2x9962288					1	1	2									2	2			6.18
SPRINGRAF   PREDICTED From In AIP is price by Prediction   AIP in 1902   0.56   1   1   1   1   1   1   1   1   1				5	1	2	5													8.10
2016/16/00 dm/Like profein 2 locform 3 [Homo saplems] 0.54 8 8 1 2 5 5 240 270 0 6.6 4 40402377 W To repeat containing profein? 2 locform 4 [Homo saplems] 0.54 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				10	1	1	1													7.68 5.33
444402377 WD repeat-containing protein 2 knotrom a [frience spients] 0.54 1 1 1 102 12.33 6.6   454.09 27   457.00						2	5									5				6.60
13256556 voltage-dependent calcium duamer subunit alpha-yeights 4 [Horn O. 53   1   1   1   1   1   1   1   1   1				1	1	1	1									1	1			6.67
4648921 strotactin-1 isoform 2 precursor [Homo sapiens] 0.49 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				1	1	1	1								0.53	1	1			5.35
5/881045 PREDICTED: AT Palegement NBA helicase DHX/9 (brown X2 (brown 1 of 1 o	578812608	PREDICTED: PHD finger protein 3 isoform X5 [Homo sapiens]	0.51	4	1	1	1							24.54	0.51	1	1	1181	133.5	8.31
116534990       transient receptor potential cation channel subfamily A member 1       0.45       9       1       1       5       9       1       1       5       1       10       2       1       1       1       2       3       1       1       2       2       1       1       1       2       2       1       1       1       3<							1								W- 1.1	1				5.15
24552822   Colgin subtamily B member 1 losform 4 (Homo suplers)   0.44   11   1   2   3   5.5							1									1				8.29
182583555         collagen alpha = 5(VI) chain isoform 2 precursor [Homo sapiens]         0.44         2         1         1         1         2526         27.98         7.3           578839833         PREDICTED: Price Practive Al soform A [Homo sapiens]         0.41         5         1         1         2         1119         10.0         7.2           578837337         PREDICTED: Enr. finger Price (domain-containing protein & 0.35         3         1         1         2         1         10.38         8.4           578837656         PREDICTED: Enr. finger Price (domain-containing protein & 6 soform         0.32         2         2         2         2479         27.9         6.2           578811634         PREDICTED: Inc. finger Price (domain-containing protein & 6 soform         0.32         2         2         2479         27.9         6.2           578811634         PREDICTED: Inc. finger Price (domain-containing protein & 6 soform         0.32         2         1         1         2         2.2         2479         27.9         6.2           578811634         PREDICTED: Inc. finger protein 40 isoform X/2 [feloro saperns]         0.30         2         1         1         2         8.3         8.3         8.3         8.3         8.3         8.3         8.3						1	5									3				7.12
5/8883833     PREDICTED: plesh-v3 knotown X4 [Homo saplens]     0.41     5     1     1     2     17/9     190.1     7.2       5/8827337     PREDICTED: EF-hand calcium-binding domain containing protein 6     0.35     3     1     1     2     1     8.4       5/8825666     PREDICTED: zinc finger [PVE domain-containing protein 6]     0.32     2     1     1     2						2	3									3				5.02
578837377 PREDICTED: EF-hand calcium-binding domain-containing protein 6 0.35 3 1 1 2 1 2 1 1 2 3 1 1 3 1 1 2 3 1 1 3 1 1 2 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1 1 3 1						1	1													7.36
578831556     PREDICTED: arc (linger PTVE downsin-containing protein 26 kolforn     0.32     2     1     1     2     6.2       578811634     PREDICTED: zinc (linger protein 40 kolform X2 (linton spiers)     0.30     2     1     1     1     30.94     0.30     1     1     2     8.3       8807138     TRIQ and Facilit-indring protein inclinal indring protein inclination (linton spiers)     0.25     2     2     256     22.12     8.3       8807138     TRIQ and Facilit-indring protein inclination (linton spiers)     0.25     2     2     256     2     2     266     261.2     8.3				3	1	1	2													7.25 8.46
578811634         PREDICTED: zinc finger protein 40 Isoform X2 [Homo sapiens]         0.30         2         1         1         202         22.21         8.3           88501738         TRIO and F-actin-binding protein Isoform 6 [Homo sapiens]         0.25         1         1         1         2         2         2365         261.2         8.4				2	1	1	2													6.28
88501738 TRIQ and F-actin-binding protein isoform 6 [Homo sapiens] 0.25 1 1 1 2 34.52 0.25 2 2 2365 261.2 8.4				2	1	1	1									1	1			8.31
	88501738		0.25	1	1	1	2							34.52	0.25	2	2 2		261.2	8.48
	222144249		0.21	60	1	2	6							57.32	0.21	4	1 6	4753	533.3	6.71

## Appendix C Cytokine

Antibody Array Assay Results	Assay Data
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Cytokine Profiling Antibody Array

Median Signal 681 378

	Fold Change between Samples	Wiedian Signal	Average Signal o	f Replicate Spots
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
Beta actin	2.62	Beta actin	14532	21117
TGF beta Receptor III	2.27	TGF beta Receptor III	1459	1841
Total PSA	2.18	Total PSA	2236	2701
Catenin-alpha1	2.02	Catenin-alpha1	9018	10087
CEA	2.01	CEA	4750	5298
MMP-2	1.98	MMP-2	5091	5584
FSH	1.88	FSH	1146	1199
IL-12	1.88	IL-12	7715	8054
Catenin-gamma	1.87	Catenin-gamma	2756	2866
TYRO3	1.86	TYRO3	1093	1130
LEC	1.85	LEC	772	792
FGFR1 Oncogene Partner	1.83	FGFR1 Oncogene Partner	1356	1380
C-Kit	1.82	C-Kit	2664	2685
VEGFB	1.82	VEGFB	6366	6259
BCL-10	1.77	BCL-10	6891	6770
	1.77	TGF-beta1	3778	3708
TGF-beta1 MMP-10	1.77	MMP-10	8395	8192
	1.75		1304	1265
gAcrp30/Adipolean		gAcrp30/Adipolean CD14		970
CD14 TGF beta2	1.67 1.59	TGF beta2	1048 1365	1204
			1590	1380
NGF beta	1.56	NGF beta		
FGF-5	1.56	FGF-5	1466	1272
MCP-2	1.54 1.54	MCP-2	419 351	358 300
AKT1		AKT1	404	
IL-1 beta	1.52	IL-1 beta		340
STAT6	1.51	STAT6	387	325
GAPDH	1.49	GAPDH (1990)	432	358
Myeloperoxidase (MPO)	1.49	Myeloperoxidase (MPO)	684	566
Prolactin	1.49	Prolactin	341	281
MDC	1.48	MDC	382	313
HER3	1.48	HER3	399	327
E-Selectin	1.47	E-Selectin	389	318
sFas Ligand/Apo1L	1.47	sFas Ligand/Apo1L	416	340
Leptin	1.46	Leptin	865	700
srankl	1.45	srankl	13558	10914
SCGF-beta	1.45	SCGF-beta	458	368
GSK3 beta	1.45	GSK3 beta	796	639
EGR1	1.45	EGR1	477	383
PDGFB	1.45	PDGFB	759	609
SCF	1.44	SCF	471	377
Hepatocyte Growth Factor (HGF)	1.44	Hepatocyte Growth Factor (HGF)	392	313
IL-6	1.44	IL-6	404	322
Adiponectin	1.44	Adiponectin	452	360
MCP-4	1.43	MCP-4	378	300
L-Selectin	1.42	L-Selectin	461	365
4E-BP1	1.42	4E-BP1	347	274
TSH	1.42	TSH	371	293
HGH	1.42	HGH	330	261
IL-7	1.42	IL-7	346	273
BMP-7/OP-1	1.42	BMP-7/OP-1	379	298
EGF	1.42	EGF	540	426

Coefficient of Varia	ation for Replicates			
Bigger Sample	Smaller Sample			
0.04	0.04			
0.07	0.05			
0.10	0.07			
0.20	0.23			
0.06	0.08			
0.35	0.66			
0.05	0.08			
0.08	0.12			
0.07	0.11			
0.03	0.10			
0.07	0.11			
0.06	0.04			
0.04	0.06			
0.10	0.07			
0.09	0.11			
0.15	0.16			
0.08	0.05			
0.12	0.02			
0.15	0.13			
0.03	0.04			
0.03	0.07			
0.05	0.10			
0.03	0.13			
0.03	0.02			
0.01	0.03			
0.02	0.05			
0.02	0.05			
0.11	0.06			
0.03	0.03			
0.03	0.09			
0.02	0.02			
0.02	0.05			
0.02	0.01			
0.02	0.03			
0.08	0.06			
0.04	0.04			
0.09	0.07			
0.02	0.02			
0.11	0.04			
0.02	0.02			
0.03	0.02			
0.02	0.01			
0.04	0.02			
0.02	0.07			
0.02	0.02			
0.03	0.03			
0.02	0.02			
0.02	0.01			
0.01	0.04			
0.02	0.02			
0.03	0.03			

Data Normalized	to Median Signal			
Bigger Sample	Smaller Sample			
21.34	55.87			
2.14	4.87			
3.28	7.15			
13.24	26.69			
6.98	14.01			
7.48	14.77			
1.68	3.17			
11.33	21.31			
4.05	7.58			
1.61	2.99			
1.13	2.09			
1.99	3.65			
3.91	7.10			
9.35	16.56			
10.12	17.91			
5.55	9.81			
12.33	21.67			
1.92	3.35			
1.54	2.57			
2.00	3.18			
2.33	3.65			
2.15	3.36			
0.61	0.95			
0.51	0.79			
0.59	0.90			
0.57	0.86			
0.63	0.95			
1.00	1.50			
0.50	0.74			
0.56	0.83			
0.59	0.86			
0.57	0.84			
0.61	0.90			
1.27	1.85			
19.91	28.87			
0.67	0.97			
1.17	1.69			
0.70	1.01			
1.11	1.61			
0.69	1.00			
0.58	0.83			
0.59	0.85			
0.66	0.95			
0.56	0.79			
0.68	0.96			
0.51	0.72			
0.55	0.78			
0.49	0.69			
0.51	0.72			
0.56	0.79			
0.79	1.13			
	•			

Antibody Array Assay Results	Assay Data

Cytokine Profiling Antibody Array

Median Signal 681 378

		Median Signal	681	3/8
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal o Bigger Sample	f Replicate Spots Smaller Sample
MCP-1/MCAF	1.42	MCP-1/MCAF	402	317
hCG	1.42	hCG	339	266
NAP-2	1.42	NAP-2	374	294
Myostatin (GDF-8)	1.41	Myostatin (GDF-8)	3265	2560
RANTES	1.41	RANTES	462	359
beta hCG	1.40	beta hCG	431	334
LH (Human Luteinizing Hormone)	1.39 1.39	LH (Human Luteinizing Hormone) FGF-basic	339 368	263 285
FGF-basic				
IFN-gamma	1.39	IFN-gamma	388	299
VEGF	1.39	VEGF	14260	10992
sIL-2R alpha	1.39	sIL-2R alpha	509	391
MIP-3beta	1.38	MIP-3beta	984	752
TECK	1.37	TECK	515	391
PTK6	1.37	PTK6	408	310
IL-15	1.36	IL-15	2094	1585
MCP-3	1.36	MCP-3	740	558
ICAM-1	1.36	ICAM-1	428	323
MMP-23	1.36	MMP-23	465	350
EPCAM	1.35	EPCAM	467	350
PSA-ACT	1.35	PSA-ACT	839	629
Thyroglobulin	1.35	Thyroglobulin	481	360
IL-20	1.35	IL-20	437	327
Insulin	1.35	Insulin	468	350
Free PSA	1.35	Free PSA	325	243
MIP-5	1.34	MIP-5	372	277
GATA1	1.34	GATA1	478	356
BMP-4	1.34	BMP-4	494	367
BAFF	1.33	BAFF	618	458
S 100A10/P11	1.33	S 100A10/P11	459	340
TIMP2	1.33	TIMP2	808	598
Neurturin	1.33	Neurturin	418	308
HDAC5	1.33	HDAC5	1718	1267
TPO	1.33	TPO	367	271
alpha hCG	1.32	alpha hCG	404	297
		· ·		
FAK	1.32	FAK	605	445
MIP-3alpha	1.32	MIP-3alpha	383	282
Osteopontin	1.32	Osteopontin	663	487
ALCAM	1.32	ALCAM	1433	1052
4-1BB Receptor	1.32	4-1BB Receptor	392	287
IP-10	1.32	IP-10	385	282
FGF-16	1.32	FGF-16	474	348
Angiopoietin-1	1.31	Angiopoietin-1	441	321
LYN	1.31	LYN	472	344
BD-2	1.31	BD-2	425	309
Androgen receptor	1.31	Androgen receptor	2888	2097
TNF-alpha	1.30	TNF-alpha	423	306
MMP-9	1.30	MMP-9	399	289
EG-VEGF	1.30	EG-VEGF	462	334
ApoE3	1.30	ApoE3	1204	870
C-reactive Protein (CRP)	1.30	C-reactive Protein (CRP)	344	249
Eotaxin-3	1.30	Eotaxin-3	471	340
ITGA5	1.30	ITGA5	493	355

Coefficient of Varia	ation for Replicates			
Bigger Sample	Smaller Sample			
0.02	0.03			
0.01	0.02			
0.02	0.02			
0.14	0.21			
0.02	0.03			
0.01	0.04			
0.02	0.01			
0.01	0.03			
0.03	0.03			
0.14	0.08			
0.03	0.01			
0.11	0.13			
0.07	0.02			
0.03	0.02			
0.03	0.04			
0.02	0.03			
0.02	0.04			
0.03	0.05			
0.02	0.03			
0.16	0.09			
0.02	0.06			
0.02	0.03			
0.02	0.03			
0.03	0.03			
0.01	0.02			
0.04	0.04			
0.02	0.03			
0.02	0.05			
0.01	0.06			
0.04	0.08			
0.02	0.05			
0.09	0.09			
0.02	0.04			
0.06	0.04			
0.02	0.01			
0.01	0.02			
0.05	0.03			
0.07	0.10			
0.02	0.02			
0.01	0.01			
0.05	0.03			
0.02	0.03			
0.02	0.08			
0.02	0.00			
0.10	0.13			
0.02	0.03			
0.02	0.02			
0.03	0.02			
0.05	0.07			
0.02	0.03			
0.03	0.03			
0.02	0.06			

Data Normalized	to Median Signal			
Bigger Sample	Smaller Sample			
0.59	0.84			
0.50	0.70			
0.55	0.78			
4.79	6.77			
0.68	0.95			
0.63	0.88			
0.50	0.69			
0.54	0.75			
0.57	0.79			
20.94	29.08			
0.75	1.03			
1.44	1.99			
0.76	1.04			
0.60	0.82			
3.08	4.19			
1.09	1.48			
0.63	0.85			
0.68	0.93			
0.69	0.93			
1.23	1.66			
0.71	0.95			
0.64				
	0.87			
0.69	0.92			
0.48	0.64			
0.55	0.73			
0.70	0.94			
0.73	0.97			
0.91	1.21			
0.67	0.90			
1.19	1.58			
0.61	0.82			
2.52	3.35			
0.54	0.72			
0.59	0.79			
0.89	1.18			
0.56	0.75			
0.97	1.29			
2.10	2.78			
0.57	0.76			
0.56	0.75			
0.70	0.92			
0.65	0.85			
0.69	0.91			
0.62	0.82			
4.24	5.55			
0.62	0.81			
0.59	0.76			
0.68	0.88			
1.77	2.30			
0.51	0.66			
0.69	0.90			
0.72	0.94			

Antibody Array Assay Results	Assay Data
Cytokine Profiling Antihody Array	

Median Signal **Average Signal of Replicate Spots Protein List** Protein List **Bigger Sample** IL-11 1.29 IL-11 413 296 Eotaxin 1.29 Eotaxin 405 291 AKT2 1.29 AKT2 599 430 NT-3 1.29 NT-3 402 288 GSK3 alpha 1.29 GSK3 alpha 532 381 TWEAK 1.29 TWEAK 438 313 CA125 1.28 CA125 373 264 FGFR2 1.28 FGFR2 585 414 549 CIB1 1.27 CIB1 389 PDGFR beta 1.27 PDGFR beta 446 315 TACI 1.27 TACI 998 702 CD40 1.27 CD40 2920 2053 IGF-BP5 1.27 IGF-BP5 1216 855 NGFR 1.26 NGFR 475 333 IGF 1R 1.26 IGF 1R 603 421 Angiopoietin-2 483 337 Angiopoietin-2 1.26 TGF beta3 1.26 TGF beta3 542 378 Beta-2-Microglobulin 1.25 Beta-2-Microglobulin 6782 4723 FLI1 1.25 FLI1 661 460 BRAK 1.25 BRAK 515 358 Artemin 1.25 Artemin 446 309 KDR (VEGFR2) 1.25 KDR (VEGFR2) 414 286 LD78beta LD78beta 1.24 655 450 MLL 1.23 MLL 1244 849 sCD40 Ligand 1.23 sCD40 Ligand 469 320 CA19-9 526 356 CA19-9 1.22 489 330 1.21 Flt-1 Flt-1 TGF beta Receptor II 1.21 TGF beta Receptor II 680 457 PDGFR alpha 1.20 PDGFR alpha 891 594 HCC-1 1.20 HCC-1 653 435 VCAM-1 1.20 VCAM-1 576 383 NP-1 1.20 NP-1 743 494 1394 926 CTGF 1.20 CTGF 454 AXL 1.19 AXL 301 PIGF 1.19 PIGF 717 473 MMP-16 1.19 MMP-16 469 309 TIMP3 1.19 TIMP3 618 407 1.19 480 316 Eotaxin-2 Eotaxin-2 MMP-14 1.19 MMP-14 463 305 MMP-8 1.18 MMP-8 652 428 FGF-10 1.18 FGF-10 506 331 CA15-3 1.18 CA15-3 471 308 NT-4 1.17 NT-4 514 335 2016 1314 Galectin-3 1.17 Galectin-3 455 HDAC1 1.17 HDAC1 701 CD44 1.16 CD44 515 333 Vaspin 1.16 Vaspin 698 450 MMP-7 1.16 MMP-7 725 467 1.16 RON 438 281 RON MMP-3 508 MMP-3 1.15 326 537 343 SOX2 1.15 SOX2 AFP 1.15 AFP 2387 1521 HDAC7 1.15 HDAC7 466 297 PROZ 1.14 PROZ 2063 1302 YES 1 1.14 YES 1 491 310 MEC 1.13 MEC 713 448 IGF-BP3 1.13 IGF-BP3 964 603 S 100B 1.13 S 100B 485 303

Coefficient of Varia	ation for Replicates
Bigger Sample	Smaller Sample
0.02	0.02
0.03	0.01
0.03	0.04
0.05	0.02
0.02	0.04
0.01	0.04
0.02	0.02
0.05	0.05
0.06	0.02
0.04	0.03
0.06	0.04
0.02	0.08
0.10	0.06
0.02	0.03
0.02	0.01
0.03	0.03
0.01	0.08
0.02	0.05
0.08	0.03
0.02	0.04
0.04	0.03
0.02	0.02
0.03	0.10
0.08	0.05
0.03	0.03
0.01	0.00
0.04	0.03
0.07	0.08
0.05	0.06
0.05 0.03	0.04 0.02
0.03	0.02
0.07	0.10
0.04	0.03
0.10	0.07
0.04	0.04
0.02	0.02
0.05	0.03
0.06	0.04
0.04	0.22
0.02	0.02
0.03	0.02
0.03	0.02
0.04	0.04
0.07	0.05
0.02	0.02
0.06	0.07
0.15	0.09
0.02	0.03
0.19	0.06
0.02	0.11
0.12	0.09
0.05	0.02
0.06	0.06
0.02	0.04
0.07	0.18
0.05	0.07
0.01	0.03

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.61	0.78
0.59	0.77
0.88	1.14
0.59	0.76
0.78	1.01
0.64	0.83
0.55	0.70
0.86	1.10
0.81	1.03
0.65	0.83
1.47	1.86
4.29	5.43
1.79	2.26
0.70	0.88
0.89	1.11
0.71	0.89
0.80	1.00
9.96	12.49
0.97	1.22
0.76	0.95
0.66	0.93
0.61	0.76
0.96	1.19
1.83	2.25
0.69	0.85
0.77	0.94
0.72	0.87
1.00	1.21
1.31	1.57
0.96	1.15
0.85	1.01
1.09	1.31
2.05	2.45
0.67	0.79
1.05	1.25
0.69	0.82
0.91	1.08
0.70	0.84
0.68	0.81 1.13
0.96	0.88
0.69	0.82
0.76	0.82
2.96	3.48
1.03	1.20
0.76	0.88
1.03	1.19
1.07 0.64	1.24 0.74
	0.74
0.75 0.79	0.86
3.51	4.02
0.68	0.79
	3.44
3.03	
0.72	0.82
1.05	1.19
1.41	1.60
0.71	0.80

Antibody Array Assay Results	Assay Data

Cytokine Profiling Antibody Array

Median Signal 681 378

Protein Lat			Median Signal	681	3/8	
Smaller Sample   Smaller Sampler   Smaller Sample   Smaller Sample   Smaller Sample   Smaller Sampler   Smaller Sampler Sampler Sampler   Smaller Sampler   Smaller Sampler Sampler Sampler   Smaller Sampler Sampler Samp	Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		
STATSA						
WNT-1						
GRADYME B   1.11	STAT5A	1.12	STAT5A	481	299	
MIG 1.11 MIG 554 349 MIMP-11 1.11 MIG 1.500 A1 651 440 S100 A1 1.11 S100 A1 651 460 LC2 1.10 LC2 527 322 Hergulin 1.10 Hc2 527 322 Hergulin 1.10 Hc2 527 322 Hergulin 1.10 Hc2 527 788 467 STAT1 1.09 STAT1 544 330 FGFR3 1.09 FGFR3 741 449 HGFR3 1.109 FGFR3 741 4	WNT-1	1.12	WNT-1	599	372	
MMP-11	Granzyme B	1.11	Granzyme B	846	523	
S100 AL	MIG	1.11	MIG	564	349	
MMP-19	MMP-11	1.11	MMP-11	715	440	
L2	S100 A1	1.11	S100 A1	651	401	
Heregulin	MMP-19	1.11	MMP-19	820	504	
Heregulin	IL-2	1.10	IL-2	527	322	
SCD22   1.10   SCD22   768   467   STAT1   1.09   STAT1   5.44   330   STAT1   5.44   340   STAT1	Heregulin		Heregulin	885	539	
STAT1					467	
FGFR3		1.09	STAT1	544	330	
International Content						
CIGFL/MSP-2						
L16						
HDAC6  1.07  HDAC6  1.08  HDAC6  1.07  HDAC6  1.07  HDAC6  1.08  HDAC6  HDA						
SRC						
STNF-receptor         1.07         STNF-receptor         628         374           LIGE BP7         1.06         JG-BP7         91         539           Apolipoprotein LI (APOLI)         1.06         Apolipoprotein LI (APOLI)         557         329           SDF-Lalpha         1.06         SDF-Lalpha         1605         945           LI-8         682         399           SDF-Lebta         1.05         SDF-Libeta         557         326           RELIM beta         647         378         378         378           IL-19         1.05         IL-19         1172         680           WNT-3a         572         332         354         1172         680           GATA3         1.04         WNT-3a         572         332         354         1172         680           GATA3         1.04         WNT-3a         572         332         354         1813         354         1813         354         1813         354         1813         354         1813         354         1813         354         1813         354         1813         354         1813         354         1813         354         1813         354         1813 <td></td> <td></td> <td></td> <td></td> <td></td>						
IGF-BPT						
Apolipoprotein LI (APOL1)         557         329           SDF-Jalpha         1.06         SDF-Jalpha         1.605         945           L-8         1.05         LL-8         682         399           SDF-Ibeta         1.05         SDF-Ibeta         557         326           SDF-Ibeta         1.05         SDF-Ibeta         557         326           IL-19         1.05         IL-19         1.172         680           WNT-3a         1.04         WNT-3a         572         332           GATA3         1.04         GATA3         613         354           STRAIL/APO2L         1.04         STRAIL/APO2L         551         324           HDAC9         1.04         HDAC9         548         315           Tyrosinase         1.03         Tyrosinase         605         347         MMF-1         717         440           IFN-lambda2         1.03         IFN-lambda2         1230         704         44         312         44         440         440         440         440         440         440         440         440         440         440         440         440         440         440         440         440						
SDF-1alpha						
1.05						
SDF-1Deta   1.05   SDF-1Deta   557   326						
RELM beta         1.05         RELM beta         647         378           L-19         1.05         IL-19         1172         680           WNT-3a         572         332         660         680           WNT-3a         572         332         661         324           GATA3         1.04         GATA3         613         354           STRAIL/APOZL         1.04         HDAC9         561         324           HDAC9         548         315         315         377         377         410           HDAC9         548         315         315         377         410         417         417         410         <						
L-19						
WNT-3a						
GATA3         1.04         GATA3         613         354           STRAIL/APO2L         1.04         STRAIL/APO2L         561         324           HDAC9         1.04         HDAC9         548         315           Tyrosinase         1.03         Tyrosinase         605         347           MMP-1         1.03         MMP-1         717         410           IFN-lambda2         1.03         IFN-lambda2         1230         704           BD-3         1.03         BD-3         548         312           IL-10         1.02         IL-10         796         453           HDAC10         1.02         HDAC10         603         340           Apolipoprotein F (APOF)         1.01         76F-17         552         309           GDNF         1.00         GDNF         553         309           GDNF         1.00         GDNF         553         309           CTACK         1.00         CTACK         631         352           MASpin         706         393         308         344           GCP-2         1.00         MCSF         623         345           IL-4         0.99						
STRAIL/APO2L         1.04         STRAIL/APO2L         561         324           HDACG         1.04         HDACG         548         315           Tyrosinase         6.05         347           MMP-1         1.03         MMP-1         717         410           FFN-lambda2         1.03         IFN-lambda2         1230         704           BD-3         548         312         11-10         796         453           IL-10         1.02         IL-10         796         453           HDAC10         1.02         HDAC10         603         340           Apolipoprotein F (APOF)         1.01         Apolipoprotein F (APOF)         675         380           FGF-17         1.01         FGF-17         552         309           CTACK         1.00         GDNF         553         309           CTACK         1.00         GDNF         553         309           CTACK         1.00         MSpin         706         393           MMP-15         1.00         MSpin         706         393           MAP-15         1.00         MSpin         706         393           MSP-2         1.00						
HDAC9						
Tyrosinase         1.03         Tyrosinase         605         347           MMP-1         1.03         MMP-1         717         410           IFN-lambda2         1.03         IFN-lambda2         1230         704           BD-3         1.03         BD-3         548         312           IL-10         1.02         IL-10         796         453           HDAC10         1.02         HDAC10         603         340           Apolipoprotein F (APOF)         675         380           FGF-17         1.01         FGF-17         552         309           GDNF         1.00         GDNF         553         309           CTACK         1.00         CTACK         631         352           Maspin         706         393         308           MMP-15         553         308         6CP-2         534         297           M-CSF         1.00         MMP-15         553         309           MCSF         1.00         MMP-15         553         309           M-CSF         1.00         MC-SF         623         344         297           M-CSF         1.00         MC-SF         623<						
MMP-1         1.03         MMP-1         717         410           IFN-lambda2         1.03         IFN-lambda2         1230         704           BD-3         1.03         IBN-lambda2         1230         704           IL-10         1.02         IL-10         796         453           HDAC10         1.02         HDAC10         603         340           Apolipoprotein F (APOF)         675         380         765         380           FGF-17         552         309						
FN-lambda2						
BD-3         1.03         BD-3         548         312           IL-10         1.02         IL-10         796         453           HDAC10         1.02         HDAC10         603         340           Apolipoprotein F (APOF)         1.01         Apolipoprotein F (APOF)         675         380           FGF-17         1.01         FGF-17         552         309           GDNF         1.00         GDNF         553         309           CTACK         631         352           Maspin         706         393           MSP-15         1.00         MMP-15         553         308           GCP-2         1.00         MMP-15         553         308           M-CSF         1.00         M-CSF         623         345           IL-4         0.99         IL-4         641         353           IL-4         0.99         TSLP         619         340           Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BMP-2         766         416						
IL-10			IFN-lambda2			
HDAC10	BD-3	1.03	BD-3		312	
Apolipoprotein F (APOF)         1.01         Apolipoprotein F (APOF)         675         380           FGF-17         1.01         FGF-17         552         309           GDNF         1.00         GDNF         553         309           CTACK         1.00         CTACK         631         352           Maspin         1.00         Maspin         706         393           MMP-15         1.00         MMP-15         553         308           GCP-2         1.00         GCP-2         534         297           M-CSF         623         345         11.4         641         353           IL-4         0.99         IL-4         641         353         345           IL-4         0.99         ITSLP         619         340         345	IL-10	1.02	IL-10	796	453	
FGF-17         1.01         FGF-17         552         309           GDNF         1.00         GDNF         553         309           CTACK         1.00         CTACK         631         352           Maspin         1.00         Maspin         706         393           MMP-15         1.00         MMP-15         553         308           GCP-2         1.00         GCP-2         534         297           M-CSF         1.00         M-CSF         623         345           IL-4         0.99         IL-4         641         353           TSLP         0.99         TSLP         619         340           Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BD-4         594         324           BMP-2         0.98         BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         604         325	HDAC10		HDAC10		340	
GDNF         1.00         GDNF         553         309           CTACK         1.00         CTACK         631         352           Maspin         1.00         Maspin         706         393           MMP-15         1.00         MMP-15         553         308           GCP-2         534         297           M-CSF         623         345           IL-4         641         353           TSLP         619         340           Integrin beta5         0.99         TSLP         619         340           Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BD-4         594         324           BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         604         325           MIP-1beta         588         316           ERCC6         0.97         ERCG6         931         500	Apolipoprotein F (APOF)	1.01	Apolipoprotein F (APOF)	675	380	
CTACK         1.00         CTACK         631         352           Maspin         1.00         Maspin         706         393           MMP-15         1.00         MMP-15         553         308           GCP-2         1.00         GCP-2         534         297           M-CSF         623         345         1.00         M-CSF         623         345           IL-4         641         353         354         354         354         354         354         354         354         354         354         354	FGF-17	1.01	FGF-17	552	309	
Maspin         1.00         Maspin         706         393           MMP-15         1.00         MMP-15         553         308           GCP-2         1.00         GCP-2         534         297           M-CSF         623         345         1.00         M-CSF         623         345           IL-4         0.99         IL-4         641         353         354         354         354         354         354         354         354         354         354         354         354         354         354         354         354	GDNF	1.00	GDNF	553	309	
MMP-15         1.00         MMP-15         553         308           GCP-2         1.00         GCP-2         534         297           M-CSF         1.00         M-CSF         623         345           IL-4         0.99         IL-4         641         353           TSLP         619         340           Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         FGF-acidic         748         398	CTACK	1.00	CTACK	631	352	
GCP-2         1.00         GCP-2         534         297           M-CSF         1.00         M-CSF         623         345           IL-4         0.99         IL-4         641         353           TSLP         0.99         TSLP         619         340           Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BD-4         594         324           BMP-2         0.98         BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERC66         931         500           Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398	Maspin	1.00	Maspin	706	393	
M-CSF         1.00         M-CSF         623         345           IL-4         0.99         IL-4         641         353           TSLP         0.99         ISLP         619         340           Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BD-4         594         324           BMP-2         0.98         BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         588         316         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398	MMP-15	1.00	MMP-15	553	308	
IL-4     0.99     IL-4     641     353       TSLP     0.99     TSLP     619     340       Integrin beta5     0.99     Integrin beta5     599     328       GDF-3     0.98     GDF-3     874     478       BD-4     0.98     BD-4     594     324       BMP-2     0.98     BMP-2     766     416       STAT3     0.98     STAT3     568     308       Ubiquitin     0.97     Ubiquitin     841     454       IL-17D     0.97     IL-17D     604     325       MIP-1beta     588     316       ERCC6     0.97     ERCC6     931     500       Cardiotrophin-1     0.96     Cardiotrophin-1     947     504       FGF-acidic     0.96     FGF-acidic     748     398	GCP-2	1.00	GCP-2	534	297	
IL-4     0.99     IL-4     641     353       TSLP     0.99     TSLP     619     340       Integrin beta5     0.99     Integrin beta5     599     328       GDF-3     0.98     GDF-3     874     478       BD-4     0.98     BD-4     594     324       BMP-2     0.98     BMP-2     766     416       STAT3     0.98     STAT3     568     308       Ubiquitin     0.97     Ubiquitin     841     454       IL-17D     0.97     IL-17D     604     325       MIP-1beta     588     316       ERCC6     0.97     ERCC6     931     500       Cardiotrophin-1     0.96     Cardiotrophin-1     947     504       FGF-acidic     0.96     FGF-acidic     748     398	M-CSF	1.00	M-CSF	623	345	
TSLP         0.99         TSLP         619         340           Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BD-4         594         324           BMP-2         766         416         55AT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
Integrin beta5         0.99         Integrin beta5         599         328           GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BD-4         594         324           BMP-2         766         416         554         308           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
GDF-3         0.98         GDF-3         874         478           BD-4         0.98         BD-4         594         324           BMP-2         0.98         BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         604         325           MIP-1beta         588         316           ERCC6         0.97         ERCG6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
BD-4         0.98         BD-4         594         324           BMP-2         0.98         BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
BMP-2         0.98         BMP-2         766         416           STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
STAT3         0.98         STAT3         568         308           Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
Ubiquitin         0.97         Ubiquitin         841         454           IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
IL-17D         0.97         IL-17D         604         325           MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
MIP-1beta         0.97         MIP-1beta         588         316           ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         748         398						
ERCC6         0.97         ERCC6         931         500           Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
Cardiotrophin-1         0.96         Cardiotrophin-1         947         504           FGF-acidic         0.96         FGF-acidic         748         398						
FGF-acidic 0.96 FGF-acidic 748 398						
TL-1A 0.96 TL-1A 597 317						
	TL-1A	0.96	TL-1A	597	317	

Coefficient of Variation for Replicate		
Bigger Sample	Smaller Sample	
0.03	0.03	
0.04	0.04	
0.06	0.04	
0.05	0.07	
0.03	0.04	
0.07	0.04	
0.05	0.06	
0.17	0.09	
0.01	0.02	
0.09	0.06	
0.08	0.04	
0.03	0.02	
0.14	0.05	
0.04	0.05	
0.04	0.02	
0.05	0.02	
0.09	0.06	
0.01	0.03	
0.03	0.02	
0.08	0.02	
0.07	0.02	
0.14	0.11	
0.05	0.04	
0.03	0.04	
0.05	0.04	
0.04	0.03	
0.05	0.02	
0.03	0.02	
0.03	0.02	
0.05	0.03	
0.04	0.02	
0.08	0.04	
0.07	0.07	
0.02	0.01	
0.05	0.05	
0.08	0.04	
0.05	0.02	
0.04	0.02	
0.04	0.02	
0.04	0.03	
0.04	0.02	
0.01	0.02	
0.05	0.02	
0.04	0.04	
0.03	0.03	
0.03	0.03	
0.05	0.04	
0.05	0.04	
0.05	0.01	
0.03	0.03	
0.08	0.08	
0.03	0.04	
0.03	0.00	
0.07	0.01	
0.06	0.03	
0.07	0.04	
0.07	0.04	
0.03	0.02	

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.74	0.83
0.71	0.79
0.88	0.98
1.24	1.38
0.83	0.92
1.05	1.16
0.96	1.06
1.20	1.33
0.77	0.85
1.30	1.42
1.13	1.24
0.80	0.87
1.09	1.19
0.99	1.08
1.09	1.19
0.77	0.82
0.97	1.04
0.77	0.82
0.92	0.99
1.34	1.43
0.82	0.87
2.36	2.50
1.00	1.06
0.82	0.86
0.95	1.00
1.72 0.84	1.80 0.88
0.90	0.88
0.90	0.94
0.82	0.83
0.89	0.83
1.05	1.09
1.81	1.86
0.80	0.83
1.17	1.20
0.89	0.90
0.99	1.01
0.81	0.82
0.81	0.82
0.93	0.93
1.04	1.04
0.81	0.81
0.78	0.78
0.92	0.91
0.94	0.93
0.91	0.90
0.88	0.87
1.28	1.26
0.87	0.86
1.12	1.10
0.83	0.82
1.24	1.20
0.89	0.86
0.86	0.84
1.37	1.32
1.39	1.33
1.10	1.05
0.88	0.84

Antibody	Array	Assay	/ Results	Assay	/ Data
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Cytokine Profiling Antibody Array

	Fold Change between Samples	Wiedian Signal	Average Signal of Replicate Spots		
Protein List	Smaller Sample/Bigger Sample	Protein List			
	1 . 00 1		Bigger Sample	Smaller Sample	
MIP-1alpha	0.95	MIP-1alpha	606	320	
BDNF	0.95	BDNF	610	321	
IGF-I	0.95	IGF-I	747	393	
Oncostatin M	0.94	Oncostatin M	568	298	
Persephin	0.94	Persephin	695	363	
IL-33	0.94	IL-33	685	358	
sDLL-4	0.94	sDLL-4	975	509	
MIP-3	0.94	MIP-3	562	292	
PDGF-AA	0.93	PDGF-AA	642	333	
Apolipoprotein L2 (APOL2)	0.93	Apolipoprotein L2 (APOL2)	657	338	
GRO-gamma	0.93	GRO-gamma	627	322	
LIGHT	0.92	LIGHT	776	397	
HER2	0.92	HER2	683	350	
OPG	0.92	OPG	757	386	
GM-CSF	0.91	GM-CSF	647	328	
	0.91		16635	8370	
Resistin		Resistin			
Follistatin	0.90	Follistatin	829	415	
TARC	0.90	TARC	595	298	
STAT5A/B	0.90	STAT5A/B	783	391	
PDGF-BB	0.90	PDGF-BB	666	332	
Neuroserpin	0.89	Neuroserpin	820	407	
Endostatin	0.89	Endostatin	967	479	
NCoR1	0.89	NCoR1	778	383	
IL-17B	0.88	IL-17B	765	375	
CXCL16	0.88	CXCL16	782	383	
IGF-BP1	0.87	IGF-BP1	1073	518	
MIA-2	0.87	MIA-2	902	434	
sTRAIL Receptor-2	0.86	sTRAIL Receptor-2	804	385	
APC	0.86	APC	1047	500	
IL-9	0.86	IL-9	687	328	
MMP-13	0.86	MMP-13	712	339	
APRIL	0.86	APRIL	703	334	
I-TAC	0.85	I-TAC	629	298	
IL-17E	0.85	IL-17E	745	353	
Fractalkine	0.85	Fractalkine	651	307	
E-cadherin	0.85	E-cadherin	1001	473	
IL-17F	0.85	IL-17F	729	343	
Catenin-beta 1	0.85	Catenin-beta 1	687	323	
FGF-4	0.85	FGF-4	1047	492	
FAS	0.84	FAS	1395	653	
PF-4	0.84	PF-4	1366	637	
BCA-1	0.84	BCA-1	663	309	
EMAP-II	0.84	EMAP-II	894	417	
TRADD	0.84	TRADD	901	420	
PAI-1	0.83	PAI-1	1019	472	
1-309	0.83	I-309	728	337	
CNTF	0.83	CNTF	1052	486	
MIA	0.83	MIA	1055	487	
NNT-1/BCSF-3	0.83	NNT-1/BCSF-3	747	344	
NOV	0.83	NOV	843	388	
TFF-2	0.83	TFF-2	773	355	
4-1BBL	0.82	4-1BBL	939	428	
		AITRL	1020		
AITRL	0.82			463	
FER	0.82	FER	793	360	
IL-31	0.82	IL-31	965	437	
MIP-4	0.81	MIP-4	686	309	
Nanog	0.81	Nanog	1004	451	
TIMP4	0.80	TIMP4	857	382	

Median Signal

681

378

Coefficient of Varia	ation for Replicates
Bigger Sample	Smaller Sample
0.02	0.02
0.05	0.05
0.05	0.03
0.02	0.04
0.04	0.04
0.06	0.03
0.04	0.02
0.03	0.03
0.02	0.03
0.07	0.04
0.09	0.01
0.02	0.05
0.02	0.03
0.06	0.05
0.05	0.01
0.11	0.09
0.06	0.09
0.03	0.02
0.02	0.07
0.03	0.02
0.03	0.03
0.04	0.06
0.04	0.03
0.12	0.02
0.03	0.03
0.03	0.04
0.02	0.04
0.05	0.02
0.10	0.10
0.02	0.03
0.06	0.03
0.01	0.03
0.02	0.02
0.06	0.02
0.03	0.02
0.03	0.07
0.05	0.02
0.04	0.03
0.07	0.04
0.06	0.05
0.09	0.08
0.08	0.03
0.11	0.02
0.06	0.04
0.08	0.03
0.04	0.01
0.06	0.07
0.04	0.03
0.10	0.02
0.08	0.05
0.10	0.05
0.07	0.03
0.07	0.03
0.06	0.03
0.08	0.08
0.04	0.04
0.07	0.07
0.05	0.04

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.89	0.85
0.90	0.85
1.10	1.04
0.83	0.79
1.02	0.96
1.01	0.95
1.43	1.35
0.82	0.77
0.94	0.88
0.96	0.89
0.92	0.85
1.14	1.05
1.00	0.93
1.11	1.02
0.95	0.87
24.43	22.14
1.22	1.10
0.87	0.79
1.15	1.03
0.98	0.88
1.20	1.08
1.42	1.27
1.14	1.01
1.12	0.99
1.15	1.01
1.58	1.37
1.32	1.15
1.18	1.02
1.54	1.32
1.01	0.87
1.05	0.90
1.03	0.88
0.92	0.79
1.09	0.93
0.96	0.81
1.47	1.25
1.07	0.91
1.01	0.86
1.54	1.30
2.05	1.73
2.01	1.69
0.97	0.82
1.31	1.10
1.32	1.11
1.50	1.25
1.07	0.89
1.54	1.29
1.55	1.29
1.10	0.91
1.24	1.03
1.14	0.94
1.38	1.13
1.50	1.22
1.16	0.95
1.42	1.16
1.42	0.82
1.47	1.19
1.26	1.01

	ay Assay Results	Assay Data						
Cytokine Profiling Antibody Array		Median Signal	681	378				
D	Fold Change between Samples	December 15th	Average Signal o	of Replicate Spots	Coefficient of Varia	ation for Replicates	Data Normalized	to Median Signal
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
rGF-alpha	0.80	TGF-alpha	1039	463	0.03	0.04	1.53	1.22
/isfatin	0.79	Visfatin	1456	640	0.07	0.06	2.14	1.69
Betacellulin	0.79	Betacellulin	907	398	0.10	0.03	1.33	1.05
IL-17 (IL-17A)	0.78	IL-17 (IL-17A)	801	348	0.13	0.02	1.18	0.92
BLK	0.77	BLK	1084	466	0.09	0.06	1.59	1.23
IL-1alpha	0.76	IL-1alpha	747	317	0.03	0.03	1.10	0.84
Exodus-2	0.76	Exodus-2	931	394	0.03	0.02	1.37	1.04
Galectin-1	0.76	Galectin-1	1304	551	0.04	0.05	1.91	1.46
Cadherin-pan	0.76	Cadherin-pan	1206	508	0.08	0.06	1.77	1.34
TIMP-1	0.75	TIMP-1	2690	1127	0.09	0.08	3.95	2.98
GRO/MGSA	0.75	GRO/MGSA	1114	466	0.08	0.02	1.64	1.23
Midkine	0.75	Midkine	959	401	0.10	0.02	1.41	1.06
GRO-beta	0.75	GRO-beta	811	338	0.03	0.01	1.19	0.89
IL-21	0.75	IL-21	919	382	0.09	0.05	1.35	1.01
L-5	0.74	IL-5	897	370	0.03	0.08	1.32	0.98
Ferritin	0.73	Ferritin	13829	5575	0.05	0.16	20.31	14.75
L-3	0.72	IL-3	836	334	0.16	0.04	1.23	0.88
IL-22	0.72	IL-22	1008	401	0.04	0.03	1.48	1.06
Adipolean Variant	0.71	Adipolean Variant	1093	429	0.02	0.03	1.60	1.13
HDAC3	0.71	HDAC3	1067	418	0.08	0.04	1.57	1.11
IL-1RA	0.70	IL-1RA	1380	535	0.05	0.05	2.03	1.42
G-CSF	0.70	G-CSF	952	369	0.11	0.03	1.40	0.98
KGF	0.68	KGF	843	320	0.03	0.04	1.24	0.85
TNF-beta	0.68	TNF-beta	1090	412	0.04	0.03	1.60	1.09
IL-13	0.68	IL-13	971	365	0.14	0.03	1.43	0.97
sRANK Receptor	0.68	sRANK Receptor	1132	425	0.07	0.03	1.66	1.12
Flt3-Ligand	0.67	Flt3-Ligand	791	293	0.05	0.07	1.16	0.77
BD-1	0.66	BD-1	1145	420	0.05	0.04	1.68	1.11
GF-II	0.66	IGF-II	1393	511	0.05	0.04	2.05	1.35
TNF-receptor II	0.66	sTNF-receptor II	1234	451	0.05	0.02	1.81	1.19
ENA-78	0.65	ENA-78	1100	395	0.03	0.02	1.62	1.05
IFN-beta	0.65	IFN-beta	1294	464	0.06	0.05	1.90	1.23
EGFR	0.61	EGFR	1308	441	0.04	0.04	1.92	1.17
Heregulin-beta1	0.58	Heregulin-beta1	1689	547	0.06	0.05	2.48	1.45
PTHrP	0.10	PTHrP	7919	421	0.11	0.06	11.63	1.11
							-	
N	1.18	Average of Empty Spots	383	274	0.03	0.02		
N	lax 2.62	Average of Negative Controls	356	295	0.02	0.02		
Me	an 1.42	Average of Positive Makers	33394	27966	0.08	0.07		

## Appendix D Explorer

	Antibody Array Assay Results	Assay Data			
Explor	er Antibody Array		Madian Sianal	120	02

		Median Signal	Average Signal of Replicate Spots		
Protein List	Fold Change between Samples	Protein List			
Vacular Fadathalial Crowth Factor(VECE)	Smaller Sample/Bigger Sample 4.59	Vacular Endathalial Crouth Factor(VECE)	Bigger Sample 222	Smaller Sample 663	
Vacular Endothelial Growth Factor(VEGF)	3.40	Vacular Endothelial Growth Factor(VEGF)			
Actin beta		Actin beta	136	299	
Survivin CD57	2.78 2.47	Survivin	426	768	
CD2		CD57	263	422	
	2.33	CD2	2757 1063	4179 1575	
ADP-ribosylation Factor (ARF-6)	2.28	ADP-ribosylation Factor (ARF-6)		3571	
HPV 16-E7 FSH	2.23	HPV 16-E7 FSH	2467 382	547	
	2.20 2.20		554	791	
Golgi Complex CD1	2.12	Golgi Complex CD1	5802	8008	
Laminin-s	2.11	Laminin-s	1225	1680	
	2.01	MHC I (HLA25 and HLA-Aw32)	804	1050	
MHC I (HLA25 and HLA-Aw32)	2.01				
Thymidylate Synthase	1.92	Thymidylate Synthase	162 695	211 868	
CEA / CD66e		CEA / CD66e			
IgG	1.91	IgG	24504	30440	
Keratin, Multi	1.85	Keratin, Multi	529	637 1227	
CD45/T200/LCA	1.85	CD45/T200/LCA	1020		
Kappa Light Chain	1.81	Kappa Light Chain	1489	1752	
Plasminogen	1.80	Plasminogen	234 399	274 466	
Glucagon	1.80	Glucagon			
Calmodulin	1.80 1.79	Calmodulin	658	769	
B-cell Linker Protein (BLNK)		B-cell Linker Protein (BLNK)	104	121	
NGF-Receptor (p75NGFR)	1.79	NGF-Receptor (p75NGFR)	81	94	
HPV 16	1.66	HPV 16	687	742	
L1 Cell Adhesion Molecule	1.65	L1 Cell Adhesion Molecule	140	151	
c-erbB-4/HER-4 CD43	1.65 1.63	c-erbB-4/HER-4 CD43	176 1682	189	
				1777	
Retinoid X Receptor (hRXR)	1.62	Retinoid X Receptor (hRXR)	418	441 196	
Parathyroid Hormone Receptor Type 1	1.62	Parathyroid Hormone Receptor Type 1	186		
MHC II (HLA-DP and DR)	1.60	MHC II (HLA-DP and DR)	1362	1417	
c-Abl	1.60	c-Abl	684	711	
DR3	1.59	DR3	303	312	
Biotin	1.58	Biotin	63691	65535	
Oct-2/	1.58	Oct-2/	63	64	
CD1b	1.57	CD1b	269	275	
CD53	1.57	CD53	96	98	
XRCC1	1.57	XRCC1	106	108	
Int-2 Oncoprotein	1.56	Int-2 Oncoprotein	145	147	
Lambda Light Chain	1.54	Lambda Light Chain	65535	65535	
XPG Strontovidin	1.53	XPG	123	123	
Streptavidin	1.53	Streptavidin	6876	6848	
CD29	1.52	CD29	124	123	
Alpha Lactalbumin	1.51	Alpha Lactalbumin	259	254	
Retinoic Acid Receptor (b)	1.51	Retinoic Acid Receptor (b)	336	329	
alpha-1-antitrypsin	1.51	alpha-1-antitrypsin	13221	12929	
CA19-9	1.50	CA19-9	111	108	
CD105	1.50	CD105	127	124	
IgM (m-Heavy Chain)	1.50	IgM (m-Heavy Chain)	579	565	
BrdU	1.50	BrdU	159	154	
Keratin 15	1.49	Keratin 15	1599	1545	
Synuclein pan	1.49	Synuclein pan	57	55	

Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample	
0.07	0.02	
0.14	0.00	
0.18	0.05	
0.08	0.10	
0.47	0.07	
0.24	0.20	
0.03	0.12	
0.19	0.21	
0.20	0.13	
0.30	0.06	
0.86	0.00	
0.24	0.03	
0.10	0.11	
0.53	0.05	
0.01	0.03	
0.07	0.08	
0.76	0.08	
0.16	0.06	
0.02	0.05	
0.10	0.18	
0.03	0.14	
0.03	0.22	
0.00	0.05	
0.25	0.07	
0.43	0.30	
0.22	0.09	
0.33	0.00	
0.10	0.05	
0.14	0.16	
0.02	0.05	
0.04	0.13	
0.19	0.16	
0.04	0.00	
0.17	0.00	
0.11	0.06	
0.00	0.12	
0.05	0.03	
0.03	0.00	
0.00	0.00	
0.11	0.16	
0.13	0.08	
0.03	0.04	
0.02	0.17	
0.13	0.11	
0.01	0.14	
0.04	0.17	
0.17	0.07	
0.16	0.08	
0.08	0.11	
0.18	0.01	
0.07	0.21	

Data Normalized	to Median Signal	
Bigger Sample	Smaller Sample	
1.74	7.98	
1.06	3.60	
3.33	9.25	
2.05	5.08	
21.58	50.35	
8.32	18.97	
19.31	43.02	
2.99	6.58	
4.33	9.52	
45.42	96.48	
9.59	20.23	
6.29	12.64	
1.27	2.54	
5.44	10.45	
191.81	366.75	
4.14	7.67	
7.98	14.78	
11.65	21.11	
1.83	3.30	
3.12	5.61	
5.15	9.26	
0.81	1.46	
0.63	1.13	
5.38	8.94	
1.10	1.81	
1.37	2.27	
13.16	21.40	
3.27	5.31	
1.46	2.36	
10.66	17.07	
5.35	8.56	
2.37	3.76	
498.56	789.58	
0.49	0.77	
2.10	3.31	
0.75	1.18	
0.83	1.30	
1.14	1.77	
512.99	789.58	
0.96	1.48	
53.82	82.51	
0.97	1.48	
2.02	3.06	
2.63	3.96	
103.49	155.77	
0.86	1.30	
0.99	1.49	
4.53	6.81	
1.24	1.86	
12.52	18.61	
0.45	0.66	

Antibody Array Assay Results	Assay Data
Explorer Antibody Array	

Median Signal **Average Signal of Replicate Spots** Protein List Protein List **Bigger Sample** MGMT 1.48 MGMT 61 59 1.47 PDGFR, beta PDGFR, beta 967 923 1.47 93 Microphthalmia Microphthalmia 98 1.47 bcl-XL bcl-XL 4442 4236 PLC gamma 1 1.47 PLC gamma 1 2132 2033 118 112 Bovine Serum Albumin 1.47 Bovine Serum Albumin Gamma Glutamyl Transferase (gGT) 1.46 Gamma Glutamyl Transferase (gGT) 80 76 F.VIII/VWF 1.46 F.VIII/VWF 70 66 erbB-2/HER-2/neu Ab-1 (21N) 1.46 c-erbB-2/HER-2/neu Ab-1 (21N) 176 167 Androgen Receptor 68 1.45 Androgen Receptor 72 p170 1.45 p170 54 51 Integrin beta5 1.45 Integrin beta5 231 218 Laminin B1/b1 1.45 Laminin B1/b1 13478 12663 1.45 476 447 Adenovirus Adenovirus CA125 1.44 CA125 73 68 E2F-4 1.44 E2F-4 125 117 1.44 Dysferlin Dysferlin 75 70 Superoxide Dismutase 1.44 Superoxide Dismutase 67 63 Thymine Glycols 1.43 Thymine Glycols 57 53 Cryptococcus neoformans 1.43 49 46 Cryptococcus neoformans Cdk7 1.43 Cdk7 324 301 Moesin 1.43 Moesin 444 411 p300 / CBP 1.42 p300 / CBP 73 68 E3-binding protein (ARM1) 1.41 E3-binding protein (ARM1) 66 61 Bonzo / STRL33 / TYMSTR 1.41 Bonzo / STRL33 / TYMSTR 2024 1849 Interferon-a(II) 1.41 Interferon-a(II) 64 58 CD56/NCAM-1 1.41 CD56/NCAM-1 1625 1483 14.3.3, Pan 1.40 14.3.3, Pan 107 98 1.40 680 617 Epithelial Specific Antigen Epithelial Specific Antigen Prohibitin 1.39 Prohibitin 5922 5350 CD59 / MACIF / MIRL / Protectin 1.39 CD59 / MACIF / MIRL / Protectin 61 55 LRP / MVP 1.39 LRP / MVP 61 55 Interferon-g 77 1.39 Interferon-g 85 p35nck5a 1.38 p35nck5a 144 130 IPO-38 Proliferation Marker 1.38 IPO-38 Proliferation Marker 151 135 1.38 498 Notch Notch 446 Axonal Growth Cones 1.38 Axonal Growth Cones 429 385 MHC I (HLA-B) 1.38 MHC I (HLA-B) 212 190 Perforin 1.38 120 108 173 Cystic Fibrosis Transmembrane Regulato 1.38 Cystic Fibrosis Transmembrane Regulator 155 IL-1 beta 1.38 IL-1 beta 58 52 CD3zeta 1.38 CD3zeta 206 185 1.38 47 Glycophorin A Glycophorin A 53 1.38 100 90 Thrombospondin Thrombospondin Ruv C 1.38 Ruv C 199 178 IL-3 1.38 47 42 IL-3 XPF 1.37 XPF 186 165 FGF-1 1.37 FGF-1 50 44 Progesterone Receptor (phospho-specifi 1.37 Progesterone Receptor (phospho-specific) - Serine 19 1052 934 1.37 67 59 Fascin Fascin 1.37 84 Cvtochrome c Cytochrome c 75 mGluR1 1.36 mGluR1 53 47

Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample	
0.19	0.30	
0.29	0.09	
0.34	0.03	
0.16	0.04	
0.22	0.14	
0.02	0.06	
0.13	0.25	
0.03	0.04	
0.05	0.04	
0.02	0.04	
0.01	0.01	
0.08	0.13	
0.08	0.02	
0.08	0.12 0.12	
0.17	0.19	
0.09	0.21	
0.00	0.01	
0.19	0.01	
0.03	0.05	
0.04	0.01	
0.46	0.44	
0.08	0.05	
0.06	0.13	
0.26	0.21	
0.06	0.02	
0.06	0.05	
0.01	0.05	
0.11	0.04	
0.07	0.20	
0.00	0.00	
0.06	0.04	
0.05	0.18	
0.09	0.09	
0.00	0.02	
0.02	0.04	
0.01	0.02	
0.12	0.05	
0.05	0.01	
0.09	0.12	
0.04	0.01	
0.03	0.16	
0.01	0.03	
0.11	0.17	
0.07	0.03	
0.00	0.03	
0.23	0.24	
0.07	0.03	
0.22	0.23	
0.03	0.02	
0.08	0.01	
0.04	0.02	

Data Normalized	to Modian Signal	
	Smaller Sample	
0.48	0.70	
7.57	11.11	
0.76	1.12	
34.77	51.03	
16.69	24.49	
0.92		
	1.35	
0.62	0.91 0.80	
	2.01	
1.38 0.56	0.82	
0.42		
	0.61	
1.81	2.62	
105.50	152.56	
3.72	5.38	
0.57	0.82	
0.98	1.41	
0.58	0.84	
0.52	0.75	
0.44	0.63	
0.38	0.55	
2.54	3.62	
3.47	4.95	
0.57	0.81	
0.52	0.73	
15.84	22.28	
0.50	0.70	
12.72	17.87	
0.84	1.17	
5.32	7.43	
46.36	64.46	
0.48	0.66	
0.47	0.66	
0.67	0.92	
1.13	1.56	
1.18	1.63	
3.89	5.37	
3.36	4.63	
1.66	2.28	
0.94	1.30	
1.35	1.86	
0.45	0.62	
1.61	2.22	
0.41	0.57	
0.78	1.08	
1.55	2.14	
0.37	0.51	
1.45	1.99	
0.39	0.53	
8.23	11.25	
0.52	0.71	
0.66	0.90	
0.41	0.56	

Antibody Array Assay Results	Assay Data
Explorer Antibody Array	

Median Signal 128

	Fold Change between Samples	ivieululi Signui	Average Signal o	f Donlicato Cnots
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
Calling 2 (CHI 2)		Cultin 2 (Cut 2)	2588	2289
Cullin-3 (CUL-3)	1.36	Cullin-3 (CUL-3)		
TNF alpha CD155/PVR (Polio Virus Receptor)	1.36 1.36	TNF alpha	43 90	38 80
CDw17	1.36	CD155/PVR (Polio Virus Receptor) CDw17	56	49
Heat Shock Protein 90a/hsp86	1.36	Heat Shock Protein 90a/hsp86	629	554
IL-10	1.35	IL-10	54	48
Thyroid Hormone Receptor, Human	1.35	Thyroid Hormone Receptor, Human	1032	906
Fyn	1.35	Fyn	94	83
Milk Fat Globule Membrane Protein	1.35	Milk Fat Globule Membrane Protein	1413	1240
PGP9.5	1.35	PGP9.5	61	54
TIMP-1	1.35	TIMP-1	69	61
Human Sodium Iodide Symporter (hNIS)	1.35	Human Sodium Iodide Symporter (hNIS)	170	149
IL-10R	1.35	IL-10R	52	46
tau	1.34	tau	103	90
Hepatocyte Growth Factor	1.34	Hepatocyte Growth Factor	95	83
Ret Oncoprotein	1.34	Ret Oncoprotein	75	66
Collagen IV	1.34	Collagen IV	95	83
Casein	1.34	Casein	213	186
SIM Ag (SIMA-4D3)	1.34	SIM Ag (SIMA-4D3)	59	52
IL-6	1.34	IL-6	67	58
Keratin 14	1.34	Keratin 14	51	44
TR2	1.34	TR2	897	781
IL-30	1.34	IL-30	43	37
Neurofilament	1.34	Neurofilament	54	47
Gamma Glutamylcysteine Synthetase(GC	1.34	Gamma Glutamylcysteine Synthetase(GCS)/Glutamate	1494	1300
Insulin Receptor Substrate-1	1.34	Insulin Receptor Substrate-1	61	53
Cdk1/p34cdc2	1.34	Cdk1/p34cdc2	570	495
Amyloid A	1.34	Amyloid A	65	56
Adrenocorticotrophic Hormone	1.34	Adrenocorticotrophic Hormone	72	63
SHP-1	1.34	SHP-1	212	184
Thomsen-Friedenreich Antigen	1.34	Thomsen-Friedenreich Antigen	61	53
CD94	1.34	CD94	117	102
TGF-beta 2	1.34	TGF-beta 2	83	72
TIMP-2	1.33	TIMP-2	49	43
Caspase 9	1.33	Caspase 9	53	46
McI-1	1.33	Mcl-1	71	62
Negative Control for Mouse IgG2a	1.33	Negative Control for Mouse IgG2a	90	78
SRF (Serum Response Factor)	1.33	SRF (Serum Response Factor)	104	90
Surfactant Protein A	1.33	Surfactant Protein A	45	39
CD68	1.33	CD68	63	55
CDw78	1.33	CDw78	67	58
Prolactin	1.33	Prolactin	77	67
Retinol Binding Protein	1.33	Retinol Binding Protein	909	785
Ku (p80)	1.33	Ku (p80)	77	66
G-CSF	1.33	G-CSF	44	38
Tyrosinase	1.33	Tyrosinase	76	66
Pneumocystis jiroveci	1.33	Pneumocystis jiroveci	51	44
ER Ca+2 ATPase2	1.32	ER Ca+2 ATPase2	68	59
GCDFP-15	1.32	GCDFP-15	47	40
Bcl-6	1.32	Bcl-6	72	62
Synaptophysin	1.32	Synaptophysin	118	101
CD42b	1.32	CD42b	442	380
Activin Receptor Type II	1.32	Activin Receptor Type II	71	61
CD54/ICAM-1	1.32	CD54/ICAM-1	71	61
mGluR5	1.32	mGluR5	212	182
TdT	1.32	TdT	67	58
Hepatocyte	1.32	Hepatocyte	46	39

Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample	
0.10	0.12	
0.03	0.00	
0.24	0.13	
0.01	0.00	
0.49	0.20	
0.10	0.01	
0.06	0.03	
0.11	0.04	
0.02	0.03	
0.02	0.07	
0.08	0.06	
0.12	0.06	
0.03	0.02	
0.01	0.17	
0.07	0.09	
0.00	0.05	
0.11	0.01	
0.01	0.01	
0.00	0.01	
0.03	0.10	
0.01	0.00	
0.18	0.01	
0.02	0.00	
0.03	0.00	
0.17	0.19	
0.00	0.05	
0.04	0.11	
0.01	0.00	
0.00	0.06	
0.08	0.05	
0.01	0.01	
0.06	0.03	
0.02	0.14	
0.00	0.05	
0.01	0.02	
0.06	0.01	
0.12	0.14	
0.08	0.09	
0.02	0.02	
0.02	0.06	
0.20	0.01	
0.04	0.01	
0.35	0.13	
0.03	0.02	
0.02	0.02	
0.00	0.08	
0.01	0.05	
0.02	0.01	
0.05 0.01	0.00	
0.01	0.01	
0.12	0.22	
0.08	0.07	
0.02	0.02	
0.01	0.07	
0.00	0.06	
0.02	0.00	

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
20.25	27.58	
0.34	0.46	
0.70	0.96	
0.43	0.59	
4.92	6.67	
0.42	0.57	
8.07	10.92	
0.74	0.99	
11.06	14.94	
0.48	0.64	
0.54	0.73	
1.33	1.79	
0.41	0.55	
0.81	1.08	
0.74	1.00	
0.59	0.79	
0.74	0.99	
1.66	2.23	
0.46	0.62	
0.52	0.70	
0.40	0.53	
7.02	9.41	
0.33	0.45	
0.42	0.57	
11.69	15.66	
0.48	0.64	
4.46	5.96	
0.50	0.67	
0.56	0.75	
1.66	2.22	
0.47	0.63	
0.92	1.22	
0.65	0.87	
0.38	0.51	
0.41	0.55	
0.56	0.74	
0.70	0.93	
0.81	1.08	
0.35	0.46	
0.49	0.66	
0.52	0.69	
0.60	0.80	
7.12	9.45	
0.60	0.80	
0.34	0.45	
0.59	0.79	
0.40	0.52	
0.53	0.70	
0.36	0.48	
0.56	0.74	
0.92	1.22	
3.46	4.57	
0.56	0.73	
0.56	0.73	
1.66	2.19	
0.52	0.69	
0.36	0.47	
0.30	0.47	

Antibody Array Assay Results	Assay Data		
Explorer Antibody Array			
	Median Signal	128	83

**Average Signal of Replicate Spots Protein List** Protein List **Bigger Sample Smaller Sample** Mucin 2 1.32 Mucin 2 81 69 DNA Ligase I 1.32 DNA Ligase I 70 60 GSK-3 1.32 GSK-3 56 48 TNFa 1.32 TNFa 49 42 Ku (p70/p80) 1.32 Ku (p70/p80) 159 136 Tubulin-b 1.32 Tubulin-b 76 65 23097 CNPase 1.32 CNPase 19750 CD32/Fcg Receptor II CD32/Fcg Receptor II 107 1.32 91 406 346 CD84 1.31 CD84 RPA/p32 1.31 RPA/p32 109 93 TRAP 1.31 TRAP 44 38 CD21 1.31 CD21 64 55 SRC1 (Steroid Receptor Coactivator-1) 1.31 SRC1 (Steroid Receptor Coactivator-1) 98 83 1.31 110 94 Lck DNA-PKcs 1.31 DNA-PKcs 107 91 Glycogen Synthase Kinase 3b (GSK3b) 1.31 Glycogen Synthase Kinase 3b (GSK3b) 1219 1034 CD15 1.31 CD15 79 67 CD9 1.31 CD9 63 53 Glicentin 1.30 Glicentin 69 59 Apolipoprotein D 1.30 Apolipoprotein D 85 72 CD5 1.30 CD5 52 44 Bromodeoxyuridine (BrdU) 1.30 Bromodeoxyuridine (BrdU) 140 118 Prostate Specific Antigen 1.30 Prostate Specific Antigen 162 137 IFN gamma 1.30 IFN gamma 55 47 MMP-15 / MT2-MMP 1.30 MMP-15 / MT2-MMP 49 41 PCTAIRE2 PCTAIRE2 120 1.30 101 Estriol 1.30 Estriol 20155 17032 p21WAF1 1.30 p21WAF1 109 92 mRANKL 1.30 mRANKL 61 51 Dystrophin 1.29 88 74 Dystrophin DNA Polymerase Beta 1.29 DNA Polymerase Beta 72 61 Cyclin D3 1.29 Cyclin D3 91 76 1.29 59 49 Keratin 16 Keratin 16 CITED1 1.29 CITED1 231 193 Neurofilament (200kDa) 1.29 Neurofilament (200kDa) 68 57 Xanthine Oxidase 1.29 Xanthine Oxidase 68 57 FGF-2 1.29 FGF-2 52 44 52 44 Laminin B2/g1 1.29 Laminin B2/g1 5012 4191 Amyloid Beta (APP) 1.29 Amyloid Beta (APP) 1.29 156 130 Collagen II Collagen II Mucin 5AC 1.29 Mucin 5AC 76 91 uPA 1.28 uPA 58 48 TID-1 1.28 TID-1 61 51 ER beta 1.28 ER beta 70 58 1.28 Ruv A 103 86 Ruv A p130 1.28 p130 105 88 CCK-8 1.28 CCK-8 72 60 CD50/ICAM-3 1.28 CD50/ICAM-3 436 363 14862 Granulocyte 1.28 Granulocyte 12370 CD26/DPP IV 1.28 CD26/DPP IV 525 437 Ubiquitin 1.28 Ubiquitin 48 40 CD10 1.28 CD10 460 383 Prostate Specific Acid Phosphatase 1.28 Prostate Specific Acid Phosphatase 210 175 NuMA 1.28 NuMA 92 76 1.28 Progesterone Receptor 120 100 Progesterone Receptor IL-4 1.27 IL-4 58 48 1.27 1121 928 Acinus Acinus

Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample	
0.04	0.06	
0.10	0.05	
0.05	0.00	
0.07	0.02	
0.00	0.03	
0.00	0.00	
0.03	0.07	
0.11	0.03	
0.01	0.20	
0.08	0.01	
0.00 0.04	0.02	
0.01	0.01	
0.08	0.17	
0.03	0.04	
0.00	0.16	
0.04	0.04	
0.06	0.08	
0.14	0.01	
0.02	0.04	
0.03	0.06	
0.04	0.06	
0.15	0.07	
0.08	0.05	
0.07	0.07	
0.03	0.08	
0.05	0.05	
0.01	0.02	
0.04	0.03	
0.02	0.08	
0.06	0.06	
0.04	0.11	
0.06	0.00	
0.09	0.11	
0.05	0.01	
0.03	0.01	
0.05	0.02	
0.08	0.05	
0.12	0.17	
0.11	0.08	
0.05	0.04	
0.06	0.03	
0.04	0.01	
0.05	0.05	
0.01	0.04	
0.01	0.06	
0.00	0.07	
0.04	0.05	
0.02	0.01	
0.14	0.01	
0.04	0.02	
0.01	0.09	
0.43	0.13	
0.04	0.02	
0.13	0.11	
0.02	0.00	
0.35	0.30	

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.63	0.83	
0.55	0.72	
0.44	0.58	
0.38	0.50	
1.24	1.64	
0.59	0.78	
180.80	237.95	
0.83	1.10	
3.17	4.17	
0.85	1.11	
0.34	0.45	
0.50	0.66	
0.76	1.00	
0.86	1.13	
0.83	1.09	
9.54	12.46	
0.62	0.81	
0.49	0.64	
0.54	0.70	
0.67	0.87	
0.41	0.53	
1.09	1.42	
1.27	1.65	
0.43	0.56	
0.38	0.49	
0.94	1.22	
157.77	205.20	
0.85	1.11	
0.47	0.61	
0.69	0.89	
0.56	0.73	
0.71	0.92	
0.46	0.59	
1.80	2.33	
0.53	0.68	
0.53	0.68	
0.41	0.52	
0.41	0.52	
39.23	50.49	
1.22	1.57	
0.71	0.92	
0.45	0.58	
0.47	0.61	
0.54	0.70	
0.80	1.03	
0.82	1.05	
0.56	0.72	
3.41	4.37	
116.34	149.04	
4.11	5.26	
0.37	0.48	
3.60	4.61	
1.64	2.10	
0.72	0.92	
0.94	1.20	
0.45	0.58	
8.77	11.17	

Antibody Array Assay Results	Assay Data		
Explorer Antibody Array			
	Median Signal	128	83

	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots	
Protein List			Bigger Sample	Smaller Sample
Fibrillin-1	1.27	Fibrillin-1	93	77
Heparan Sulfate Proteoglycan	1.27	Heparan Sulfate Proteoglycan	64	53
Factor VIII Related Antigen	1.27	Factor VIII Related Antigen	186	153
MAGE-1	1.27	MAGE-1	117	97
CD79b	1.27	CD79b	74	61
IRAK	1.27	IRAK	2954	2435
IL-5	1.27	IL-5	60	49
Fibronectin	1.27	Fibronectin	170	140
Inhibin alpha	1.27	Inhibin alpha	48	40
Thyroglobulin	1.27	Thyroglobulin	68	56
Transglutaminase II	1.27	Transglutaminase II	186	153
CD100/Leukocyte Semaphorin	1.26	CD100/Leukocyte Semaphorin	70	58
Synuclein	1.26	Synuclein	146	120
CLAUDIN 7	1.26	CLAUDIN 7	53	44
Keratin 10	1.26	Keratin 10	198	163
	1.26		136	112
Medroxyprogesterone Acetate (MPA)		Medroxyprogesterone Acetate (MPA)		
EMA/CA15-3/MUC-1	1.26	EMA/CA15-3/MUC-1	78	64
IL17	1.26	IL17	64	52
Phospho-Ser/Thr/Tyr	1.26	Phospho-Ser/Thr/Tyr	77	63
CD98	1.26	CD98	58	47
Ruv B	1.26	Ruv B	112	92
Negative Control for Mouse IgG1	1.26	Negative Control for Mouse IgG1	169	138
Heat Shock Factor 2	1.26	Heat Shock Factor 2	63	51
Keratin 18	1.26	Keratin 18	65	53
MDM2	1.25	MDM2	79	64
LewisB	1.25	LewisB	203	165
ZAP-70	1.25	ZAP-70	92	75
Hepatocyte Factor Homologue-4	1.25	Hepatocyte Factor Homologue-4	75	61
MHC I (HLA-A)	1.25	MHC I (HLA-A)	83	68
Tubulin-a	1.25	Tubulin-a	193	157
Maltose Binding Protein	1.25	Maltose Binding Protein	70	57
Caspase 3	1.25	Caspase 3	67	54
Stat5	1.25	Stat5	59	48
bcl-2a	1.25	bcl-2a	177	144
Negative Control for Mouse IgM	1.25	Negative Control for Mouse IgM	66	53
Retinoblastoma	1.25	Retinoblastoma	66	53
Toxoplasma Gondii	1.25	Toxoplasma Gondii	66	53
Urocortin	1.24	Urocortin	71	57
Actin, Muscle Specific	1.24	Actin, Muscle Specific	65	53
Nitric Oxide Synthase, brain (bNOS)	1.24	Nitric Oxide Synthase, brain (bNOS)	3136	2531
DR5	1.24	DR5	57	46
CD46	1.24	CD46	215	174
IL-1 alpha	1.24	IL-1 alpha	47	38
	1.24		65	52
Synuclein beta		Synuclein beta		
Insulin Receptor	1.24	Insulin Receptor	69	56
CDw75	1.24	CDw75	97	78
CD24	1.24	CD24	230	185
Rad18	1.24	Rad18	3367	2706
TRP75 / gp75	1.23	TRP75 / gp75	61	49
Cadherin-E	1.23	Cadherin-E	73	59
TTF-1	1.23	TTF-1	81	65
FITC	1.23	FITC	153	123
CDC25C	1.23	CDC25C	60	48
GluR4	1.23	GluR4	60	48
p130cas	1.23	p130cas	75	60
Cyclin B1	1.23	Cyclin B1	1284	1026
Thyroid Stimulating Hormone (TSH)	1.23	Thyroid Stimulating Hormone (TSH)	202	

Coefficient of Variation for Replicates			
Bigger Sample	Smaller Sample		
0.01	0.08		
0.14	0.04		
0.10	0.01		
0.19	0.11		
0.04	0.05		
0.10	0.02		
0.04	0.03		
0.02	0.04		
0.00	0.02		
0.05	0.01		
0.10	0.09		
0.04	0.01		
0.03	0.05		
0.03	0.02		
0.03	0.04		
0.07	0.07		
0.03	0.08		
0.03	0.00		
0.04	0.09		
0.04	0.03		
0.08	0.01		
0.02	0.02		
0.06	0.03		
0.04	0.03		
0.03	0.07		
0.14	0.15		
0.04	0.05		
0.08	0.07		
0.09	0.07		
0.08	0.02		
0.05	0.04		
0.03	0.03		
0.04	0.01		
0.05	0.03		
0.08	0.03		
0.05	0.03		
0.05	0.13		
0.09	0.12		
0.04	0.04		
0.19	0.16		
0.00	0.03		
0.00	0.10 0.06		
0.03	0.03		
0.00	0.06		
0.22	0.09		
0.13	0.13		
0.04	0.07		
0.06	0.04		
0.10	0.05		
0.02	0.16		
0.05	0.06		
0.02	0.03		
0.04	0.09		
0.19	0.02		
0.17	0.14		

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.72	0.92	
0.50	0.63	
1.45	1.84	
0.92	1.16	
0.58	0.73	
23.12	29.33	
0.47	0.59	
1.33	1.68	
0.38	0.48	
0.53	0.67	
1.45	1.84	
0.55		
	0.69	
1.14	1.44	
0.41	0.52	
1.55	1.96	
1.06	1.34	
0.61	0.77	
0.50	0.63	
0.60	0.76	
0.45	0.57	
0.88	1.10	
1.32	1.66	
0.49	0.61	
0.51	0.64	
0.61	0.77	
1.59	1.99	
0.72	0.90	
0.59	0.73	
0.65	0.81	
1.51	1.89	
0.54	0.68	
0.52	0.65	
0.46	0.57	
1.39	1.73	
0.51	0.64	
0.51	0.64	
0.51	0.64	
0.55	0.69	
0.51	0.63	
24.54	30.49	
0.45	0.55	
1.68	2.09	
0.36	0.45	
0.50	0.63	
0.54	0.67	
0.76	0.94	
1.80	2.22	
26.35	32.60	
0.47	0.58	
0.57	0.70	
0.63	0.78	
1.20	1.48	
0.47	0.58	
0.47	0.58	
0.59	0.72	
10.05	12.36	
1.58	1.94	
1.30	1.74	

Antibody Array Assay Results	Assay Data	
Explorer Antibody Array		

Average Signal of Replicate Spots **Protein List** Protein List **Bigger Sample** Leukotriene (C4, D4, E4) Leukotriene (C4, D4, E4) 1.23 70 56 Claudin 3 1.23 Claudin 3 72 57 Rhodopsin (Opsin) 1.23 Rhodopsin (Opsin) 488 389 Adenovirus Fiber 1.23 Adenovirus Fiber 3326 2648 CD106 / VCAM 1.22 CD106 / VCAM 71 57 179 142 XPA 1.22 XPA MMP-10 (Stromilysin-2) 1.22 MMP-10 (Stromilysin-2) 456 362 TrxR2 1.22 TrxR2 63 50 Adenovirus Type 5 E1A 1.22 Adenovirus Type 5 E1A 179 142 77 MMP-9 (92kDa Collagenase IV) 1.22 MMP-9 (92kDa Collagenase IV) 97 Ezrin/p81/80K/Cytovillin 1.22 Ezrin/p81/80K/Cytovillin 68 54 GnRH Receptor 1.22 GnRH Receptor 169 134 Plasma Cell Marker 1.22 Plasma Cell Marker 1947 1543 Cdk5 1.22 50 Cdk5 63 Alpha Fetoprotein (AFP) 1.22 Alpha Fetoprotein (AFP) 108 86 CD165 1.22 CD165 98 78 GSTmu 53 42 GSTmu 1.22 1.22 141 pS2 pS2 111 14.3.3 gamma 14.3.3 gamma 1.22 150 119 p19ARF 1.22 p19ARF 2067 1632 CD61 / Platelet Glycoprotein IIIA 1.21 CD61 / Platelet Glycoprotein IIIA 64 50 CD25/IL-2 Receptor a 1.21 CD25/IL-2 Receptor a 132 104 FHIT 1.21 FHIT 68 54 CD4 1.21 CD4 70 55 CD30 (Reed-Sternberg Cell Marker) CD30 (Reed-Sternberg Cell Marker) 1.21 89 70 1.21 Pax-5 49 Pax-5 63 MART-1/Melan-A 1.21 MART-1/Melan-A 81 64 LewisA 1.21 LewisA 74 58 IGF-1R 1.21 IGF-1R 102 80 SODD (Silencer of Death Domain) 1.20 SODD (Silencer of Death Domain) 561 439 1.20 108 85 Catenin gamma Catenin gamma Vimentin 1.20 Vimentin 62 48 p15INK4b 1.20 52 p15INK4b 66 744 580 Ras 1.20 Ras Presenillin 1.20 Presenillin 75 59 1.20 6-Histidine 6-Histidine 89 69 IGF-I 1.20 IGF-I 66 51 Neutrophil Elastase Neutrophil Elastase 1.20 4223 3287 1.20 sm 428 333 HIF-1a 1.20 HIF-1a 77 60 MHC II (HLA-DP) 1.20 MHC II (HLA-DP) 101 79 Amylin Peptide 1.20 Amylin Peptide 51 65 MMP-7 (Matrilysin) 1.19 MMP-7 (Matrilysin) 121 94 CD40 1.19 CD40 116 90 Parkin 1.19 Parkin 203 158 Collagen VII 1.19 Collagen VII 71 55 p170 / MDR-1 1.19 p170 / MDR-1 87 67 EGFR 1.19 EGFR 184 143 Hepatic Nuclear Factor-3B 1.19 Hepatic Nuclear Factor-3B 162 125 MMP-2 (72kDa Collagenase IV) 1.19 MMP-2 (72kDa Collagenase IV) 93 72 1.19 hPL 51 Neurofilament (160kDa) 1.19 Neurofilament (160kDa) 95 73 AIF (Apoptosis Inducing Factor) 1.19 AIF (Apoptosis Inducing Factor) 5419 4184 IP10/CRG2 1.19 IP10/CRG2 75 58 Heat Shock Factor 1 1.19 Heat Shock Factor 1 66 51 CDC6 1.18 CDC6 113 87 Collagen IX 1.18 Collagen IX 87 67

Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample	
0.03	0.01	
0.05	0.05	
0.08	0.34	
0.24	0.06	
0.02	0.09	
0.05	0.00	
0.10	0.16	
0.00	0.03	
0.22	0.08	
0.17	0.01	
0.03	0.01	
0.02	0.10	
0.19	0.02	
0.03	0.04	
0.08	0.12	
0.07	0.01	
0.09	0.02	
0.06	0.01	
0.01	0.07	
0.13	0.09	
0.10	0.00	
0.08	0.02	
0.02	0.09	
0.08	0.08	
0.01	0.01	
0.03	0.09	
0.14		
0.08	0.15	
0.09	0.03	
0.18	0.06	
0.09	0.06	
0.08	0.04	
0.05	0.22	
0.08	0.08	
0.01	0.04	
0.05	0.04	
0.06	0.08	
0.05	0.05	
0.12	0.01	
0.06	0.10	
0.09	0.01	
0.03	0.13	
0.01	0.00	
0.01	0.15	
0.08	0.03	
0.08	0.03	
0.16	0.06	
0.12	0.07	
0.09	0.07	
0.02	0.00	
0.02	0.04	
0.02	0.04	
0.07	0.09	
0.03	0.01	
0.02	0.04	
0.11	0.03	

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.54	0.67	
0.56	0.69	
3.82	4.68	
26.04	31.90	
0.56	0.68	
1.40	1.71	
3.57	4.36	
0.49	0.60	
1.40	1.71	
0.76	0.92	
0.53	0.64	
1.32	1.61	
15.24	18.58	
0.49	0.60	
0.85	1.03	
0.77	0.93	
0.41	0.50	
1.10	1.34	
1.17	1.43	
16.18	19.66	
0.50	0.60	
1.03	1.25	
0.53	0.64	
0.55	0.66	
0.69	0.84	
0.49	0.59	
0.63	0.77	
0.58	0.70	
0.79	0.96	
4.39	5.29	
0.85	1.02	
0.48	0.58	
0.52	0.62	
5.82	6.99	
0.59	0.70	
0.69	0.83	
0.51	0.61	
33.06	39.60	
3.35	4.01	
0.60	0.72	
0.79	0.95	
0.51	0.61	
0.94	1.13	
0.91	1.08	
1.59	1.90	
0.56	0.66	
0.68	0.81	
1.44	1.72	
1.26	1.51	
0.72	0.86	
0.52	0.61	
0.74	0.88	
42.41	50.40	
0.58	0.69	
0.51	0.61	
0.88	1.04	
0.68	0.80	

Antibody Array Assay Results	Assay Data
Explorer Antibody Array	
	Median Signal 128

**Average Signal of Replicate Spots Protein List** Protein List **Bigger Sample** Claudin 2 1.18 Claudin 2 67 52 Keratin 10/13 1.18 Keratin 10/13 61 47 BAG-1 1.18 BAG-1 84 65 MMP-1 (Collagenase-I) MMP-1 (Collagenase-I) 1.18 65 50 339 260 B-Cell 1.18 B-Cell E2F-3 1.18 E2F-3 69 53 MADD 1.18 MADD 682 522 Chromogranin A 1.18 Chromogranin A 162 124 CD18 1.18 CD18 102 78 CDw60 1.18 CDw60 70 54 Clathrin 261 199 Clathrin 1.18 1.18 146 112 Thyroid Hormone Receptor beta, humar Thyroid Hormone Receptor beta, human Heat Shock Protein 75/hsp75 Heat Shock Protein 75/hsp75 1.17 95 73 Cadherin-P 1.17 Cadherin-P 51 39 SV40 Large T Antigen 1.17 SV40 Large T Antigen 135 103 FSH-b 1.17 FSH-b 147 112 Renal Cell Carcinoma 1.17 Renal Cell Carcinoma 69 53 Testosterone 1.17 82 62 Testosterone 107 von Hippel-Lindau Protein 1.17 von Hippel-Lindau Protein 81 JNK Activating kinase (JKK1) 1.17 JNK Activating kinase (JKK1) 653 496 CD95 / Fas CD95 / Fas 121 92 1.17 O ct-1 1.17 O ct-1 98 74 Insulin 1.17 Insulin 79 60 alpha-1-antichymotrypsin 1.17 alpha-1-antichymotrypsin 3160 2394 MMP-19 1.17 MMP-19 68 52 Keratin 20 1.16 Keratin 20 109 83 74 Myelin / Oligodendrocyte 1.16 Myelin / Oligodendrocyte 56 Nucleophosmin (NPM) Nucleophosmin (NPM) 1.16 80 61 487 Exo1 1.16 Exo1 645 ATM ATM 1.16 80 60 Growth Hormone (hGH) 1.16 Growth Hormone (hGH) 116 88 IL-8 1.16 388 293 IL-8 b Galactosidase 1.16 b Galactosidase 108 81 Heat Shock Protein 70/hsp70 Heat Shock Protein 70/hsp70 77 1.16 58 Parathyroid Hormone 1.16 Parathyroid Hormone 77 58 TAG-72 52 TAG-72 1.16 69 Calretinin 1.16 Calretinin 71 53 4826 3628 Calponin 1.16 Calponin MCM5 MCM5 113 1.16 85 CD23 1.15 CD23 70 53 Cdk2 1.15 Cdk2 80 60 Claudin 5 1.15 Claudin 5 64 48 GFAP 1.15 GFAP 62 47 UCP3 UCP3 1.15 76 57 Ang-1 1.15 Ang-1 70 52 CD6 1173 1.15 CD6 876 79 MCM2 1.15 MCM2 59 Actin, skeletal muscle 1.15 Actin, skeletal muscle 71 53 Progesterone Receptor (phospho-specifi 1.15 Progesterone Receptor (phospho-specific) - Serine 29 99 74 MyoD1 1.15 MyoD1 5791 4316 Rabies Virus 1.15 Rabies Virus 139 104 PPAR-gamma PPAR-gamma 48 1.15 65 PCNA PCNA 113 1.14 84 IL-2 1.14 IL-2 76 56 HRP 1.14 HRP 89 66 1.14 Ang-2 Ang-2 68 50

	ation for Replicates
Bigger Sample	Smaller Sample
0.11	0.01
0.06	0.02
0.03	0.03
0.03	0.04
0.14	0.08
0.05	0.01
0.18	0.22
0.12	0.08
0.08	0.02
0.08	0.01
0.10	0.08
0.17	0.07
0.19	0.03
0.13	0.06
0.07	0.05
0.02	0.02
0.16	0.01
0.04	0.02
0.05	0.02
0.20	0.19
0.02	0.07
0.08	0.08
0.12	0.06
0.02	0.05
0.02	0.01
0.08	0.11
0.00	0.03
0.07	0.08
0.15	0.03
0.17	0.05
0.06	0.09
0.09	0.08
0.27	0.02
0.06	0.02
0.00	0.10
0.05	0.01
0.05	0.03
0.04	0.20
0.18	0.11
0.02	0.12
0.04	0.05
0.02	0.12
0.11	0.08
0.13	0.10
0.05	0.03
0.19	0.04
0.02	0.10
0.06	0.00
0.27	0.11
0.13	0.15
0.23	0.06
0.05	0.03
0.01	0.03
0.14	0.05
0.05	0.04
0.03	0.00

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.52	0.62	
0.47	0.56	
0.66	0.78	
0.50	0.60	
2.65	3.13	
0.54	0.63	
5.33	6.29	
1.27	1.49	
0.80	0.94	
0.55	0.64	
2.04	2.40	
1.14	1.34	
0.74	0.87	
0.40	0.46	
1.05	1.23	
1.15	1.34	
0.54	0.63	
0.64	0.75	
0.64	0.75	
5.11	5.98	
0.94	1.10	
0.76	0.89	
0.61	0.72	
24.73	28.84	
0.53	0.62	
0.85	0.99	
0.58	0.67	
0.63	0.73	
5.05	5.87	
0.62	0.72	
0.91	1.05	
3.04	3.52	
0.84	0.98	
0.60	0.70	
0.60	0.70	
0.54	0.62	
0.55	0.64	
37.77	43.70	
0.88	1.02	
0.55	0.63	
0.63	0.72	
0.50	0.58	
0.49	0.56	
0.59	0.69	
0.54	0.63	
9.18	10.55	
0.62	0.71	
0.56	0.64	
0.77	0.89	
45.33	52.00	
1.09	1.25	
0.50	0.58	
0.88	1.01	
0.59	0.67	
0.70	0.80	
0.53	0.60	

Antibody Array Assay Results	Assay Data		
Explorer Antibody Array			
	Median Signal	128	83
	ivieaian Signai	128	

Protein List	Fold Change between Samples	Destain List	Average Signal of Replicate Spots	
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
ITK	1.14	ITK	165	122
S100A4	1.14	S100A4	126	93
PSCA	1.14	PSCA	71	52
Topo II beta	1.13	Topo II beta	70	52
CD138	1.13	CD138	104	77
Keratin, LMW	1.13	Keratin, LMW	95	70
Prostate Apoptosis Response Protein-4	1.13	Prostate Apoptosis Response Protein-4	66	49
IgA	1.13	IgA	16036	11781
Caspase 1	1.13	Caspase 1	1082	794
GAPDH	1.13	GAPDH	166	122
Surfactant Protein B	1.13	Surfactant Protein B	77	57
CD14	1.13	CD14	137	101
Caldesmon	1.13	Caldesmon	113	83
CD79a mb-1	1.13	CD79a mb-1	114	84
Retinoblastoma (Rb) (Phospho-specific S	1.13	Retinoblastoma (Rb) (Phospho-specific Serine 608)	69	51
Osteopontin	1.13	Osteopontin	82	60
PMP-22	1.12	PMP-22	76	56
a-B-Crystallin	1.12	a-B-Crystallin	74	54
CXCR4 / Fusin	1.12	CXCR4 / Fusin	305	222
Gastrin 1	1.12	Gastrin 1	134	97
Ornithine Decarboxylase	1.12	Ornithine Decarboxylase	101	73
CD20	1.12	CD20	148	108
PDGF	1.12	PDGF	79	57
Transforming Growth Factor a	1.12	Transforming Growth Factor a	146	106
CD45RB	1.12	CD45RB	118	86
Mek6	1.11	Mek6	639	462
MHC II (HLA-DQ)	1.11	MHC II (HLA-DQ)	163	118
MMP-11 (Stromelysin-3)	1.11	MMP-11 (Stromelysin-3)	88	63
Caspase 7 (Mch 3)	1.11	Caspase 7 (Mch 3)	1128	812
Fli-1	1.11	Fli-1	79	57
MAP2a,b	1.11	MAP2a,b	123	88
CD16	1.10	CD16	223	160
HDAC1	1.10	HDAC1	73	52
CIDE-A	1.10	CIDE-A	691	496
MLH1	1.10	MLH1	80	57
GM-CSF	1.10	GM-CSF	51	37
ERCC1	1.10	ERCC1	677	484
Prolactin Receptor	1.10	Prolactin Receptor	4449	3179
CD115/c-fms/CSF-1R/M-CSFR	1.10	CD115/c-fms/CSF-1R/M-CSFR	212	152
c-iun	1.10	c-jun	154	110
Mucin 3 (MUC3)	1.10	Mucin 3 (MUC3)	202	144
Raf-1 (Phospho-specific)	1.10	Raf-1 (Phospho-specific)	152	108
Neurofilament (68kDa)	1.10	Neurofilament (68kDa)	162	115
Alkaline Phosphatase (AP)	1.10	Alkaline Phosphatase (AP)	655	466
CD36GPIIIb/GPIV	1.09	CD36GPIIIb/GPIV	220	157
HDJ-2/DNAJ	1.09	HDJ-2/DNAJ	120	85
S100A6	1.09	\$100A6	154	110
Vitamin D Receptor (VDR)	1.09	Vitamin D Receptor (VDR)	738	525
p95VAV	1.09	p95VAV		
PLAP	1.09	PLAP	80 93	57 66
Myosin Smooth Muscle Heavy Chain	1.09	Myosin Smooth Muscle Heavy Chain	93	66
Cdk4	1.09	Cdk4	154	109
p63 (p53 Family Member)	1.09	p63 (p53 Family Member)	115	81
Rad51	1.09	Rad51	229	162
MHC II (HLA-DR)	1.09	MHC II (HLA-DR)	190	134
E2F-1	1.09	E2F-1	758	535

	ation for Replicates		
Bigger Sample	Smaller Sample		
0.13	0.09		
0.07	0.09		
0.13	0.05		
0.04	0.04		
0.16	0.01		
0.04	0.01		
0.00	0.04		
0.04	0.02		
0.32	0.14		
0.01	0.04		
0.09	0.06		
0.03	0.04		
0.18	0.13		
0.04	0.31		
0.08	0.01		
0.00	0.12		
0.07	0.01		
0.01	0.12		
0.05	0.09		
0.11	0.03		
0.02	0.04		
0.21	0.16		
0.10	0.07		
0.02	0.11		
0.11	0.11		
0.16	0.22		
0.13	0.04		
0.02	0.11		
0.02			
	0.10		
0.10	0.04		
0.02	0.03		
0.08	0.00		
0.03	0.00		
0.43	0.29		
0.06	0.07		
0.22	0.02		
0.11	0.00		
0.24	0.34		
0.23	0.08		
0.00	0.10		
0.08	0.01		
0.06	0.03		
0.03	0.06		
0.25	0.01		
0.03	0.06		
0.11	0.22		
0.27	0.10		
0.08	0.08		
0.13	0.06		
0.11	0.09		
0.07	0.12		
0.08	0.00		
0.02	0.07		
0.04	0.00		
0.02	0.12		
0.02	0.12		
0.13	0.13		

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.29	1.46
0.99	1.12
0.55	0.63
0.55	0.62
0.81	0.92
0.74	0.84
0.52	0.58
125.52	141.93
8.47	9.57
1.30	1.46
0.60	0.68
1.07	1.21
0.88	0.99
0.89	1.01
0.54	0.61
0.64	0.72
0.59	0.67
0.58	0.64
2.38	2.67
1.05	1.17
0.79	0.88
1.16	1.30
0.61	0.69
1.14	1.27
0.92	1.03
5.00	5.57
1.27	1.42
0.68	0.76
8.83	9.78
0.61	0.68
0.96	1.06
1.75	1.93
0.57	0.63
5.41	5.97
0.62	0.69
0.40	0.44
5.30	5.83
34.82	38.30
1.66	1.83
1.20	1.32
1.58	1.73
1.19	1.30
1.26	1.39
5.13	5.61
1.72	1.89
0.94	1.02
1.21	1.32
5.78	6.32
0.62	0.68
0.73	0.80
0.72	0.79
1.21	1.31
0.90 0.98	
1.79 1.95	
1.48	1.61
5.93	6.45

Antibody Array Assay Results	Assay Data
Explorer Antibody Array	Adulius Simula 420

	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots	
Protein List			Bigger Sample	Smaller Sample
DD2 (Dastelane 2)		DD2 (Duntainess 2)		
PR3 (Proteinase 3)	1.09	PR3 (Proteinase 3)	7675	5416
GRIP1	1.09	GRIP1	95 78	67
CDC14A Phosphatase	1.09	CDC14A Phosphatase		55
bcl-X	1.08	bcl-X	71	50
b-2-Microglobulin	1.08	b-2-Microglobulin	73	51
Phosphotyrosine	1.08	Phosphotyrosine	204	144
Erk1	1.08	Erk1	228	160
GLUT-3	1.08	GLUT-3	101	71
Claudin 4	1.08	Claudin 4	64	45
14-3-3 beta	1.08	14-3-3 beta	107	75
p16INK4a	1.08	p16INK4a	68	48
Chorionic Gonadotropin beta (hCG-beta)	1.07	Chorionic Gonadotropin beta (hCG-beta)	123	86
CD1a	1.07	CD1a	113	79
Surfactant Protein B (Pro)	1.07	Surfactant Protein B (Pro)	141	98
Progesterone	1.07	Progesterone	1623	1130
Epithelial Membrane Antigen (EMA / CA1	1.07	Epithelial Membrane Antigen (EMA / CA15-MUC-1)	179	125
GST	1.07	GST	133	93
Calcium Pump ATPase	1.07	Calcium Pump ATPase	148	103
Cyclin E	1.07	Cyclin E	3647	2532
CD81/TAPA-1	1.06	CD81/TAPA-1	94	65
MHC I (HLA-A,B,C)	1.06	MHC I (HLA-A,B,C)	159	110
Tubulin	1.06	Tubulin	443	305
p53	1.06	p53	87	60
TGF beta 3	1.05	TGF beta 3	186	127
Heregulin	1.05	Heregulin	117	80
Myeloid Specific Marker	1.05	Myeloid Specific Marker	177	121
Oct-3/	1.05	Oct-3/	79	54
CD71 / Transferrin Receptor	1.05	CD71 / Transferrin Receptor	111	76
CD231	1.05	CD231	166	113
MHC II (HLA-DR) Ia	1.05	MHC II (HLA-DR) Ia	155	106
L-Plastin	1.05	L-Plastin	348	237
MMP-13 (Collagenase-3)	1.04	MMP-13 (Collagenase-3)	120	81
Flt-4	1.04	Flt-4	76	52
Chk1	1.04	Chk1	1520	1029
RPA/p70	1.04	RPA/p70	176	119
COX2	1.04	COX2	83	56
GLUT-1	1.03	GLUT-1	79	53
p73a/b	1.03	p73a/b	81	54
Connexin 43	1.03	Connexin 43	93	62
Mitochondria	1.03	Mitochondria	80	53
Fas-ligand	1.02	Fas-ligand	81	54
Bax	1.02	Bax	107	71
Tropomyosin	1.02	Tropomyosin	167	111
Ga0	1.02	Ga0	92	61
Glucose-Regulated Protein 94	1.02	Glucose-Regulated Protein 94	86	57
P504S	1.02	P504S	74	49
	1.02		96	63
Filaggrin E2F-2	1.02	Filaggrin E2F-2	9241	6087
Cathepsin D	1.01	Cathepsin D	9241 81	53
<u> </u>	1.01		305	200
Laminin Receptor		Laminin Receptor		
Muc-1	1.01	Muc-1	97	64
Keratin 8 (phospho-specific Ser73)	1.00	Keratin 8 (phospho-specific Ser73)	178	116
APC11	1.00	APC11	551	359
NF kappa B / p65 (Rel A)	1.00	NF kappa B / p65 (Rel A)	675	439
RAD1	1.00	RAD1	174	113
Actin, Pan	1.00	Actin, Pan	115	75

Coefficient of Variation for Replicates			
Bigger Sample	Smaller Sample		
0.02	0.05		
0.02	0.04		
0.07	0.05		
0.04	0.03		
0.20	0.03		
0.12	0.06		
0.04	0.04		
0.05	0.11		
0.08	0.05		
0.14	0.07		
0.04	0.13		
0.01	0.01		
0.06	0.14		
0.02	0.06		
0.04	0.08		
0.05	0.03		
0.15	0.07		
0.11	0.03		
0.21	0.06		
0.00	0.02		
0.06	0.01		
0.17	0.31		
0.14	0.08		
0.11	0.11		
0.00	0.14		
0.00	0.06		
0.09	0.03		
0.10	0.05		
0.13	0.08		
0.16	0.09		
0.10	0.16		
0.16	0.16		
0.17	0.01		
0.09	0.04		
0.03	0.05		
0.03	0.06		
0.18	0.08		
0.11	0.00		
0.04	0.07		
0.29	0.05		
0.13	0.01		
0.09	0.03		
0.02	0.11		
0.10	0.08		
0.14	0.04		
0.09	0.04		
0.08	0.00		
0.07	0.13		
0.24	0.03		
0.03	0.03		
0.10	0.03		
0.06	0.12		
0.21	0.05		
0.08	0.17		
0.46	0.09		
0.31	0.09		

Data Normalized to Median Signal			
Bigger Sample	Smaller Sample		
60.08	65.25		
0.74	0.81		
0.61	0.66		
0.56	0.60		
0.57	0.61		
1.60	1.73		
1.78	1.93		
0.79	0.85		
0.50	0.54		
0.83	0.90		
0.53	0.57		
0.96	1.03		
0.88	0.95		
1.10	1.18		
12.70	13.61		
1.40	1.50		
1.04	1.11		
1.15	1.23		
28.54	30.50		
0.74	0.78		
1.24	1.32		
3.46	3.67		
0.68	0.72		
1.45	1.53		
0.92	0.96		
1.39	1.46		
0.62	0.65		
0.86	0.91		
1.30	1.36		
1.21	1.27		
2.72	2.85		
0.94	0.98		
0.59	0.62		
11.90	12.39		
1.38	1.43		
0.65	0.67		
0.62	0.64		
0.63	0.65		
0.72	0.75		
0.62	0.64		
0.63	0.64		
0.83	0.85		
1.31	1.33		
0.72	0.73		
0.67	0.68		
0.58	0.58		
0.75	0.76		
72.33	73.34		
0.63	0.64		
2.39	2.41		
0.76	0.77		
1.39	1.40		
4.31	4.32		
5.28	5.29		
1.36	1.36		
0.90	0.90		
0.50	0.50		

Antibody	y Array	Assay	y Results	Assa	y Data
Alltibou	y <del>M</del> ilay	Mooa	y nesults	ASSA	y Date

Explorer Antibody Array

Median Signal 128 83

Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
Heat Shock Protein 60/hsp60	0.99	Heat Shock Protein 60/hsp60	120	77
Estradiol	0.99	Estradiol	194	125
CD45RO	0.99	CD45RO	8930	5753
Mast Cell Chymase	0.99	Mast Cell Chymase	8147	5239
Tenascin	0.99	Tenascin	91	59
Gai1	0.99	Gai1	6158	3943
Luciferase	0.97	Luciferase	90	57
GABA a Receptor 1	0.97	GABA a Receptor 1	94	60
Estrogen Receptor	0.97	Estrogen Receptor	96	61
CD8	0.97	CD8	110	69
SIRP a1	0.97	SIRP a1	949	598
LH	0.97	LH	166	104
S100	0.96	S100	101	63
MMP-16 / MT3-MMP	0.96	MMP-16 / MT3-MMP	384	240
DcR1	0.95	DcR1	121	75
Macrophage	0.95	Macrophage	27363	16885
Keratin 8/18	0.95	Keratin 8/18	3273	2018
CD137 (4-1BB)	0.95	CD137 (4-1BB)	94	58
Keratin 5/6/18	0.95	Keratin 5/6/18	367	226
cdh1	0.95	cdh1	118	73
PHAS-II	0.94	PHAS-II	152	93
Neuron Specific Enolase	0.94	Neuron Specific Enolase	3636	2230
I-Kappa-B Kinase b (IKKb)	0.94	I-Kappa-B Kinase b (IKKb)	171	104
p73a	0.94	p73a	160	98
Myogenin	0.94	Myogenin	189	115
GluR6/7	0.94	GluR6/7	93	57
Keratin 8	0.93	Keratin 8	4890	2969
Caspase 5	0.93	Caspase 5	101	61
Keratin 5/8	0.93	Keratin 5/8	150	91
c-fos	0.93	c-fos	98	59
Desmin	0.93	Desmin	102	61
Ki67	0.92	Ki67	244	146
Melanoma (gp100)	0.92	Melanoma (gp100)	4679	2795
GluR 2/3	0.92	GluR 2/3	91	54
CREB	0.91	CREB	607	360
Green Fluorescent Protein (GFP)	0.91	Green Fluorescent Protein (GFP)	131	78
Pds1	0.91	Pds1	418	247
claudin 11	0.91	claudin 11	103	61
Keratin 19	0.91	Keratin 19	313	184
MAP1B	0.90	MAP1B	4433	2604
CD35/CR1	0.89	CD35/CR1	269	156
DJ-1	0.89	DJ-1	103	59
Grb2	0.88	Grb2	695	400
GluR1	0.88	GluR1	102	58
CREB-Binding Protein	0.88	CREB-Binding Protein	124	71
Cdk8	0.88	Cdk8	814	463
Paxillin	0.88	Paxillin	146	83
Keratin, Pan	0.87	Keratin, Pan	114	65
Bcl10 / CIPER / CLAP / mE10	0.87	Bcl10 / CIPER / CLAP / mE10	352	199
APC	0.87	APC	107	60
Negative Control for Mouse IgG3	0.87	Negative Control for Mouse IgG3	254	143
SREBP-1 (Sterol Regulatory Element Bindi	0.86	SREBP-1 (Sterol Regulatory Element Binding Protein-1	127	71
Catenin alpha	0.84	Catenin alpha	88	48
Myeloperoxidase	0.84	Myeloperoxidase	4854	2654
Adenovirus Type 2 E1A	0.84	Adenovirus Type 2 E1A	5639	3080
NF kappa B / p50	0.83	NF kappa B / p50	1080	584
иг карра в / рэс	0.83	Int rahha p / hon	1090	384

Coefficient of Variation for Replicates			
Bigger Sample	Smaller Sample		
0.15	0.06		
0.13	0.18		
0.04	0.01		
0.11	0.09		
0.11	0.01		
0.19	0.11		
0.27	0.10		
0.21	0.04		
0.10	0.43		
0.03	0.08		
0.00	0.02		
0.15	0.07		
0.20	0.20		
0.40	0.01		
0.22	0.10		
0.08	0.07		
0.16	0.13		
0.04	0.06		
0.28	0.01		
0.06	0.01		
0.03	0.02		
0.01	0.01		
0.02	0.20		
0.19	0.12		
0.07	0.04		
0.05	0.01		
0.01	0.05		
0.08	0.00		
0.14	0.10		
0.16	0.02		
0.01	0.05		
0.06	0.09		
0.06	0.09		
0.16	0.05		
0.34	0.30		
0.18	0.12		
0.06	0.00		
0.06	0.08		
0.05	0.07		
0.17	0.24		
0.00	0.10		
0.19	0.02		
0.01	0.08		
0.03	0.15		
0.03	0.01		
0.16	0.03		
0.10	0.03		
0.12	0.03		
0.05	0.15		
0.05	0.07		
0.01	0.09		
0.01	0.11		
0.09	0.03		
0.03	0.00		
0.15	0.17		
0.31	0.15		

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.94	0.93
1.52	1.51
69.90	69.31
63.77	63.12
0.71	0.70
48.20	47.51
0.70	0.69
0.74	0.72
0.75	0.73
0.86	0.83
7.42	7.20
1.30	1.25
0.79	0.76
3.00	2.89
0.94	0.90
214.19	203.43
25.62	24.31
0.73	0.69
2.87	2.72
0.92	0.87
1.19	1.12
28.46	26.86
1.33	1.25
1.25	1.17
1.48	1.39
0.73	0.68
38.27	35.77
0.79	0.73
1.17	1.09
0.77	0.71
0.79	0.73
1.91	1.76
36.63	33.67
0.71	0.65
4.75	4.33
1.03	0.93
3.27	2.97
0.80	0.73
2.45	2.22
34.70 2.10	31.37 1.88
0.80	0.71
5.44	4.81
0.79	0.70
0.79	0.70
6.37	5.58
1.14	1.00
0.89	0.78
2.76	2.39
0.83	0.72
1.99	1.72
0.99	0.85
0.68	0.58
37.99	31.97
44.14	37.11
8.45	7.04
	-

Antibody Array Assay Results	Assay Data
Explorer Antibody Array	

Median Signal 128 83

Fold Change between Samples Average Signal of Replicate Spots

		Median Signal	128	83
Protein List	Fold Change between Samples	Protein List		f Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
Wnt-1	0.83	Wnt-1	94	51
Cyclin C	0.82	Cyclin C	247	132
Heat Shock Protein 27/hsp27	0.81	Heat Shock Protein 27/hsp27	4058	2135
Mekk-1	0.79	Mekk-1	148	76
Stat6	0.79	Stat6	103	53
Fra2	0.79	Fra2	212	109
Granzyme B	0.78	Granzyme B	198	101
Raf1	0.78	Raf1	492	249
Vinculin	0.78	Vinculin	200	101
p27Kip1	0.77	p27Kip1	179	89
Syk	0.76	Syk	480	238
B7-H2	0.76	B7-H2	3527	1741
nm23	0.76	nm23	146	72
Topoisomerase IIa	0.76	Topoisomerase IIa	172	85
Myoglobin	0.75	Myoglobin	121	59
Thymidine Phosphorylase	0.75	Thymidine Phosphorylase	124	61
ERK2	0.75	ERK2	189	92
Caspase 8 (FLICE)	0.74	Caspase 8 (FLICE)	139	67
Ferritin	0.74	Ferritin	1686	815
Heat Shock Protein 90b/hsp84	0.74	Heat Shock Protein 90b/hsp84	139	67
Zip kinase	0.73	Zip kinase	260	124
Helicobacter pylori	0.73	Helicobacter pylori	265	125
Claudin-1	0.71	Claudin-1	184	85
Cyclin E2	0.71	Cyclin E2	148	69
ROC	0.71	ROC	119	55
I-FLICE / CASPER	0.71	I-FLICE / CASPER	186	85
CD63	0.70	CD63	2280	1038
D4-GDI	0.69	D4-GDI	201	91
DNA Polymerase Gamma	0.68	DNA Polymerase Gamma	141	63
Bim (BOD)	0.68	Bim (BOD)	385	170
Filamin	0.67	Filamin	2149	939
MMP-14 / MT1-MMP	0.67	MMP-14 / MT1-MMP	183	80
DP-2	0.67	DP-2	212	92
Caspase 6 (Mch 2)	0.67	Caspase 6 (Mch 2)	163	71
DFF45 / ICAD	0.65	DFF45 / ICAD	583	247
CDC37	0.65	CDC37	1435	605
NOS-i	0.64	NOS-i	202	85
Histone H1	0.64	Histone H1	1208	503
TNF-R2	0.64	TNF-R2	176	73
E2F-5	0.63	E2F-5	374	154
Flk-1 / KDR / VEGFR2	0.63	Flk-1 / KDR / VEGFR2	146	60
Amphiregulin	0.63	Amphiregulin	170	69
DcR2 / TRAIL-R4 / TRUNDD	0.62	DcR2 / TRAIL-R4 / TRUNDD	130	53
Negative Control for Rabbit IgG	0.62	Negative Control for Rabbit IgG	160	65
Somatostatin Receptor-I	0.62	Somatostatin Receptor-I	243	98
Mek2	0.62	Mek2	308	124
Daxx	0.62	Daxx	162	65
APC2	0.61	APC2	129	51
A-Raf	0.60	A-Raf	198	78
Ask1 / MAPKKK5	0.60	Ask1 / MAPKKK5	227	89
Calcitonin	0.60	Calcitonin	174	68
	0.60			70
Caspase 2 Bak	0.59	Caspase 2 Bak	180 299	116
	0.59		852	
Involucrin		Involucrin		328
TACE (TNF-alpha converting enzyme) / Al	0.59	TACE (TNF-alpha converting enzyme) / ADAM17	246	95
Gab-1	0.59	Gab-1	316	121

Coefficient of Variation for Replicates			
Bigger Sample	Smaller Sample		
0.37	0.13		
0.26	0.04		
0.20	0.01		
0.18	0.13		
0.02	0.04		
0.02	0.15		
0.30	0.13		
0.45	0.29		
0.19	0.06		
0.02	0.06		
0.03	0.01		
0.14	0.18		
0.15	0.00		
0.12	0.01		
0.06	0.05		
0.05	0.04		
0.45	0.04		
0.14	0.08		
0.08	0.09		
0.10	0.07		
0.04	0.01		
0.16	0.09		
0.20	0.15		
0.68	0.09		
0.23	0.05		
0.01	0.13		
0.03	0.06		
0.06	0.20		
0.23	0.03		
0.16	0.01		
0.09	0.10		
0.03	0.08		
0.08	0.06		
0.03	0.09		
0.19	0.06		
0.24	0.19		
0.01	0.18		
0.18	0.01		
0.11	0.07		
0.06	0.08		
0.16	0.08		
0.02	0.08		
0.07	0.12		
0.03	0.05		
0.15	0.14		
0.00	0.09		
0.07	0.07		
0.05	0.03		
0.03	0.10		
0.11	0.14		
0.21	0.12		
0.01	0.17		
0.16	0.14		
0.04	0.07		
0.01	0.07		
0.17	0.10		

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.73	0.61
1.93	1.58
31.77	25.72
1.16	0.92
0.80	0.63
1.66	1.31
1.55	1.21
3.85	2.99
1.57	1.22
1.40	1.07
3.75	2.86
27.61	20.98
1.14	0.87
1.35	1.02
0.94	0.71
0.97	0.73
1.48	1.10
1.08	0.81
13.20	9.82
1.08	0.80
2.03	1.49
2.07	1.51
1.44	1.02
1.16	0.83
0.93	0.66
1.45	1.02
17.85	12.50
1.57	1.09
1.10	0.75
3.01	2.05
16.82	11.31
1.43	0.96
1.66	1.11
1.28	0.85
4.56	2.97
11.23	7.28
1.58	1.02
9.46	6.06
1.37	0.87
2.92	1.86
1.14	0.72
1.33	0.83
1.01	0.63
1.25	0.78
1.90	1.18
2.41	1.49
1.26	0.78
1.01	0.61
1.55	0.93
1.78	1.07
1.36	0.81
1.41	0.84
2.34	1.39
6.67	3.95
1.93	1.14
2.47	1.45
2.17	1110

Antibody Array Assay Results	Assay Data
Explorer Antibody Array	
	Median Sianal 128 83

	Fold Change between Samples		Average Signal of Replicate Spots	
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
Amyloid A4 Protein Precursor	0.58	Amyloid A4 Protein Precursor	214	80
PHAS-I	0.58	PHAS-I	420	157
Lck (p56lck)	0.57	Lck (p56lck)	270	101
CIDE-B	0.57	CIDE-B	321	120
ARC	0.57	ARC	380	142
Nck	0.57	Nck	208	77
p73	0.56	p73	420	153
FLIP	0.56	FLIP	218	79
FADD (FAS-Associated death domain-con	0.55	FADD (FAS-Associated death domain-containing Prote	188	67
Cyclin D1	0.55	Cyclin D1	244	87
p57Kip2 Ab-7	0.54	p57Kip2 Ab-7	309	109
CDC47	0.54	CDC47	279	98
Flt-1 / VEGFR1	0.54	Flt-1 / VEGFR1	230	81
GAD65	0.54	GAD65	272	95
Catenin beta	0.54	Catenin beta	178	62
Mek1	0.54	Mek1	241	84
H.Pylori	0.53	H.Pylori	185	64
p14ARF	0.53	p14ARF	167	58
Cadherin, (Pan)	0.53	Cadherin, (Pan)	231	80
Nitric Oxide Synthase, endothelial (eNOS	0.53	Nitric Oxide Synthase, endothelial (eNOS)	276	95
Stat3	0.53	Stat3	226	78
Stat5b	0.53	Stat5b	172	59
RAIDD	0.52	RAIDD	224	76
DNA Primase (p49)	0.52	DNA Primase (p49)	195	66
p19Skp1	0.52	p19Skp1	207	70
Stat5a	0.51	Stat5a	225	75
TRADD	0.51	TRADD	225	75
NOS-u	0.51	NOS-u	354 210	118 69
DNA Primase (p58)	0.51 0.51	DNA Primase (p58)	265	87
PDGFR, alpha	0.50	PDGFR, alpha	257	84
p18INK4c DFF40 (DNA Fragmentation Factor 40) / 0	0.50	p18INK4c DFF40 (DNA Fragmentation Factor 40) / CAD	257	84
c-Src	0.50	c-Src	233	76
PARP	0.50	PARP	231	75
Endostatin	0.49	Endostatin	174	56
Cullin-1 (CUL-1)	0.49	Cullin-1 (CUL-1)	160	51
PARP (Poly ADP-Ribose Polymerase)	0.49	PARP (Poly ADP-Ribose Polymerase)	314	99
XRCC2	0.48	XRCC2	211	66
MyD88	0.48	MyD88	218	68
Cdk3	0.44	Cdk3	357	103
MMP-23	0.44	MMP-23	301	86
Cullin-2 (CUL-2)	0.42	Cullin-2 (CUL-2)	213	58
Stat-1	0.42	Stat-1	414	112
CDC34	0.41	CDC34	254	68
BRCA2 (aa 1323-1346)	0.35	BRCA2 (aa 1323-1346)	275	62
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Coefficient of Variation for Replicate		
Bigger Sample	Smaller Sample	
0.31	0.12	
0.20	0.05	
0.19	0.11	
0.44	0.29	
0.34	0.16	
0.15	0.01	
0.38	0.13	
0.43	0.12	
0.34	0.14	
0.13	0.17	
0.31	0.08	
0.32	0.01	
0.18	0.17	
0.32	0.18	
0.03	0.00	
0.06	0.03	
0.38	0.20	
0.37	0.01	
0.24	0.13	
0.45	0.16	
0.59	0.05	
0.06	0.06	
0.40	0.11	
0.06	0.04	
0.27	0.04	
0.27	0.02	
0.19	0.13	
0.08	0.04	
0.08	0.06	
0.17	0.03	
0.07	0.03	
0.11	0.17	
0.29	0.10	
0.06	0.02	
0.09	0.01	
0.30	0.04	
0.48	0.20	
0.25	0.06	
0.10	0.10	
0.37	0.08	
0.15	0.11	
0.48	0.02	
0.20	0.14	
0.41	0.03	
0.31	0.07	

Data Normalized	to Median Signal
	Smaller Sample
1.67	0.96
3.28	1.89
2.11	1.21
2.51	1.44
2.97	1.70
1.63	0.92
3.28	1.84
1.70	0.95
1.47	0.80
1.91	1.04
2.41	1.31
2.18	1.18
1.80	0.97
2.13	1.14
1.39	0.75
1.88	1.01
1.44	0.77
1.30	0.69
1.81	0.96
2.16	1.14
1.77	0.93
1.34	0.70
1.75	0.92
1.52	0.80
1.62	0.84
1.76	0.90
1.76	0.90
2.77	1.42
1.64	0.83
2.07	1.05
2.01	1.01
2.02	1.01
1.82	0.91
1.81	0.90
1.36	0.67
1.25	0.61
2.46	1.19
1.65	0.80
1.70	0.82
2.79	1.23
2.35	1.03
1.67	0.70
3.24	1.35
1.99	0.81
2.15	0.75

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Min	1.33
Max	4.59
Mean	1.55

## Appendix E<br/>Signaling

Antibody Array Assay Results	Assay Data
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Durantin Line	Fold Change between Samples	Parada tita	Average Signal of Replicate Spots	
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
Tubulin alpha	4.41	Tubulin alpha	2453	8594
BAD	2.15	BAD	1315	2247
GAD1	1.91	GAD1	1756	2666
MAP4K4	1.88	MAP4K4	849	1268
p42 MAPK	1.87	p42 MAPK	5165	7674
Caveolin-1	1.73	Caveolin-1	2848	3910
CDH9	1.67	CDH9	4784	6330
TNFA	1.63	TNFA	2503	3249
SND1/P100	1.63	SND1/P100	2801	3633
CA 15-3	1.58	CA 15-3	516	648
Keratin 15	1.58	Keratin 15	2304	2884
NYREN18	1.57	NYREN18	203	253
SP3/4	1.57	SP3/4	1299	1622
KCNMB2	1.56	KCNMB2	4242	5261
CDH24	1.55	CDH24	9045	11150
CEA	1.55	CEA	328	403
CMC1	1.53	CMC1	1311	1596
Retinoic Acid Receptor beta	1.53	Retinoic Acid Receptor beta	1367	1662
Claudin 5	1.53	Claudin 5	5219	6339
Cytochrome b561 D1	1.52	Cytochrome b561 D1	17291	20861
MMP-10	1.52	MMP-10	2050	2468
mGluR2/3	1.51	mGluR2/3	2648	3184
IgG	1.51	lgG	53652	64397
GRB14	1.51	GRB14	13254	15852
GRTP1	1.50	GRTP1	1155	1372
mGluR4	1.49	mGluR4	1387	1637
Actin-alpha-1	1.47	Actin-alpha-1	10264	11984
STAT3	1.47	STAT3	263	307
LPA	1.47	LPA	267	311
GAD1/2	1.46	GAD1/2	2230	2578
TNF Receptor II	1.45	TNF Receptor II	1461	1680
inos	1.44	iNOS	1275	1456
RIT1	1.43	RIT1	1861	2117
Actin-gamma2	1.43	Actin-gamma2	839	954
KIF4A	1.42	KIF4A	1486	1675
ARSI	1.41	ARSI	7206	8095
Desmin	1.41	Desmin	13560	15175
Beta-Actin	1.40	Beta-Actin	2110	2342
UBR1	1.40	UBR1	1665	1847
Thrombin Receptor	1.39	Thrombin Receptor	2550	2825
CD40	1.39	CD40	785	870
TP53INP1	1.39	TP53INP1	2418	2664
AKT2	1.39	AKT2	188	207
CDYL2	1.38	CDYL2	1128	1238
MAGE-1	1.38	MAGE-1	1021	1118
BCL-10	1.37	BCL-10	765	834
ABCD1	1.37	ABCD1	3413	3719
PIP5K1C	1.37	PIP5K1C	647	704
Heregulin	1.37	Heregulin	396	430
HDAC5	1.37	HDAC5	567	616
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Coefficient of Variation for Replicates		
	Smaller Sample	
0.04	0.47	
0.21	0.50	
0.13	0.04	
0.45	0.01	
0.41	0.32	
0.08	0.25	
0.58	0.75	
0.01	0.06	
0.01	0.17	
0.27	0.02	
0.01	0.04	
0.41	0.08	
0.15	0.01	
0.05	0.04	
0.08	0.12	
0.05	0.08	
0.06	0.04	
0.01	0.05	
0.00	0.12	
0.04	0.06	
0.04	0.08	
0.07	0.05	
0.10	0.02	
0.05	0.02	
0.05	0.01	
0.07	0.10	
0.09	0.05	
0.41	0.22	
0.05	0.04	
0.05	0.03	
0.08	0.07	
0.14	0.08	
0.13	0.10	
0.07	0.10	
0.09	0.08	
0.03	0.16	
0.26	0.42	
0.05	0.06	
0.03	0.05	
0.07	0.02	
0.02	0.00	
0.08	0.13	
0.16	0.11	
0.05	0.01	
0.05	0.11	
0.20	0.20	
0.08	0.07	
0.03	0.03	
0.13	0.12	
0.13	0.11	

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
8.67	38.24
4.65	10.00
6.20	11.86
3.00	5.64
18.25	34.14
10.06	17.39
16.90	28.16
8.84	14.46
9.90	16.16
1.82	2.88
8.14	12.83
0.72	1.13
4.59	7.22
14.99	23.41
31.96	49.61
1.16	1.79
4.63	7.10
4.83	7.39
18.44	28.20
61.10	92.82
7.24	10.98
9.36	14.16
189.58	286.53
46.83	70.53
4.08	6.10
4.90	7.28
36.27	53.32
0.93	1.36
0.94	1.38
7.88	11.47
5.16	7.47
4.50	6.48
6.57	9.42
2.96	4.24
5.25	7.45
25.46	36.02
47.92	67.52
7.46	10.42
5.88	8.22
9.01	12.57
2.77	3.87
8.54	11.85
0.66	0.92
3.99	5.51
3.61	4.97
2.70	3.71
12.06	16.55
2.28	3.13
1.40	1.91
2.00	2.74

Antibody Array Assay Results	<b>Assay Data</b>
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Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
i iotem List	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
RCBTB1	1.36	RCBTB1	1117	1209
Claudin 3	1.36	Claudin 3	2312	2495
HSP105	1.35	HSP105	857	918
GLUT1	1.35	GLUT1	1375	1473
ACTR-1C	1.34	ACTR-1C	1701	1811
VEGFB	1.34	VEGFB	1088	1155
MYLIP	1.34	MYLIP	2509	2663
GADD45 beta	1.33	GADD45 beta	1310	1388
MTA1	1.33	MTA1	940	994
ARC	1.33	ARC	5210	5498
ARFIP1	1.32	ARFIP1	6420	6754
CSF2 (GM-CSF)	1.32	CSF2 (GM-CSF)	265	278
BAGE2	1.32	BAGE2	773	810
ORAV1	1.32	ORAV1	2248	2353
GRP75	1.31	GRP75	275	287
GPRIN2	1.31	GPRIN2	1367	1424
Thyroid Hormone Receptor alpha	1.31	Thyroid Hormone Receptor alpha	526	547
DP-1	1.31	DP-1	1807	1877
GNPAT	1.31	GNPAT	1053	1092
CDK7	1.30	CDK7	314	325
Actin-pan	1.30	Actin-pan	3203	3312
Angiopoietin-2	1.30	Angiopoietin-2	116	120
CAGE1	1.30	CAGE1	187	192
Galectin 3	1.30	Galectin 3	673	692
HSP90A	1.29	HSP90A	9403	9642
MMP-9	1.29	MMP-9	198	203
Testosterone	1.29	Testosterone	63928	65535
кітн	1.29	KITH	184	189
FGFR1 Oncogene Partner	1.29	FGFR1 Oncogene Partner	441	452
lk3-2	1.29	lk3-2	364	372
SRPK1	1.28	SRPK1	622	634
Lamin A (Cleaved-Asp230)	1.28	Lamin A (Cleaved-Asp230)	960	978
CREB-BP	1.28	CREB-BP	641	650
KCNJ2	1.27	KCNJ2	411	416
CATD (heavy chain,Cleaved-Leu169)	1.27	CATD (heavy chain,Cleaved-Leu169)	2159	2184
IP3KC	1.27	IP3KC	1023	1033
CD80	1.27	CD80	1448	1462
COX1	1.27	COX1	1366	1379
MASP1 (heavy chain, Cleaved-Arg448)	1.27	MASP1 (heavy chain,Cleaved-Arg448)	330	333
Collagen alpha1 XVIII	1.27	Collagen alpha1 XVIII	1610	1623
TGF beta Receptor III	1.26	TGF beta Receptor III	496	498
RAB11FIP4	1.26	RAB11FIP4	1126	1130
Catenin-alpha1	1.26	Catenin-alpha1	756	759
Pax-5	1.26	Pax-5	2647	2658
Patched	1.26	Patched	2038	2046
UBE1L	1.26	UBE1L	442	442
INSL4	1.26	INSL4	265	265
REN	1.26	REN	1108	1107
	1.26			†
MAP3K10	1.26	MAP3K10	208	207
PLD4	1.26	PLD4	395	394

	ation for Replicates
Bigger Sample	Smaller Sample
0.11	0.04
0.07	0.04
0.08	0.03
0.04	0.10
0.11	0.28
0.11	0.18
0.15	0.12
0.10	0.10
0.08	0.09
0.06	0.05
0.14	0.01
0.08	0.36
0.06	0.22
0.03	0.04
0.15	0.22
0.08	0.05
0.07	0.05
0.01	0.06
0.10	0.26
0.03	0.06
0.05	0.03
0.26	0.05
0.00	0.01
0.01	0.06
0.28	0.11
0.10	0.08
0.04	0.00
0.10	0.06
0.07	0.08
0.00	0.05
0.07	0.08
0.01	0.08
0.02	0.28
0.07	0.01
0.07	0.21
0.11	0.00
0.12	0.02
0.01	0.03
0.04	0.01
0.01	0.09
0.01	0.14
0.12	0.04
0.10	0.04
0.06	0.15
0.02	0.07
0.16	0.07
0.03	0.12
0.05	0.01
0.09	0.02
0.02	0.06

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
3.95	5.38
8.17	11.10
3.03	4.08
4.86	6.55
6.01	8.06
3.84	5.14
8.87	11.85
4.63	6.18
3.32	4.42
18.41	24.46
22.69	30.05
0.93	1.23
2.73	3.60
7.94	10.47
0.97	1.28
4.83	6.34
1.86	2.43
6.38	8.35
3.72	4.86
1.11	1.45
11.32	14.74
0.41	0.53
0.66	0.85
2.38	3.08
33.23	42.90
0.70	0.90
225.89	291.59
0.65	0.84
1.56	2.01
1.29	1.65
2.20	2.82
3.39	4.35
2.26	2.89
1.45	1.85
7.63	9.72
3.61	4.60
5.11	6.50
4.83	6.13
1.16	1.48
5.69	7.22
1.75	2.21
3.98	5.03
2.67	3.38
9.35	11.82
7.20	9.10
1.56	1.97
0.93	1.18
3.91	4.92
0.73	0.92
1.39	1.75
1.33	1./3

Antibody Array Assay Results	Assay Data
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	Fold Change between Samples	- Treatan signal	Average Signal of Replicate Spots	
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
Catenin-beta 1	1.25	Catenin-beta 1	242	241
MAPK 11	1.25	MAPK 11	5705	5669
NFYC	1.25	NFYC	835	829
C-Kit	1.25	C-Kit	575	570
KCNA1	1.25	KCNA1	668	661
TUBGCP3	1.24	TUBGCP3	631	624
AIRE	1.24	AIRE	736	725
Tubulin beta	1.24	Tubulin beta	474	465
SLC27A5	1.23	SLC27A5	370	363
XRCC6	1.23	XRCC6	247	242
TGF beta2	1.23	TGF beta2	443	433
	1.23	SERPINB9	199	195
SERPINB9		MAT1	461	450
MAT1	1.23 1.23	TRXR2	702	
TRXR2				685
Tubulin gamma	1.23	Tubulin gamma	454	442
EMR3	1.23	EMR3	1221	1189
MAP3K4	1.23	MAP3K4	188	183
ACAD10	1.23	ACAD10	317	308
Notch 1 (Cleaved-Val1754)	1.23	Notch 1 (Cleaved-Val1754)	408	397
FAS	1.22	FAS	306	297
APC6	1.22	APC6	410	399
p73	1.22	p73	327	317
NKX3.1	1.22	NKX3.1	419	405
GAS6	1.22	GAS6	371	359
NCoR1	1.22	NCoR1	288	279
14-3-3 theta	1.22	14-3-3 theta	398	384
IgA	1.21	IgA	1040	1003
Survivin	1.21	Survivin	169	163
NM23	1.21	NM23	600	578
CD302	1.21	CD302	337	324
GPR151	1.21	GPR151	2754	2651
TIMP3	1.21	TIMP3	261	251
CSF-1 (MCSF)	1.21	CSF-1 (MCSF)	180	173
GFR alpha-1	1.21	GFR alpha-1	221	212
IRF4	1.21	IRF4	312	299
CIDEB	1.21	CIDEB	351	336
TIMP4	1.20	TIMP4	254	243
PLK5	1.20	PLK5	655	627
Tyrosinase	1.20	Tyrosinase	207	198
JAB1	1.20	JAB1	387	370
TUBGCP6	1.20	TUBGCP6	371	354
SLC27A4	1.20	SLC27A4	203	194
ADCK2	1.20	ADCK2	661	630
Fibronectin	1.20	Fibronectin	964	918
FAS ligand	1.20	FAS ligand	533	508
Histone H2B (Acetyl-Lys15)	1.20	Histone H2B (Acetyl-Lys15)	209	199
FGF22	1.20	FGF22	1111	1058
IKB alpha	1.20	IKB alpha	770	731
SLC6A16	1.20	SLC6A16	698	662
СНКВ	1.19	СНКВ	302	287
Cytochrome P450 2B6	1.19	Cytochrome P450 2B6	778	738
PKCB1	1.19	PKCB1	399	378
GRP78	1.19	GRP78	520	493
Mammaglobin	1.19	Mammaglobin	245	232
NCK2	1.19	NCK2	290	275
L-:	1,1,0			

Coefficient of Varia	ation for Replicates
Bigger Sample	Smaller Sample
0.06	0.16
0.05	0.07
0.02	0.00
0.05	0.05
0.06	0.00
0.17	0.02
0.03	0.08
0.08	0.18
0.05	0.01
0.17	0.08
0.03	0.02
0.06	0.03
0.06	0.08
0.07	0.06
0.02	0.08
0.03	0.10
0.04	0.06
0.06	0.19
0.05	0.01
0.12	0.03
0.01	0.09
0.09	0.12
0.06	0.02
0.06	0.01
0.16	0.13
0.03	0.05
0.42	0.44
0.01	0.06
0.02	0.00
0.01	0.03
0.07	0.07
0.06	0.17
0.06	0.05
0.04	0.16
0.11	0.04
0.02	0.07
0.08	0.08
0.01	0.11
0.00	0.10
0.12	0.10
0.01	0.09
0.03	0.05
0.03	0.12
0.14	0.12
0.06	0.10
0.04	0.14
0.11	0.14
0.14	0.08
0.06	0.08
0.25	0.09
0.09	0.17
0.09	0.01
0.11	0.21
0.06	0.09
0.03	0.11

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.85	1.07
20.16	25.22
2.95	3.69
2.03	2.53
2.36	2.94
2.23	2.77
2.60	3.23
1.67	2.07
1.31	1.61
0.87	1.07
1.56	1.92
0.70	0.87
1.63	2.00
2.48	3.05
1.60	1.97
4.31	5.29
0.66	0.81
1.12	1.37
1.44	1.77
1.08	1.32
1.45	1.77
1.16	1.41
1.48	1.80
1.31	1.60
1.02	1.24
1.40	1.71
3.67	4.46
0.60	0.72
2.12	2.57
1.19	1.44
9.73	11.80
0.92	1.11
0.63	0.77
0.78	0.94
1.10	1.33
1.24	1.49
0.90	1.08
2.31	2.79
0.73	0.88
1.37	1.64
1.31	1.57
0.72	0.86
2.34	2.80
3.40	4.08
1.88	2.26
0.74	0.88
3.93	4.71
2.72	3.25
2.46	2.95
1.07	1.27
2.75	3.28
1.41	1.68
1.84	2.19
0.87	1.03
1.02	1.22

Antibody Array Assay Results	Assay Data
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Manufact   1.99	Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
F6F82         1.19         F6F82         278         263           molhide         1.19         molhide         2.20         236           Kerain 5         1.19         Rectain 5         2.28         2.28         1.59           PSA-ACT         1.28         1.92         1.92         Numan Albumin         5646         3.317           DMOKOH         1.19         Mode Molh         7.29         6.87           TL22         1.19         TL2         2.29         2.81           NSE         1.18         NSE         2.70         2.54           SEPP2         1.18         SEMP2         388         365           Firellin-1         1.18         Firellin-1         32.7         308           Synuclein gamma         1.18         GEB         1.18         400         376           GB3         1.18         Qual mark         400         376         182           Bar         1.18         Res         751         705           TMP1         1.18         Res         751         705           RMA (michin alpha)         1.18         Res         751         705           SWY         1.18         Res		Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
mGUING         1.19         MGUING         250         236           PSA-ACT         1.19         PSA-ACT         628         3.92           DMGDH         1.19         PSA-ACT         628         3.92           DMGDH         1.19         DMGDH         7.29         687           DMGDH         1.19         DMGDH         7.29         687           TL2         1.11         DMGDH         7.29         2.81           NSE         1.118         NSE         2.70         2.94           SEWP2         1.118         NSE         2.70         2.94           Florilla-1         1.118         NSE         3.27         3.08           Florilla-1         1.118         NSY Under garma         4.00         3.75           GB3         1.118         NSY Under garma         4.00         3.75           GB3         1.118         RSE         1.75         1.705           GB3         1.118         NSY Under garma         4.00         1.75           GB3         1.118         NS Yes         1.18         1.01         1.02           GB3         1.118         NS Yes         1.08         1.17           YSK<	Claudin 2	1.19	Claudin 2	516	488
Keratin 5         1.19         Keratin 5         285         269           PSA ACT         1.19         PSA ACT         6.28         592           human Alburin         1.19         human Alburin         566         1.5317           MAGOH         1.19         human Alburin         566         1.5317           TL2         1.19         HL2         2.90         2.24           SEW         1.18         MSS         2.70         1.24           SEW2         1.18         MSS         2.70         1.24           SEW2         1.18         MSS         2.70         1.24           SEW2         1.18         MSS         3.83         3.65           SFW2         1.18         MSS         3.27         3.08           Synuclei gamma         1.18         MSS         1.18 <td>FGFR2</td> <td>1.19</td> <td>FGFR2</td> <td>278</td> <td>263</td>	FGFR2	1.19	FGFR2	278	263
PSA-ACT	mGluR6	1.19	mGluR6	250	236
human Albumin         5-646         3.317           DMGOH         1.19         boMOPH         729         687           TLZ         1.19         boMOPH         729         687           TLZ         1.18         NS         270         2.24           SER         1.18         NS         270         2.24           SFNPZ         1.18         SEMPZ         388         365           Fellin-1         1.18         Fellin-1         327         308           Synuclein gamma         1.18         Fellin-1         327         308           Synuclein gamma         1.18         Fellin-1         1.26         370           Sw         1.18         GES         1.18	Keratin 5	1.19	Keratin 5	285	269
DMGDH	PSA-ACT	1.19	PSA-ACT	628	592
TLE2  SE 1.18  SE 1.18  SE 270  254  SENP2  1.18  SENP2  1.18  SENP2  1.18  SENP2  1.18  SENP2  3.88  3.55  SEMINITAL  SEMINITAL  1.18  SEMINITAL  SEMINIT	human Albumin	1.19	human Albumin	5646	5317
SEE	DMGDH	1.19	DMGDH	729	687
SENP2         1.18         SENP2         3.88         365           Firefillin-1         1.18         Firefillin-1         2.37         308           Synuclein gamma         1.18         Synuclein gamma         400         3.76           CIES         1.18         OSA         1.194         1.18           CIES         1.18         DNA         1.751         1.75           CIES         1.18         DNA         1.751         1.75           TIMP1         1.18         TIMP1         742         696           TIMP1         1.18         TIMP1         742         696           TIMP1         1.18         TIMP1         742         696           SYK         1.18         SYK         355         333           GIBP2         1.18         GIFIP2         2.13         199           mGluB8         1.18         McGHP2         2.21         199           MCLOM         1.18         McCMA         2.25         2.21           CLIP1         1.17         CLIP1         1.264         1180           WECCS         1.17         CLIP1         1.264         1180           GUID3         1.17         <	TLE2	1.19	TLE2	299	281
Fibrillin-1   1.18	NSE	1.18	NSE	270	254
Synuclein gamma	SENP2	1.18	SENP2	388	365
CB3	Fibrillin-1	1.18	Fibrillin-1	327	308
Bax         1.18         Bax         751         705           TIMP1         1.18         TMP1         742         696           INHA (Inhibin alpha)         1.68         1.57           SYK         3.35         333         199           IGFBP2         1.18         INFA (Inhibin alpha)         168         1.57           SYK         3.35         333         199           mGluR8         1.18         mGluR8         301         281           ALCAM         1.18         ALCAM         225         210           CUP1         1.17         CUP1         11264         1180           SRCCS         1.17         QuP1         1264         1180           SRCS S         1.17         QuIln 2         791         737           GUT3         1.17         QuIln 2         791         737           GUT3         1.17         QuIln 2         791         737           RAB3GAP2         1.17         ARB3GAP2         2.16         201           MMP-11         1.17         MM-11         494         460           Polactin         1.17         CDM6         837         778           CLNG </td <td>Synuclein gamma</td> <td>1.18</td> <td>Synuclein gamma</td> <td>400</td> <td>376</td>	Synuclein gamma	1.18	Synuclein gamma	400	376
TIMP1         1.18         TIMP1         742         696           NHA (Inhibin alpha)         1.18         INHA (Inhibin alpha)         1.68         157           SYK         1.18         INHA (Inhibin alpha)         1.68         157           SYK         335         333         333           GFBP2         1.18         IIGHA         301         281           MISSAR         1.18         IIGHAR         301         281           ALCAM         1.18         ALCAM         225         210           CUP1         1.17         CUP1         1264         1180           XECC5         1.17         CUP1         1264         1180           XECC5         1.17         CURC5         287         288           Cullin 2         1.17         CURC5         287         288           Cullin 2         1.17         CURC5         287         288           Cullin 2         1.17         RAC5         287         288           Cullin 2         1.17         RAC5         287         288           Cullin 2         1.17         RAC5         287         288           Cullin 2         1.17         MPOBATI		1.18		194	182
NHA (Inhibin alpha)	Bax	1.18	Bax	751	705
SYK         1.18         SYK         355         333           GGFB2         1.18         GFBP2         213         199           mGIuR8         1.18         mGIuR8         301         281           ALCAM         1.18         ALCAM         225         210           CUP1         1.17         CUP1         1264         1180           KRCC5         1.17         XRCC5         287         268           CUII012         1.17         CUII02         791         737           GLIT3         1.17         GLUT3         290         270           GLIT3         1.17         MMP-11         494         460           MMP-11         1.17         MMP-11         494         460           Prolactin         1.17         PROBATION         837         778           CLTROB         1.17         CLDN6         837         778           CATROB         1.17         CNTROB         837         778           CATROB         1.17         CNTROB         253         235           STC         1.17         POTASSUM Channel Kv3.2b         644         598           STS         1.17         POTASSUM Cha	TIMP1	1.18	TIMP1	742	696
International Content   Inte	INHA (Inhibin alpha)	1.18	INHA (Inhibin alpha)	168	157
mGluRB         1.18         mGluRB         301         281           ALCAM         1.18         ALCAM         225         210           CUP1         1.17         CUP1         1264         1180           XRCC5         1.17         XRCC5         287         268           Cullin 2         791         737         737           GLUT3         1.17         GLUT3         290         270           XABSGAP2         1.17         MMP-11         494         460           WMP-11         1.17         MMP-11         494         460           Prolactin         1.17         CUTROB         837         778           CNTROB         1.17         CNTROB         837         778           CNTROB         1.17         XRCC3         316         294           POtassium Channel Kv3.2b         644         598         253         235           XRCC3         1.17         XRCC3         316         294           POtassium Channel Kv3.2b         644         598         265           STS         1.17         POTASSIUM Channel Kv3.2b         644         598           STS         1.17         POTASSIUM Channel Kv3.	SYK	1.18	SYK	355	333
ALCAM  1.18	IGFBP2	1.18	IGFBP2	213	199
CUP1         1.17         CUP1         1264         1180           XRCCS         1.17         XRCCS         287         268           Culin 2         1.17         Culin 2         791         737           GLUT3         1.17         GLUT3         290         270           RAB3GAP2         1.17         RAB3GAP2         1216         201           MMP-11         4.94         460         460           Prolactin         1.17         Prolactin         2.99         278           CLDM6         1.17         CLDM6         837         778           CNTROB         1.17         CLDM6         837         778           CNTROB         1.17         CNTROB         253         235           RXCC3         316         294         294           Potassium Channel Kv3.2b         644         598         55           STS         1.17         Potassium Channel Kv3.2b         644         598           STS         1.17         POTAS         333         309           TFS3111         1.17         TS31         341         317           POGFB         1.17         PDGFB         333         309	mGluR8	1.18	mGluR8	301	281
RRCCS         1.17         XRCCS         287         268           Cullin 2         1.17         Cullin 2         791         737           GLUT3         2.90         270         RAB3GAP2         216         201           RAB3GAP2         1.17         RAB3GAP2         216         201           MMP-11         494         460         460           Prolactin         299         278           CLDM6         1.17         CLDM6         837         778           CLDM6         1.17         CLDM6         837         778           CLDM6         1.17         CLDM6         837         778           CLDM6         1.17         XRCC3         316         294           Potassium Channel Kv3.2b         1.17         Potassium Channel Kv3.2b         644         598           ST5         1.17         Potassium Channel Kv3.2b         644         598           TS5	ALCAM	1.18	ALCAM	225	210
Cullin 2         1.17         Cullin 2         791         737           GUT3         1.17         GUT3         290         270           RAB3GAP2         1.17         RAB3GAP2         216         201           MMP-11         1.17         MMP-11         494         460           Prolactin         1.17         Prolactin         299         278           CLDM6         1.17         CLDM6         837         778           CNTROB         1.17         CNTROB         253         235           XRCC3         1.17         XRCC3         316         294           Potassium Channel Kv3.2b         1.17         Potassium Channel Kv3.2b         644         598           STS         1.17         Potassium Channel Kv3.2b	CLIP1	1.17	CLIP1	1264	1180
GLUT3         1.17         GLUT3         290         270           RAB3GAP2         1.17         RAB3GAP2         216         201           MMP-11         1.17         MMP-11         494         460           Probactin         1.17         MMP-11         494         460           Probactin         1.17         CLDN6         299         278           CLDN6         1.17         CLDN6         837         778           CLTROB         253         235         235           XRC3         316         294         294           Potassium Channel Kv3.2b         1.17         RSC3         316         294           Potassium Channel Kv3.2b         1.17         Potassium Channel Kv3.2b         644         598           ST5         1.17         Potassium Channel Kv3.2b         644         1.34           P06FB         1.17         Potassium Channel Kv3.2b         644         313 </td <td>XRCC5</td> <td>1.17</td> <td>XRCC5</td> <td>287</td> <td>268</td>	XRCC5	1.17	XRCC5	287	268
RABSGAP2         1.17         RABSGAP2         216         201           MMP-11         1.17         MMP-11         494         460           Prolactin         299         278           CLDN6         1.17         CLDN6         837         778           CLTROB         1.17         CNTROB         253         235           XRCC3         316         294         494           Potassium Channel Kv3.2b         1.17         RKCC3         316         294           Potassium Channel Kv3.2b         1.17         STS         286         265           TSS311         1.17         FPS3111         341         317           PDGFB         1.17         PDGFB         333         309           EFNA3         1.17         EFNA3         745         691           MH3         1.17         MH3         275         255           CD37         1.17         CD37         1388         1287           TMF Receptor I         1.17         TNF Receptor I         253         234           ADCKS         1.17         ADCKS         195         181           GAS1         1.16         WNT 108         138	Cullin 2	1.17	Cullin 2	791	737
MMP-11         1.17         MMP-11         494         460           Prolactin         1.17         Prolactin         299         278           CLDN6         1.17         CLDN6         837         778           CNTROB         1.17         CNTROB         253         235           XRCC3         1.17         XRCC3         316         294           Potassium Channel Kv3.2b         1.17         PROTASSIUM Channel Kv3.2b         644         598           ST5         1.17         PST         286         265         265           TP5311         1.17         TP5311         341         317           PDGFB         1.17         PD6FB         333         309           EFNA3         1.17         EFNA3         745         691           MLH3         1.17         CD37         1388         1287           TNF Receptor I         1.17         CD37         1388         1287           TNF Receptor I         1.17         ADCK5         195         181           GAS1         1.17         GAS1         443         410           MMY         1.16         MMY         326         301           WNT 1	GLUT3	1.17	GLUT3	290	270
Prolactin         1.17         Prolactin         299         278           CLDN6         1.17         CLDN6         837         778           CNTROB         1.17         CNTROB         253         235           XRCC3         1.17         XRCC3         316         294           Potassium Channel Kv3.2b         1.17         Potassium Channel Kv3.2b         644         598           ST5         1.17         PST         286         265           TP53111         1.17         PD67B         331         309           EFNA3         1.17         PD67B         333         309           EFNA3         1.17         MH3         745         691           MH3         1.17         MH3         275         255           C037         1.17         MH3         275         255           C037         1.17         ADCK5         195         181           GAS1         1.17         ADCK5         195         181           GAS1         1.17         ADCK5         195         181           GAS1         1.16         WN 10B         138         128           WWT 10B         1.16         WN 10B<	RAB3GAP2	1.17	RAB3GAP2	216	201
CLDN6         1.17         CLDN6         837         778           CNTROB         1.17         CNTROB         253         235           NRCC3         1.17         RRCC3         316         294           Potassium Channel Kv3.2b         1.17         Potassium Channel Kv3.2b         644         598           STS         1.17         PSTS         286         265           TP53111         1.17         PD6FB         333         309           EFNA3         1.17         PD6FB         333         309           EFNA3         1.17         MH3         275         255           CO37         1.17         MH3         275         255           TNF Receptor I         1.17         ADCK5         195         181           ADCKS         1.17         ADCK5         195         181           GAS1         1.17         ADCK5         195         181           IMM         1.16         JM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         1.16         ZP4         656         606           MMP-2         1.16         MP-2<	MMP-11	1.17	MMP-11	494	460
CNTROB         1.17         CNTROB         253         235           XRCC3         1.17         XRCC3         316         294           Potassium Channel Kv3.2b         644         598           ST5         1.17         Potassium Channel Kv3.2b         644         598           ST5         1.17         PS         286         265           TP53111         1.17         TP53111         341         317           PDGFB         1.17         PDGFB         333         309           EFNA3         1.17         EFNA3         745         691           MLH3         1.17         MH3         275         255           CD37         1.17         MH3         275         255           CD37         1.17         TNF Receptor I         253         234           ADCK5         1.17         ADCK5         195         181           GAS1         1.17         ADKC5         195         181           GAS1         1.17         ADKC5         195         318         128           GAS1         1.17         ADKC5         195         181         18         128           GAS1         1.17	Prolactin	1.17	Prolactin	299	278
XRCC3         1.17         XRCC3         316         294           Potassium Channel Kv3.2b         1.17         Potassium Channel Kv3.2b         644         598           STS         1.17         STS         286         265           TP53l11         1.17         TP53l11         341         317           PDGFB         1.17         PDGFB         333         309           EFNA3         1.17         EFNA3         745         691           MLH3         1.17         MH3         275         255           CD37         1.17         CD37         1388         1287           TNF Receptor I         1.17         TNF Receptor I         253         234           ADCKS         1.17         ADCKS         195         181           GAS1         1.17         GAS1         443         410           JMA         1.16         JM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         656         656         606           MMP-2         1.16         MMP-2         1154         1066           TUSCS         1.16         TKSPL	CLDN6	1.17	CLDN6	837	778
Potassium Channel Kv3.2b         1.17         Potassium Channel Kv3.2b         644         598           ST5         1.17         ST5         286         265           TP53I11         1.17         TP53I11         341         317           PDGFB         1.17         PDGFB         333         309           EFNA3         1.17         EFNA3         745         691           MLH3         1.17         MLH3         275         225           CD37         1.17         CD37         1388         1287           TNF Receptor I         1.17         TNF Receptor I         253         224           ADCKS         1.17         ADCKS         195         181           GAS1         1.17         GAS1         443         410           JM4         1.16         JM4         326         301           WNT 108         1.16         WNT 10B         138         128           ZP4         1.16         ZP4         656         606           MMP-2         1.16         MMP-2         1154         1066           TUSCS         1.16         GRK7         424         391           FKBPL         1.16	CNTROB	1.17	CNTROB	253	235
STS         1.17         STS         286         265           TPS3I11         1.17         TPS3I11         341         317           PDGFB         1.17         PDGFB         333         309           EFNA3         1.17         EFNA3         745         691           MLH3         1.17         MLH3         275         255           CD37         1388         1287           TNF Receptor I         253         234           ADCKS         1.17         ADCKS         195         181           GAS1         1.17         GAS1         443         440           JM4         326         301           WNT 108         1.16         WNT 10B         138         128           ZP4         1.16         WNT 10B         138         128           WMP-2         1.154         1066         MMP-2         1154         1066           TUSC5         1.16         MMP-2         1154         1066           GRK7         1.16         FKBPL         867         800           FKBPL         1.16         RASSF4         218         201           Catenin-gamma         1.16         Cateni	XRCC3	1.17	XRCC3	316	294
TP53	Potassium Channel Kv3.2b	1.17	Potassium Channel Kv3.2b	644	598
PDGFB         1.17         PDGFB         333         309           EFNA3         1.17         EFNA3         745         691           MLH3         1.17         MLH3         275         255           CD37         1388         1287           TNF Receptor I         1.17         TNF Receptor I         253         234           ADCKS         1.17         ADCKS         195         181           GAS1         1.17         GAS1         443         410           JM4         1.16         JM4         326         301           WNT 108         1.16         WNT 108         138         128           ZP4         1.16         ZP4         656         606           MMP-2         1.154         1066         170           TUSC5         1.16         MMP-2         1154         1066           TUSC5         1.16         GRK7         424         391           FKBPL         867         800         800           RASSF4         1.16         RASSF4         218         201           Catenin-gamma         1.09         1012         beta-2-Microglobulin         3715         3419	ST5	1.17	ST5	286	265
EFNA3         1.17         EFNA3         745         691           MLH3         1.17         MLH3         275         255           CD37         1.17         CD37         1388         1287           TNF Receptor I         1.17         TNF Receptor I         253         234           ADCK5         195         181           GAS1         443         410         413         410           JM4         1.16         JM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         656         606         606           MMP-2         1154         1066           TUSCS         1.16         MMP-2         1154         1066           TUSCS         1.16         GRK7         424         391         178           GRK7         1.16         FKBPL         867         800           RASSF4         1.16         RASSF4         218         201           Catenin-gamma         1.09         1012         218         201           Catenin-gamma         1.16         Catenin-gamma         1099         1012           beta-2-Microg	TP53I11	1.17	TP53I11	341	317
MLH3         1.17         MLH3         275         255           CD37         1.17         CD37         1388         1287           TNF Receptor I         253         234           ADCKS         1.17         ADCKS         195         181           GSS1         1.17         GAS1         443         410           JM4         1.16         JM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         1.16         WNT 10B         138         128           TUSCS         1.16         MMP-2         1154         1066           TUSCS         1.16         TUSCS         193         178           FKBPL         1.16         GRK7         424         391           FKBPL         867         800           RASSF4         218         201           Catenin-gamma         1.16         Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         ODH18         251         231           MMP-7         1.16         MMP-7         381         350	PDGFB	1.17	PDGFB	333	309
CD37         1.17         CD37         1388         1287           TNF Receptor I         253         234           ADCKS         1.17         ADCKS         195         181           GAS1         1.17         GAS1         443         410           JM4         1.16         JM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         1.16         WNT 10B         138         128           ZP4         656         606         606           MMP-2         1.154         1066         1056           TUSCS         1.16         TUSCS         193         178           FKBPL         1.16         FKBPL         867         800           RASSF4         218         201           Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         AOS1         406         374           MMP-7         381         350           GRP94         1.16         MMP-7         381         350	EFNA3	1.17	EFNA3	745	691
TNF Receptor I         1.17         TNF Receptor I         253         234           ADCKS         1.17         ADCKS         195         181           GAS1         1.17         GAS1         443         410           JM4         1.16         JM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         656         666         606           MMP-2         1154         1066         1066           TUSCS         1.16         MMP-2         1154         1066           TUSCS         1.16         GRK7         424         391         178           GRK7         1.16         GRK7         424         391         178           RASSF4         1.16         RASSF4         218         201           Catenin-gamma         1.09         1012         101           beta-2-Microglobulin         3715         3419           CDH18         251         231           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258	MLH3	1.17	MLH3	275	255
ADCKS 1.17 ADCKS 195 181  GAS1 1.17 GAS1 443 410  JM4 1.16 JM4 326 301  WNT 108 1.16 WNT 10B 138 128  ZP4 656 666  MMP-2 1.16 MMP-2 1154 1066  TUSCS 1.16 GRK7 424 391  FKBPL 1.16 FKBPL 867 800  RASSF4 1.16 RASSF4 218 201  Catenin-gamma 1.16 Catenin-gamma 1099 1012  beta-2-Microglobulin 1.16 CH18 251 231  ADS1 1.16 MMP-7 381 350  GRP94 1.16 MMP-7 381 350  GRP94 1.16 MMP-7 381 350  GRP94 281 281 258	CD37	1.17	CD37	1388	1287
GAS1         1.17         GAS1         443         410           JM4         1.16         JM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         656         666         606           MMP-2         1154         1066           TUSCS         1.16         TUSCS         193         178           GRK7         1.16         GRK7         424         391           FKBPL         867         800           RASSF4         218         201           Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           ASS1         1.16         MMP-7         381         350           GRP94         281         258         258	TNF Receptor I	1.17	TNF Receptor I	253	234
JIM4         1.16         JIM4         326         301           WNT 10B         1.16         WNT 10B         138         128           ZP4         656         656         606           MMP-2         1.154         1066           TUSCS         1.154         1066           GRK7         1.16         GRK7         424         391           FKBPL         1.16         FKBPL         867         800           RASSF4         1.16         RASSF4         218         201           Catenin-gamma         1.16         Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258	ADCK5	1.17	ADCK5	195	181
WNT 10B         1.16         WNT 10B         138         128           ZP4         1.16         ZP4         656         606           MMP-2         1.16         MMP-2         1154         1066           TUSCS         1.16         TUSCS         193         178           GRK7         424         391           FKBPL         867         800           RASSF4         218         201           Catenin-gamma         1.16         RASSF4         218         201           Catenin-gamma         1.099         1012         beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           AOS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258			GAS1		
ZP4         1.16         ZP4         656         606           MMP-2         1.16         MMP-2         1154         1066           TUSCS         1.16         TUSCS         193         178           GRK7         1.16         GRK7         424         391           FKBPL         867         800           RASSF4         218         201           Catenin-gamma         1.09         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           AOS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         281         258					
MMP-2     1.16     MMP-2     1154     1066       TUSCS     1.16     TUSCS     193     178       GRK7     1.16     GRK7     424     391       FKBPL     867     800       RASSF4     218     201       Catenin-gamma     1.09     1012       beta-2-Microglobulin     3715     3419       CDH18     1.16     CDH18     251     231       AOS1     406     374       MMP-7     1.16     MMP-7     381     350       GRP94     281     258		1.16		138	128
TUSCS         1.16         TUSCS         193         178           GRK7         1.16         GRK7         424         391           FKBPL         1.16         FKBPL         867         800           RASSF4         218         201         218         201           Catenin-gamma         1.06         Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           ASS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258					
GRK7         1.16         GRK7         424         391           FKBPL         1.16         FKBPL         867         800           RASSF4         218         201           Catenin-gamma         1.06         Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           AOS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258				1154	1066
FKBPL         1.16         FKBPL         867         800           RASSF4         1.16         RASSF4         218         201           Catenin-gamma         1.16         Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           AOS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258			TUSC5		
RASSF4         1.16         RASSF4         218         201           Catenin-gamma         1.16         Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           AOS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258	GRK7	1.16	GRK7	424	391
Catenin-gamma         1.16         Catenin-gamma         1099         1012           beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           AOS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258	FKBPL	1.16	FKBPL	867	800
beta-2-Microglobulin         1.16         beta-2-Microglobulin         3715         3419           CDH18         1.16         CDH18         251         231           AOS1         406         374           MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258					
CDH18     1.16     CDH18     251     231       AOS1     406     374       MMP-7     1.16     MMP-7     381     350       GRP94     1.16     GRP94     281     258					
AOS1     1.16     AOS1     406     374       MMP-7     1.16     MMP-7     381     350       GRP94     1.16     GRP94     281     258					
MMP-7         1.16         MMP-7         381         350           GRP94         1.16         GRP94         281         258					
GRP94 1.16 GRP94 281 258					
Myostatin 1.16 Myostatin 261 240					
	Myostatin	1.16	Myostatin	261	240

Coefficient of Varia	ation for Replicates		
Bigger Sample	Smaller Sample		
0.02	0.37		
0.09	0.05		
0.09	0.06		
0.08	0.08		
0.00	0.18		
0.27	0.28		
0.05	0.04		
0.16	0.26		
0.02	0.04		
0.01	0.01		
0.05	0.08		
0.01	0.01		
0.10	0.02		
0.09	0.06		
0.05	0.02		
0.07	0.18		
0.07	0.01		
0.14	0.05		
0.13	0.13		
0.06	0.06		
0.03	0.05		
0.10	0.07		
0.02	0.06		
0.06	0.07		
0.04	0.17		
0.00	0.12		
0.06	0.02		
0.02	0.01		
0.10	0.08		
0.11	0.07		
0.14	0.01		
0.02	0.02		
0.02	0.06		
0.00	0.03		
0.15	0.09		
0.14	0.03		
0.36	0.11		
0.06	0.06		
0.06	0.29		
0.02	0.04		
0.12	0.11		
0.04	0.08		
0.01	0.02		
0.09	0.07		
0.07	0.06		
0.07	0.02		
0.10	0.05		
0.03	0.14		
0.01	0.08		
0.07	0.15		
0.04	0.08		
0.02	0.03		
0.12	0.11		
0.03	0.09		
0.04	0.07		

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.82	2.17
0.98	1.17
0.88	1.05
1.01	1.19
2.22	2.63
19.95	23.66
2.58	3.05
1.05	1.25
0.95	1.13
1.37	1.62
1.16	1.37
1.41	1.67
0.69	0.81
2.65	3.13
2.62	3.09
0.59	0.70
1.25	1.48
0.75	0.89
1.06	1.25
0.79	0.93
4.47	5.25
1.01	1.19
2.80	3.28
1.02	1.20
0.76	0.89
1.75	2.04
1.05	1.23
2.96	3.46
0.89	1.05
1.12	1.31
2.27	2.66
1.01	1.18
1.20	1.41
1.17	1.37
2.63	3.07
0.97	1.13
4.90	5.72
0.89	1.04
0.69	0.80
1.57	1.82
1.15	1.34
0.49	0.57
2.32	2.69
4.08	4.74
0.68	0.79
1.50	1.74
3.06	3.56
0.77	0.89
3.88	4.50
13.13	15.21
0.89	1.03
1.43	1.66
1.34	1.56
0.99	1.15
0.92	1.07

Antibody Array Assay Results	Assa	y Data
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		iviealari Signal	283	223
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
Synaptophysin	1.16	Synaptophysin	267	245
KCNK17	1.16	KCNK17	490	450
USP30	1.16	USP30	173	159
RAB6C	1.16	RAB6C	195	179
SENP5	1.16	SENP5	237	217
TOP2B	1.16	TOP2B	255	234
MMP23 (Cleaved-Tyr79)	1.15	MMP23 (Cleaved-Tyr79)	2300	2109
RAB40B	1.15	RAB40B	403	370
FOXN4	1.15	FOXN4	304	279
HSPB2	1.15	HSPB2	262	240
Pirh2 (RCHY1)	1.15	Pirh2 (RCHY1)	154	141
Mammaglobin B	1.15	Mammaglobin B	484	443
TUBB3 (Tubulin beta 3)	1.15	TUBB3 (Tubulin beta 3)	444	406
Sodium Channel-pan	1.15	Sodium Channel-pan	260	238
cAMP	1.15	cAMP	293	267
GPR132	1.15	GPR132	338	309
MMP-19	1.15	MMP-19	463	423
GANP	1.15	GANP	229	209
CHP2	1.15	CHP2	227	207
Cyclin L1	1.15	Cyclin L1	182	166
Collagen II	1.15	Collagen II	400	364
MAP2K6	1.14	MAP2K6	303	276
MPS1	1.14	MPS1	1014	922
SENP7	1.14	SENP7	290	264
SRY	1.14	SRY	312	283
			224	204
DGKD	1.14	DGKD		
ACOT2	1.14	ACOT2	136	124
XRCC2	1.14	XRCC2	256	232
Claudin 11	1.14	Claudin 11	1240	1125
ERAS	1.14	ERAS	375	340
MMP-14	1.14	MMP-14	236	214
Sirp alpha1	1.14	Sirp alpha1	214	194
S6K	1.14	S6K	428	388
Nrf2	1.14	Nrf2	255	231
FOXR1	1.14	FOXR1	217	197
TPD54	1.14	TPD54	281	254
p50 CDC37	1.14	p50 CDC37	206	187
ATP5S	1.14	ATP5S	248	225
GluR5	1.14	GluR5	311	282
ERF	1.14	ERF	257	233
Vimentin	1.14	Vimentin	236	213
LDLRAD1	1.14	LDLRAD1	173	156
IP6K2	1.14	IP6K2	172	155
FAKD2	1.14	FAKD2	166	150
p44/42 MAPK	1.14	p44/42 MAPK	448	404
MAP3K1	1.14	MAP3K1	226	204
60S Ribosomal Protein L10	1.14	60S Ribosomal Protein L10	281	254
WNT1	1.13	WNT1	339	305
MARK	1.13	MARK	229	206
PARL	1.13	PARL	214	192
p44 MAPK	1.13	p44 MAPK	343	308
Lys-acetylated proteins	1.13	Lys-acetylated proteins	243	218
Cyclosome 1	1.13	Cyclosome 1	495	445
Sumo1	1.13	Sumo1	333	299
Ki67	1.13	Ki67	273	245
KIO7	1.15	NO7	2/3	243

	ation for Replicates		
Bigger Sample	Smaller Sample		
0.13	0.04		
0.02	0.01		
0.34	0.32		
0.11	0.16		
0.07	0.04		
0.05	0.08		
0.02	0.01		
0.16	0.20		
0.01	0.02		
0.04	0.21		
0.03	0.03		
0.07	0.14		
0.06	0.08		
0.11	0.01		
0.01	0.22		
0.03	0.22		
0.13	0.02		
0.02	0.06 0.05		
0.06			
0.10 0.07	0.06 0.04		
0.07	0.04		
0.05	0.03		
0.03	0.08		
0.06	0.14		
0.03	0.09		
0.04	0.05		
0.07	0.13		
0.03	0.07		
0.17	0.11		
0.05	0.04		
0.07	0.03		
0.06	0.21		
0.03	0.09		
0.09	0.04		
0.06	0.07		
0.01	0.03		
0.19	0.01		
0.03	0.12		
0.13	0.00		
0.15	0.09		
0.06	0.05		
0.04	0.06		
0.06	0.03		
0.16	0.01		
0.07	0.01		
0.00	0.10		
0.07	0.11		
0.10	0.05		
0.07	0.07		
0.25	0.07		
0.04	0.12		
0.08	0.02		
0.10	0.10		
0.14	0.00		

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.94	1.09
1.73	2.00
0.61	0.71
0.69	0.79
0.84	0.97
0.90	1.04
8.13	9.38
1.42	1.64
1.07	1.24
0.93	1.07
0.54	0.63
1.71	1.97
1.57	1.80
0.92	1.06
1.03	1.19
1.19	1.37
1.64	1.88
0.81	0.93
0.80	0.92
0.64	0.74
1.41	1.62
1.07 3.58	1.23 4.10
1.02	1.17
1.10	1.17
0.79	0.91
0.48	0.55
0.90	1.03
4.38	5.01
1.33	1.51
0.83	0.95
0.76	0.86
1.51	1.72
0.90	1.03
0.77	0.87
0.99	1.13
0.73	0.83
0.88	1.00
1.10	1.25
0.91	1.03
0.83	0.95
0.61	0.69
0.61	0.69
0.59	0.67
1.58	1.80
0.80	0.91
0.99	1.13
1.20	1.36
0.81	0.92
0.75	0.85
1.21	1.37
0.86	0.97
1.75	1.98
1.18	1.33
0.96	1.09

Antibody	/ Array	/ Assav	/ Results	Assa

Assay Data

Signaling Explorer Antibody Array

Protein List  Glucagon  SERC1  Proteinase 3  Septin-7  XPA  EKI2  AP-2  Tyk2  SENP6  SLC25A31  Granzyme B  Cytochrome P450 17A1  TGF alpha Peripherin HSP60 HNF4alpha/gamma LRP11  CLN6 HDAC1  TGF beta3 BRSK1  CCT6A  STEA2  CDK5R2 HDAC7  Somatostatin ERCC1  MMP-23 LDLRAD3 Bak	Fold Change between Samples Smaller Sample/Bigger Sample 1.13 1.13 1.13 1.13 1.13 1.13	Protein List Glucagon SERC1	Average Signal o Bigger Sample 281 164	Smaller Sample 252
Glucagon  SERC1  Proteinase 3  Septin-7  XPA  EKI2  AP-2  Tyk2  SENP6  SLC25A31  Granzyme B  Cytochrome P450 17A1  TGF alpha  Peripherin  HSP60  HNF4alpha/gamma  LRP11  CLN6  HDAC1  TGF beta3  BRSK1  CCT6A  STEA2  CDKSR2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3	1.13 1.13 1.13 1.13	Glucagon SERC1	281	252
SERC1         Proteinase 3           Septin-7         XPA           KPA         EKI2           AP-2         Tyk2           Tyk2         SENP6           SLC25A31         Granzyme B           Cytochrome P450 17A1         TGF alpha           Peripherin         HNF4alpha/gamma           LRP11         LCN6           HDAC1         TGF beta3           BRSK1         CCTGA           STEA2         CDK5R2           HDAC7         Somatostatin           ERCC1         MMP-23           LDLRAD3         LDLRAD3	1.13 1.13 1.13	SERC1		
Proteinase 3  Septin-7  XPA  EKI2  AP-2  Tyk2  SENP6  SLC25A31  Granzyme B  Cytochrome P450 17A1  TGF alpha  Peripherin  HSP60  HNF4alpha/gamma  LRP11  CLN6  HDAC1  TGF beta3  BRSK1  CCT6A  STEA2  CDK5R2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3	1.13 1.13		164	
Septin-7           XPA           EKI2           AP-2           Tyk2           SENP6           SLC25A31           Granzyme B           Cytochrome P450 17A1           TGF alpha           Peripherin           HSP60           HNF4alpha/gamma           LRP11           CLN6           HDAC1           TGF beta3           BRSK1           CCT6A           STEA2           CDK5R2           HDAC7           Somatostatin           ERCC1           MMP-23           LDLRAD3	1.13			147
XPA  EKI2  AP-2  Tyk2  SENP6  SLC25A31  Granzyme B  Cytochrome P450 17A1  TGF alpha  Peripherin  HSP60  HNF4alpha/gamma  IRP11  CLN6  HDAC1  TGF beta3  BRSK1  CCT6A  STFA2  CDK5R2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3		Proteinase 3	120	108
EKI2 AP-2 Tyk2 SENP6 SENP6 SIC25A31 Granzyme B Cytochrome P450 17A1 TGF alpha Peripherin HSP60 HNF4alpha/gamma IRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCT6A STEA2 CDKSR2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1 12	Septin-7	206	185
AP-2 Tyk2 SENP6 SLC25A31 Granzyme B Cytochrome P450 17A1 TGF alpha Peripherin HSP60 HNF4alpha/gamma IRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCTGA STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.13	XPA	302	270
Tyk2  SENP6  SLC25A31  Granzyme B  Cytochrome P450 17A1  TGF alpha  Peripherin  HSP60  HNF4alpha/gamma  LRP11  CLN6  HDAC1  TGF beta3  BRSK1  CCT6A  STEA2  CDK5R2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3	1.13	EKI2	162	145
SENP6           SLC25A31           Granzyme B           Cytochrome P450 17A1           TGF alpha           Peripherin           HSP60           HNF4alpha/gamma           LRP11           CLN6           HDAC1           TGF beta3           BRSK1           CCT6A           STEA2           CDK5R2           HDAC7           Somatostatin           ERCC1           MMP-23           LDLRAD3	1.13	AP-2	398	356
SLC25A31  Granzyme B  Cytochrome P450 17A1  TGF alpha  Peripherin  HSP60  HNF4alpha/gamma  IRP11  CLN6  HDAC1  TGF beta3  BRSK1  CCT6A  STEA2  CDK5R2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3	1.13	Tyk2	289	259
Granzyme B  Cytochrome P450 17A1  TGF alpha Peripherin HSP60 HNF4alpha/gamma IRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCT6A STEA2 CDKSR2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.13	SENP6	260	233
Cytochrome P450 17A1 TGF alpha Peripherin HSP60 HNF4alpha/gamma LRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCT6A STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.13	SLC25A31	231	206
TGF alpha Peripherin HSP60 HNF4alpha/gamma IRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCTGA STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.13	Granzyme B	343	307
TGF alpha Peripherin HSP60 HNF4alpha/gamma LRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCTGA STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	Cytochrome P450 17A1	314	280
Peripherin HSP60 HNF4alpha/gamma LRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCT6A STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	TGF alpha	453	405
HSP60 HNF4alpha/gamma LRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCT6A STFEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	Peripherin	7395	6598
HNF4alpha/gamma LRP11 CLN6 HDAC1 TGF beta3 BRSK1 CCT6A STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	HSP60	273	244
IRP11  CLN6  HDAC1  TGF beta3  BRSK1  CCT6A  STEA2  CDKSR2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3	1.12	HNF4alpha/gamma	577	514
CLN6  HDAC1  TGF beta3  BRSK1  CCTGA  STEA2  CDK5R2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3	1.12	LRP11	410	365
HDAC1 TGF beta3 BRSK1 CCT6A STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	CLN6	244	217
TGF beta3 BRSK1 CCT6A STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	HDAC1	266	237
BRSK1  CCT6A  STEA2  CDK5R2  HDAC7  Somatostatin  ERCC1  MMP-23  LDLRAD3	1.12	TGF beta3	259	231
CCT6A STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	BRSK1	418	372
STEA2 CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	CCT6A	182	162
CDK5R2 HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	STEA2	191	170
HDAC7 Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	CDK5R2	313	278
Somatostatin ERCC1 MMP-23 LDLRAD3	1.12	HDAC7	258	230
ERCC1 MMP-23 LDLRAD3	1.12	Somatostatin	317	282
MMP-23 LDLRAD3	1.12	ERCC1	528	470
LDLRAD3		MMP-23	223	198
	1.12 1.12	LDLRAD3	250	222
	1.12	Bak	418	371
			244	
Prostate-specific Antigen 5-HT-5A	1.12	Prostate-specific Antigen 5-HT-5A	384	217 341
	1.12			
FSH H 2000	1.12	FSH	247	219
IL20RB	1.12	IL20RB	198	176
Cytochrome P450 2C8	1.12	Cytochrome P450 2C8	202	179
KPB1/2	1.11	KPB1/2	192	170
PML	1.11	PML	355	314
USF2	1.11	USF2	220	195
SENP3	1.11	SENP3	203	179
PBOV1	1.11	PBOV1	215	190
Cytochrome P450 26C1	1.11	Cytochrome P450 26C1	291	257
Synuclein beta	1.11	Synuclein beta	298	263
PIAS2	1.11	PIAS2	217	191
IPKB	1.11	IPKB	238	210
p300/CBP	1.11	p300/CBP	305	269
CYB5R1	1.11	CYB5R1	448	395
Kallikrein-11 (Cleaved-Ile54)	1.11	Kallikrein-11 (Cleaved-Ile54)	215	190
PPHLN	1.11	PPHLN	207	182
HER3	1.11	HER3	2370	2089
Cytochrome P450 26A1	1.11	Cytochrome P450 26A1	825	727
CNGA2	1.11	CNGA2	508	448
STK24	1.11	STK24	214	189
LIMK2	1.11	LIMK2	633	557
FLI1				23,
FGFR3	1.11	FLI1	256	225

	ation for Replicates
Bigger Sample	Smaller Sample
0.11	0.07
0.07	0.04
0.01	0.01
0.16	0.03
0.03	0.05
0.01	0.00
0.07	0.03
0.01	0.13
0.00	0.06
0.05	0.01
0.10	0.05
0.02	0.21
0.03	0.01
0.46	0.06
0.10	0.14
0.06	0.14
0.03	0.07
0.03	0.17
0.10	0.09
0.10	0.02
0.04	0.00
0.10	0.03
0.01	0.05
0.03	0.05
0.09	0.01
0.06	0.01
0.09	0.02
0.10	0.17
0.06	0.06
0.08	0.07
0.01	0.05
0.07	0.06
0.03	0.08
0.05	0.01
0.09	0.00
0.11	0.00
0.01	0.19
0.07	0.06
0.11	0.07
0.03	0.01
0.05	0.03
0.06	0.12
0.06	0.02
0.09	0.03
0.12	0.13
0.01	0.19
0.01	0.05
0.10	0.03
0.01	0.05
0.11	0.03
0.09	0.07
0.05	0.02
0.09	0.03
0.00	0.02

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.99	1.12
0.58	0.65
0.42	0.48
0.73	0.82
1.07	1.20
0.57	0.64
1.41	1.58
1.02	1.15
0.92	1.03
0.81	0.92
1.21	1.36
1.11	1.25
1.60	1.80
26.13	29.35
0.96	1.08
2.04	2.29
1.45	1.62
0.86	0.97
0.94	1.05
0.92	1.03
1.48	1.65
0.64	0.72
0.67	0.75
1.10	1.24
0.91	1.02
1.12	1.25
1.87 0.79	2.09
0.79	0.88
1.48	1.65
0.86	0.96
1.36	1.52
0.87	0.97
0.70	0.78
0.71	0.79
0.68	0.75
1.25	1.39
0.78	0.87
0.72	0.80
0.76	0.84
1.03	1.14
1.05	1.17
0.77	0.85
0.84	0.93
1.08	1.19
1.58	1.76
0.76	0.84
0.73	0.81
8.37	9.29
2.92	3.23
1.80	1.99
0.76	0.84
2.23	2.48
0.90	1.00
1.14	1.26

Antibody Arr	ay Assay Results	Assay Data
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PACIS	Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
PATA	Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
Caudin 1	PLK3	1.11	PLK3	205	180
Systems   Syst	PLA1A	1.11	PLA1A	187	165
1512   1.11	Claudin 1	1.11	Claudin 1	652	574
MIL	Cytochrome c	1.11	Cytochrome c	401	353
MIL  1.11 MIL  1.235 207  1.002  1.11 UBA2  2.43 2.14  2.05 180  1.05 110  1.05 111  1.05 111  1.05 111  1.05 111  1.05 111  1.06 117  1.06 117  1.07 110  1	TSH2	1.11	TSH2	165	145
USAP2 USAP3 USP13	XRCC1	1.11	XRCC1	252	221
DOKSR1	MLL	1.11	MLL	235	207
USP13	UBA2	1.11	UBA2	243	214
USP13	CDK5R1	1.11	CDK5R1	205	180
IPACS	USP13	1.11	USP13	172	151
APOL2  1.10  APOL2  1.10  APOL3  APOL4  APOL4  APOL5  APOL	MMP1 (Cleaved-Phe100)	1.11	MMP1 (Cleaved-Phe100)	156	137
APOL2 1.10 APOL2 208 183 AFSH 1.10 APOL2 208 183 AFSH 1.10 APSH 771 676 GABRG1 1.10 GABRG1 226 198 VCAM1 1.10 VCAM1 1.15 127 PROZ 322 282 TIMP2 1.10 TIMP2 266 233 NPTN 1.10 NPTN 482 422 CREBZF 1.10 CREBZF 157 137 MGMT 452 395 MAP3KG 1.10 MAP3KG 205 179 LCCAL1 1.10 MAP3KG 205 179 LCCAL1 1.10 ASC 411 424 370 ASC 1.10 ASC 411 436 CELWA 1.10 CREBZF 1.10 424 370 ASC 1.10 ASC 414 361 CELWA 1.10 CREWA 234 224 226 CREBZF 364 1.10 CREBZF 1.10 424 370 ASC 1.10 ASC 414 361 CELWA 1.10 CREWA 234 204 Presentin 1 1.10 CREWA 1.		1.11		426	374
SABRG1		1.10		208	183
SABRG1	ATP5H	1.10	ATP5H	771	676
NCAM1		1.10	GABRG1	226	198
PROZ		1.10		145	127
NPTN					
CREBZF         1.10         CREBZF         157         137           MGNIT         1.10         MGMT         452         335           MAP3K6         1.10         MAP3K6         205         179           SLC4A11         1.10         SLC4A11         424         370           ASC         414         361         204         424         370           CBLM4         1.10         CBLN4         234         204           Presenilin 1         1.10         Presenilin 1         238         207           FAK         1.10         FAK         1.64         1.43           CNTNA         1.10         CNTNA         1.90         1.66           Ezrin         1.10         Oxtamer-binding transcription factor 1         368         320           Otzamer-binding transcription factor 1         1.10         Oxtamer-binding transcription factor 1         368         320           SKP1A/p19         1.10         Oxtamer-binding transcription factor 1         368         320           SKP1A/p19         1.10         Oxtamer-binding transcription factor 1         368         320           SKP1A/p19         1.10         ATS         44         405         352 <t< td=""><td></td><td>1.10</td><td>TIMP2</td><td>266</td><td>233</td></t<>		1.10	TIMP2	266	233
MGMT	NPTN	1.10	NPTN	482	422
MGMT	CREBZF	1.10	CREBZF	157	137
MAP3K6					
SLC4A11				205	179
ASC  GBLN4  1.10  CBLN4  1.10  CBLN4  1.10  CBLN4  1.10  CBLN4  1.10  CBLN4  1.10  CBLN4  1.10  FAK  1.10  FAK  1.10  CNTN4  1.10  CNTN4  1.10  CTNN4  1.10  CTNN4  1.10  Exrin  1.10  Exrin  229  260  Octamer-binding transcription factor 1  1.10  SKP1A/p19  316  275  Cytochrome P450 19A1  1.10  ATFS  ATFS  1.10  ATFS					
CBLN4         1.10         CBLN4         234         204           Presenilin 1         1.10         Presenilin 1         238         207           FAK         1.10         FAK         1.64         1.43           CNTN4         1.10         CNTN4         1.90         1.66           Ezrin         1.10         CNTN4         1.90         1.66           Ezrin         299         2.60           Octamer-binding transcription factor 1         368         320           SKP1A/p19         3.16         275           Cytochrome P450 19A1         1.10         SKP1A/p19         3.16         275           Cytochrome P450 19A1         1.10         ATFS         243         2.11           TrkA         1.10         ATFS         243         2.11           MAP383         1.10         MAP383         1.10         MAP383         338         294           IL-1beta (Cleaved-Asp210)         1.10         IL-1beta (Cleaved-Asp210)         238         207           CASP2 (p18, Cleaved-Thr325)         1.09         CASP2 (p18, Cleaved-Thr325)         345         300           Keratin 17         1.09         Marxim 17         437         380					
Presentlin 1         1.10         Presentlin 1         238         207           FAK         1.10         FAK         1.64         1.43           CNTN4         1.10         CNTN4         1.90         1.66           Ezrin         1.10         CXTNA         1.99         260           Octamer-binding transcription factor 1         1.10         Octamer-binding transcription factor 1         368         320           Octamer-binding transcription factor 1         368         320         320         320         368         320           SKP1A/p19         1.10         SKP1A/p19         316         275         275         Cytochrome P450 19A1         405         352           ATF5         1.10         ATF5         243         211         243         211           MAP3K3         1.10         ATF5         243         211         243         211           MAP3K3         1.10         MAP3K3         338         294           IL-1beta (Cleaved-Asp210)         1.10         IL-1beta (Cleaved-Asp210)         238         207           Keratin 17         437         380         380         380           Keratin 17         437         380         380				234	
FAK         1.10         FAK         164         143           CNTN4         1.10         CNTN4         190         166           Ezrin         299         260           Octamer-binding transcription factor 1         1.10         Octamer-binding transcription factor 1         368         320           SKP1A/p19         1.10         SKP1A/p19         316         275           Cytochrome P450 19A1         1.10         Cytochrome P450 19A1         405         352           ATF5         1.10         ATF5         243         211           TrkA         1.10         TrkA         196         171           MAP3K3         1.10         MAP3K3         338         294           L-Ibeta (Cleaved-Asp210)         1.10         IL-Ibeta (Cleaved-Asp210)         238         207           CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Keratin 17         1.09         Keratin 17         437         338         204           HDAC6         1.09         HDAC2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         MAPK10         492         427           MRC2         1.09					
CNTN4         1.10         CNTN4         190         166           Ezrin         1.10         Ezrin         299         260           Octamer-binding transcription factor 1         368         320           SKP1A/p19         1.10         SKP1A/p19         316         275           Cytochrome P450 19A1         1.10         Cytochrome P450 19A1         405         352           ATF5         1.10         ATF5         243         211           TrkA         1.10         TrkA         196         171           MAP3K3         1.10         MAP3K3         338         294           II-1beta (Cleaved-Asp210)         1.10         IL-1beta (Cleaved-Asp210)         238         207           CASP2 (p18,Cleaved-Th7325)         1.09         CASP2 (p18,Cleaved-Th7325)         345         300         8           Keratin 17         1.09         Keratin 17         437         380         9         A           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236         A           HDAC6         1.09         HDAC6         282         245         A         A           MAPK10         1.09         MAPK10         492 <td></td> <td>1.10</td> <td></td> <td>164</td> <td>143</td>		1.10		164	143
Ezrin         1.10         Ezrin         299         260           Octamer-binding transcription factor 1         1.10         Octamer-binding transcription factor 1         368         320           SKP1A/p19         1.10         SKP1A/p19         316         275           Cytochrome P450 19A1         1.10         Cytochrome P450 19A1         405         352           ATF5         1.10         ATF5         243         211           TrkA         1.10         TrkA         196         171           MAP3K3         1.10         MAP3K3         338         294           IL-1beta (Cleaved-Asp210)         1.10         IL-1beta (Cleaved-Asp210)         238         207           CASP2 (p18, Cleaved-Thr325)         1.09         CASP2 (p18, Cleaved-Thr325)         345         300           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         COC2         292         254			CNTN4		
SKP1A/p19         1.10         SKP1A/p19         316         275           Cytochrome P450 19A1         1.10         Cytochrome P450 19A1         405         352           ATF5         1.10         ATF5         243         211           TrkA         1.10         TrkA         1.96         171           MAP3K3         1.10         MAP3K3         338         294           IL-1beta (Cleaved-Asp210)         238         207         CASP2 (p18,Cleaved-Thr325)         345         300           CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Keratin 17         1.09         Keratin 17         437         380           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2		1.10	Ezrin	299	
SKP1A/p19         1.10         SKP1A/p19         316         275           Cytochrome P450 19A1         1.10         Cytochrome P450 19A1         405         352           ATF5         1.10         ATF5         243         211           TrkA         1.10         TrkA         196         171           MAP3K3         1.10         MAP3K3         338         294           IL-1beta (Cleaved-Asp210)         238         207         CASP2 (p18,Cleaved-Thr325)         345         300           CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09         MUC13         15	Octamer-binding transcription factor 1	1.10	Octamer-binding transcription factor 1	368	320
Cytochrome P450 19A1         1.10         Cytochrome P450 19A1         405         352           ATF5         1.10         ATF5         243         211           TrkA         1.10         TrkA         1.96         171           MAP3K3         1.10         MAP3K3         338         294           IL-1beta (Cleaved-Asp210)         1.10         IL-1beta (Cleaved-Asp210)         238         207           CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Keratin 17         437         380         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MRC2         179         156           SORL1         1.09         MRC2         179         156           SORL1         247         214         247         214           CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09				316	275
ATF5         1.10         ATF5         243         211           TrkA         1.10         TrkA         196         171           MAP3K3         1.10         MAP3K3         338         294           Li-beta (Cleaved-Asp210)         1.10         IL-ibeta (Cleaved-Asp210)         238         207           CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Keratin 17         1.09         Keratin 17         437         380           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           COllagen I alpha2         109         MUC13         151         131           TRADD         1.09         MMP-3         278	Cytochrome P450 19A1	1.10		405	352
TrkA         1.10         TrkA         196         171           MAP3K3         1.10         MAP3K3         338         294           II-1beta (Cleaved-Asp210)         1.10         II-1beta (Cleaved-Asp210)         238         207           CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Keratin 17         1.09         Keratin 17         437         380           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen Lalpha2         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         Cytochrome P450 1A2				243	
MAP3K3         1.10         MAP3K3         338         294           IL-1beta (Cleaved-Asp210)         1.10         IL-1beta (Cleaved-Asp210)         238         207           CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Keratin 17         1.09         Keratin 17         437         380           Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         Notch 2 (Cleaved-Asp1733)         271         236           MAPK10         1.09         HDAC6         282         245           MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         MRC2         179         156           SORL1         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09         MUC13         151         131           MWC13         1.09         MUC13         151         131           TRADD         1.09         MMP-3         278         241           Cytochrome P450 1A2		1.10		196	171
IL-1beta (Cleaved-Asp210)					
CASP2 (p18,Cleaved-Thr325)         1.09         CASP2 (p18,Cleaved-Thr325)         345         300           Keratin 17         1.09         Keratin 17         437         380           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           MUC13         1.09         COllagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1					
Keratin 17         1.09         Keratin 17         437         380           Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09         Collagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266		1.09		345	300
Notch 2 (Cleaved-Asp1733)         1.09         Notch 2 (Cleaved-Asp1733)         271         236           HDAC6         1.09         HDAC6         282         245           MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09         Collagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266		1.09		437	380
HDAC6				271	
MAPK10         1.09         MAPK10         492         427           MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         262         227         Collagen Lalpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266				282	
MRC2         1.09         MRC2         179         156           SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         262         227         227           Collagen I alpha2         1.09         Collagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266				492	427
SORL1         1.09         SORL1         247         214           CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09         Collagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
CDC2         1.09         CDC2         292         254           HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09         Collagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
HDAC10         1.09         HDAC10         262         227           Collagen I alpha2         1.09         Collagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
Collagen I alpha2         1.09         Collagen I alpha2         235         204           MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         307         266					
MUC13         1.09         MUC13         151         131           TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
TRADD         1.09         TRADD         316         274           MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
MMP-3         1.09         MMP-3         278         241           Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
Cytochrome P450 1A2         1.09         Cytochrome P450 1A2         237         205           Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
Prostate Apoptosis Response protein-4         1.09         Prostate Apoptosis Response protein-4         263         228           NT         1.09         NT         229         198           COX11         1.09         COX11         307         266					
NT 1.09 NT 229 198 COX11 1.09 COX11 307 266			•		
COX11 1.09 COX11 307 266					
	CDH10	1.09	CDH10	378	327

Coefficient of Variation for Replicat		
Bigger Sample	Smaller Sample	
0.01	0.02	
0.00	0.00	
0.05	0.05	
0.22	0.03	
0.05	0.01	
0.11	0.11	
0.02	0.16	
0.05	0.01	
0.06	0.06	
0.08	0.01	
0.03	0.09	
0.05	0.01	
0.12	0.05	
0.00	0.15	
0.08	0.08	
0.04	0.00	
0.07	0.05	
0.10	0.14	
0.01	0.06	
0.10	0.04	
0.08	0.09	
0.06	0.04	
0.05	0.08	
0.04	0.06	
0.10	0.02	
0.13	0.01	
0.00	0.12	
0.02	0.01	
0.02	0.05	
0.01	0.06	
0.00	0.03	
0.02	0.08	
0.06	0.07	
0.05	0.12	
0.06	0.04	
0.13	0.13	
0.43	0.05	
0.05	0.08	
0.05	0.01	
0.04	0.03	
0.06	0.09	
0.06	0.02	
0.14	0.09	
0.08	0.03	
0.03	0.09	
0.04	0.08	
0.01	0.05	
0.03	0.10	
0.10	0.08	
0.06	0.19	
0.02	0.00	
0.06	0.11	
0.03	0.14	
0.11	0.10	

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.72	0.80
0.66	0.73
2.30	2.55
1.42	1.57
0.58	0.65
0.89	0.98
0.83	0.92
0.86	0.95
0.72	0.80
0.61	0.67
0.55	0.61
1.50	1.66
0.73	0.81
2.72	3.01
0.80	0.88
0.51	0.57
1.14	1.25
0.94	1.03
1.70	1.88
0.55	0.61
1.60	1.76
0.72	0.79
1.50	1.65
1.46	1.60
0.83	0.91
0.84	0.92
0.58	0.63
0.67	0.74
1.05	1.16
1.30	1.42
1.12	1.22
1.43	1.57
0.86	0.94
0.69	0.76
1.19	1.31
0.84	0.92
1.22	1.33
1.54	1.69
0.96	1.05
1.00	1.09
1.74	1.90
0.63	0.69
0.87	0.95
1.03	1.13
0.92	1.01
0.83	0.91
0.53	0.58
1.12	1.22
0.98	1.07
0.84	0.91
0.93	1.01
0.81	0.88
1.08	1.18
1.33	1.45

	Antibody	/ Array	Assav	Resul	lts
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Assay Data

Signaling Explorer Antibody Array

		ivieaian Signai	283	225
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
BIM	1.09	BIM	348	301
DNA Polymerase lambda	1.09	DNA Polymerase lambda	178	154
Keratin 7	1.09	Keratin 7	240	208
TNK1	1.09	TNK1	203	176
CA6	1.09	CA6	236	204
EFNA2	1.09	EFNA2	221	191
RABEP2	1.09	RABEP2	463	400
нск	1.09	HCK	158	136
TUSC2	1.09	TUSC2	234	202
CHK2	1.09	CHK2	165	142
KAP0	1.09	KAPO	362	312
BARD1	1.09	BARD1	196	169
MER	1.09	MER	138	119
SIRPG	1.09	SIRPG	297	256
CA13	1.08	CA13	322	277
PIAS3	1.08	PIAS3	256	220
SLC9A9	1.08	SLC9A9	319	275
GADD45GIP1	1.08	GADD45GIP1	308	265
14-3-3 epsilon	1.08	14-3-3 epsilon	204	176
GABA-B Receptor	1.08	GABA-B Receptor	279	240
XRCC4	1.08	XRCC4	329	283
LAMC3	1.08	LAMC3	236	203
BST2	1.08	BST2	186	160
CD18 (ITGB2)	1.08	CD18 (ITGB2)	203	174
WASF3	1.08	WASF3	464	399
CD97beta (Cleaved-Ser531)	1.08	CD97beta (Cleaved-Ser531)	230	197
Histone H3 (Acetyl-Lys23)	1.08	Histone H3 (Acetyl-Lys23)	297	255
Guanylate Cyclase beta	1.08	Guanylate Cyclase beta	293	251
Octamer-binding transcription factor 6	1.08	Octamer-binding transcription factor 6	309	265
PRKX	1.08	PRKX	270	231
ATBP3	1.08	АТВРЗ	574	492
Parathyroid Hormone	1.08	Parathyroid Hormone	315	270
ABHD4	1.08	ABHD4	206	176
TNF14	1.08	TNF14	223	191
ARSK	1.08	ARSK	435	372
TGF beta Receptor II	1.08	TGF beta Receptor II	354	303
Dynamin-2	1.08	Dynamin-2	132	113
Keratin 8	1.08	Keratin 8	294	251
PHLA1	1.08	PHLA1	218	186
NEDD8	1.08	NEDD8	251	215
Caspase 10	1.08	Caspase 10	450	385
DAK	1.08	DAK	254	217
MYC	1.08	MYC	192	164
Influenza B virus Nucleoprotein	1.08	Influenza B virus Nucleoprotein	141	120
MART-1	1.08	MART-1	383	327
Ubiquitin	1.07	Ubiquitin	304	260
MOK	1.07	МОК	202	172
ADH7	1.07	ADH7	178	152
POLE1	1.07	POLE1	229	195
Cytochrome P450 24A1	1.07	Cytochrome P450 24A1	338	288
alpha hCG	1.07	alpha hCG	126	108
CDCP1	1.07	CDCP1	160	137
FRK	1.07	FRK	218	186
ATG4B	1.07	ATG4B	289	246
A1U4D	1.07	ATO40	489	∠40

Coefficient of Veri	ation for Doulineton
	ation for Replicates
Bigger Sample	Smaller Sample
0.01	0.06
0.01	0.07
0.05	0.09
0.03	0.04
0.09	0.08
0.04	0.12 0.01
0.02	0.01
0.20	
0.00	0.02 0.12
0.00	0.02
0.08	0.02
0.01	0.13
0.12	0.07
0.01	0.10
0.09	0.10
0.06	0.10
0.03	
	0.06
0.11	0.11
0.08	0.08
0.09	0.06
0.02 0.14	0.15 0.13
0.03	0.13
0.17	0.20
0.06	0.00
0.01	0.06
0.06	0.07
0.15	0.02
0.01	0.06
0.13	0.07
0.07	0.06
0.10	0.25
0.05	0.08
0.11	0.01
0.00	0.07
0.03	0.05
0.06	0.06
0.00	0.06
0.02	0.01
0.07	0.01
0.01	0.04
0.00	0.13
0.08	0.10
0.00	0.07
0.08	0.07
0.05	0.15
0.16	0.10
0.06	0.10
0.02	0.02
0.00	0.05
0.07	0.02
0.07	0.02

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.23	1.34
0.63	0.68
0.85	0.92
0.72	0.78
0.83	0.91
0.78	0.85
1.63	1.78
0.56	0.61
0.83	0.90
0.58	0.63
1.28	1.39
0.69	0.75
0.49	0.53
1.05	1.14
1.14	1.23
0.90	0.98
1.13	1.22
1.09	1.18
0.72	0.78
0.99	1.07
1.16	1.26
0.83	0.90
0.66	0.71
0.72	0.77
1.64	1.77
0.81	0.88
1.05	1.13
1.03	1.12
1.09	1.18
0.95	1.03
2.03	2.19
1.11	1.20
0.73	0.78
0.79	0.85
1.54	1.66
1.25	1.35
0.46	0.50
1.04	1.12
0.77	0.83
0.89	0.95
1.59	1.71
0.90	0.97
0.68	0.73
0.50	0.53
1.35	1.45
1.07	1.15
0.71	0.77
0.63	0.67
0.81	0.87
1.19	1.28
0.45	0.48
0.57	0.61
0.77	0.83
1.02	1.09

Array Assay Results Ass	ay Da
Array Assay Results Ass	ay D

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Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
EDD	1.07	EDD	316	269
FRS3	1.07	FRS3	265	226
SERC2	1.07	SERC2	288	245
СРМ	1.07	СРМ	253	215
SLC25A6	1.07	SLC25A6	192	163
PPRC1	1.07	PPRC1	249	212
SENP8	1.07	SENP8	366	312
DNA Polymerase zeta	1.07	DNA Polymerase zeta	292	249
USP24	1.07	USP24	181	154
Keratin 18	1.07	Keratin 18	388	330
PAK2	1.07	PAK2	167	142
CPN1	1.07	CPN1	234	199
MDM2	1.07	MDM2	330	281
SPINK6	1.07	SPINK6	220	187
SERC3	1.07	SERC3	249	212
PRPF19	1.07	PRPF19	189	161
CHST10	1.07	CHST10	216	183
LH	1.07	LH	186	158
RAB5C	1.07	RAB5C	199	169
NF1	1.07	NF1	347	295
RET	1.07	RET	142	121
Cytochrome P450 4F2	1.07	Cytochrome P450 4F2	225	191
MCM2	1.07	MCM2	225	191
ILKAP	1.07	ILKAP	258	219
CDC40	1.07	CDC40	205	174
Fra-2	1.07	Fra-2	399	339
Claudin 7	1.07	Claudin 7	464	394
CA125	1.07	CA125	112	95
AMACR	1.07	AMACR	226	191
p300	1.07	p300	324	274
TACC1	1.07	TACC1	248	210
5-HT-1F	1.07	5-HT-1F	206	174
Cytochrome P450 3A43	1.07	Cytochrome P450 3A43	209	177
Myeloperoxidase	1.07	Myeloperoxidase	228	193
NGFR	1.07	NGFR	182	154
ADD2	1.07	ADD2	234	198
	1.07		172	145
LILRA1		LILRA1		
14-3-3 gamma	1.06	14-3-3 gamma	214	181
YAP	1.06	YAP	201	170
GGH	1.06	GGH	249	211
EIF4G2	1.06	EIF4G2	291	246
FMN2	1.06	FMN2	226	191
TAF4	1.06	TAF4	187	158
HGH	1.06	HGH	158	133
MMP-16	1.06	MMP-16	264	223
5-HT-3A	1.06	5-HT-3A	196	165
RAD50	1.06	RAD50	196	165
ITIH1 (Cleaved-Asp672)	1.06	ITIH1 (Cleaved-Asp672)	141	119
LYN	1.06	LYN	135	114
TNXB	1.06	TNXB	163	138
Octamer-binding transcription factor 3	1.06	Octamer-binding transcription factor 3	272	229
Cullin 1	1.06	Cullin 1	3968	3346
	1.06	Lck	150	127
Lck				
EEF1G	1.06	EEF1G	185	156

Coefficient of Vari	ation for Replicates
Bigger Sample	Smaller Sample
0.07	0.02
0.07	0.05
0.06	0.07
0.03	0.01
0.01	0.00
0.01	0.00
0.02	0.14
0.03	0.19
0.02	0.06
0.00	0.13
0.07	0.00
0.05	0.01
0.04	0.08
0.12	0.05
0.09	0.06
0.08	0.03
0.11	0.05
0.07	0.00
0.12	0.14
0.01	0.11
0.01	0.03
0.05	0.12
0.05	0.29
0.02	0.07
0.04	0.05
0.11	0.16
0.03	0.00
0.04	0.07
0.02	0.07
0.13	0.02
0.02	0.05
0.04	0.11
0.17	0.12
0.01	0.06
0.08	0.04
0.00	0.03
0.05	0.06
0.02	0.00
0.00	0.10
0.12	0.08
0.01	0.14
0.02	0.05
0.04	0.05
0.06	0.05
0.15	0.05
0.00	0.12
0.11	0.03
0.05	0.00
0.01	0.01
0.04	0.01
0.01	0.01
0.10	0.06
0.04	0.07
0.05	0.04

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.11	1.20
0.93	1.00
1.02	1.09
0.89	0.96
0.68	0.73
0.88	0.94
1.29	1.39
1.03	1.11
0.64	0.69
1.37	1.47
0.59	0.63
0.83	0.88
1.17	1.25
0.78	0.83
0.88	0.94
0.67	0.71
0.76	0.81
0.66	0.70
0.70	0.75
1.23	1.31
0.50	0.54
0.79	0.85
0.79 0.91	0.85
0.72	0.97 0.77
1.41	1.51
1.64 0.39	1.75 0.42
0.80	0.42
1.14	1.22
0.88	0.93
0.73	
0.74	0.77 0.79
0.80	0.86
0.64	0.69
0.83	0.88
0.61	0.65
0.71 0.88	0.75 0.94
1.03	1.09
0.80	0.85
0.66	0.70
0.56 0.93	0.59 0.99
0.69	
	0.73 0.73
0.69	0.73
0.48	0.51
0.58	0.61
0.96	1.02
14.02	14.89
0.53	0.56
0.65	0.69

Antibody	Array Assay	y Results	Assay	y Data
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Signaling Explorer Antibody Array

	Fold Change between Samples	iviedian Signal	Average Signal c	of Replicate Spots
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
ABHD11	1.06	ABHD11	169	143
Involucrin	1.06	Involucrin	388	327
ALDH3B1	1.06	ALDH3B1	169	142
PKM2	1.06	PKM2	172	145
CKI-gamma1	1.06	CKI-gamma1	165	139
RAD51L1	1.06	RAD51L1	165	139
COX15	1.06	COX15	222	187
SLCO1A2	1.06	SLCO1A2	178	150
SLC39A7	1.06	SLC39A7	168	141
CARKL	1.06	CARKL	183	154
MUSK	1.06	MUSK	148	125
Collagen XX alpha1	1.06	Collagen XX alpha1	252	212
HAT	1.06	HAT	308	259
beta hCG	1.06	beta hCG	242	203
KCNK4	1.06	KCNK4	241	203
ADCY7	1.06	ADCY7	175	147
CD2 Tail-binding	1.06	CD2 Tail-binding	216	181
SLC5A2	1.06	SLC5A2	281	236
RHOBTB3	1.06	RHOBTB3	234	197
PYK2 (FAK2)	1.06	PYK2 (FAK2)	159	134
RASH/RASK	1.06	RASH/RASK	332	279
DNAJB4	1.06	DNAJB4	245	206
MAP2K4	1.06	MAP2K4	292	245
JAK1	1.06	JAK1	202	169
TUSC3	1.06	TUSC3	257	216
BUB1B	1.06	BUB1B	211	177
Dysferlin	1.06	Dysferlin	443	371
MUTYH	1.06	MUTYH	513	430
BCA3	1.06	BCA3	155	130
DNA Polymerase beta	1.06	DNA Polymerase beta	297	249
PAR4	1.06	PAR4	124	104
ELOVL4	1.06	ELOVL4	216	181
E2F4	1.06	E2F4	343	287
PPGB (32k,Cleaved-Arg326)	1.05	PPGB (32k,Cleaved-Arg326)	207	173
SPTBN1	1.05	SPTBN1	216	181
RAB37	1.05	RAB37	339	284
ERCC5	1.05	ERCC5	252	211
Thyroid Hormone Receptor beta	1.05	Thyroid Hormone Receptor beta	295	247
COX19	1.05	COX19	285	239
Cyclin A	1.05	Cyclin A	401	336
RAN	1.05	RAN	309	259
CD55	1.05	CD55	554	463
ABHD14A	1.05	ABHD14A	186	156
CFAB Bb (Cleaved-Lys260)	1.05	CFAB Bb (Cleaved-Lys260)	195	163
p63	1.05	p63	280	234
HSP40	1.05	HSP40	453	379
GAPDH	1.05	GAPDH	386	322
Laminin	1.05	Laminin	173	145
MRCKB	1.05	MRCKB	215	180
BAD (Cleaved-Asp71)	1.05	BAD (Cleaved-Asp71)	242	202
TGF beta1	1.05	TGF beta1	251	210
MADD	1.05	MADD	197	164
Keratin 16	1.05	Keratin 16	266	222
SAA4	1.05	SAA4	145	121

Coefficient of Varia	ation for Replicates
Bigger Sample	Smaller Sample
0.09	0.01
0.14	0.04
0.09	0.05
0.09	0.00
0.02	0.01
0.09	0.02
0.07	0.19
0.02	0.05
0.02	0.01
0.11	0.06
0.00	0.02
0.09	0.07
0.11	0.07
0.08	0.17
0.04	0.09
0.11	0.02
0.02	0.02
0.02	0.10
0.02	0.03
0.04	0.12
0.26	0.10
0.03	0.02
0.26	0.00
0.00	0.03
0.01	0.04
0.01	0.06
0.03	0.08
0.01	0.00
0.05	0.01
0.04	0.03
0.04	0.03
0.09	0.02
0.10	0.05
0.02	0.20
0.02	0.04
0.04	0.13
0.07	0.06
0.03	0.01
0.06	0.10
0.01	0.02
0.08	0.01
0.03	0.08
0.08	0.02
0.04	0.12
0.08	0.02
0.02	0.04
0.05	0.05
0.02	0.05
0.09	0.03
0.03	0.24
0.00	0.12
0.10	0.12
0.01	0.11
0.03	0.02
0.03	0.02

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.60	0.63
1.37	1.45
0.60	0.63
0.61	0.64
0.58	0.62
0.58	0.62
0.78	0.83
0.63	0.67
0.59	0.63
0.65	0.69
0.52	0.55
0.89	0.94
1.09	1.15
0.85	0.90
0.85	0.90
0.62	0.65
0.76	0.81
0.99	1.05
0.83	0.87
0.56	0.59
1.17	1.24
0.87	0.91
1.03	1.09
0.71	0.75
0.91	0.96
0.74	0.79
1.56	1.65
1.81	1.91
0.55	0.58
1.05	1.11
0.44	0.46
0.76	0.81
1.21	1.28
0.73	0.77
0.76	0.80
1.20	1.26
0.89	0.94
1.04	1.10
1.01	1.06
1.42	1.49
1.09	1.15
1.96	2.06
0.66	0.69
0.69	0.73
0.99	1.04
1.60	1.68
1.36	1.43
0.61	0.64
0.76	0.80
0.86	0.90
0.89	0.93
0.69	0.73
0.94	0.99
0.51	0.54

Antibody Array Assay Results
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Assay Data

Signaling Explorer Antibody Array

		Median Signal	283	225
Protein List	Fold Change between Samples	Protein List		f Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
BMP8A	1.05	BMP8A	220	183
TUBGCP5	1.05	TUBGCP5	277	231
CD247 (CD3Z)	1.05	CD247 (CD3Z)	132	110
CD31	1.05	CD31	144	120
MMP-13	1.05	MMP-13	384	320
MMP-8	1.05	MMP-8	399	333
Collagen XXIII alpha1	1.05	Collagen XXIII alpha1	294	245
KIAA1967	1.05	KIAA1967	219	182
NKX26	1.05	NKX26	189	157
Collagen III	1.05	Collagen III	820	683
RAB38	1.05	RAB38	259	216
CD253	1.05	CD253	310	258
Octamer-binding transcription factor 2	1.05	Octamer-binding transcription factor 2	301	250
GADD153	1.05	GADD153	390	324
GPR120	1.05	GPR120	443	368
LRRK1	1.05	LRRK1	235	195
POLDIP3	1.05	POLDIP3	327	272
Collagen IV alpha4	1.05	Collagen IV alpha4	229	190
DOK7	1.05	DOK7	297	247
PPP1R8	1.05	PPP1R8	225	187
CA14	1.05	CA14	240	199
DDR2	1.05	DDR2	157	130
Cytochrome P450 3A7	1.05	Cytochrome P450 3A7	186	155
TPD52	1.05	TPD52	298	248
FA13A (Cleaved-Gly39)	1.05	FA13A (Cleaved-Gly39)	207	172
GPR174	1.05	GPR174	159	132
CDKL1	1.05	CDKL1	209	174
PARP	1.05	PARP	127	105
STEAP4	1.04	STEAP4	252	209
Collagen IX alpha3	1.04	Collagen IX alpha3	278	230
Gastrin	1.04	Gastrin	245	203
POLD3	1.04	POLD3	201	166
EPN3	1.04	EPN3	230	190
ITGA7 (light chain,Cleaved-Glu959)	1.04	ITGA7 (light chain,Cleaved-Glu959)	288	238
CST9L	1.04	CST9L	180	149
MAP4K6	1.04	MAP4K6	215	178
PIAS4	1.04	PIAS4	324	268
TENS3	1.04	TENS3	269	223
hCG	1.04	hCG	185	153
CDH2	1.04	CDH2	304	251
APOL1	1.04	APOL1	211	175
Mlx	1.04	Mlx	220	182
IGF 1R	1.04	IGF 1R	159	131
Insulin	1.04	Insulin	265	219
NCOA7	1.04	NCOA7	215	178
SHC3	1.04	SHC3	204	168
ABHD12	1.04	ABHD12	206	170
SKP2/p45	1.04	SKP2/p45	328	271
XRCC3	1.04	XRCC3	200	165
ARHGEF9	1.04	ARHGEF9	194	160
SENP1	1.04	SENP1	544	448
THRB (AP2,Cleaved-Arg327)	1.04	THRB (AP2,Cleaved-Arg327)	341	281
SPTBN5	1.04	SPTBN5	168	138

Coefficient of Vari	ation for Replicates
Bigger Sample	Smaller Sample
0.17	0.08
0.05	0.06
0.04	0.06
0.03	0.06
0.02	0.09
0.02	0.10
0.04	0.07
0.04	0.09
0.06	0.02
0.10	0.04
0.02	0.24
0.05	0.01
0.04	0.01
0.06	0.01
0.09	0.03
0.04	0.04
0.00	0.01
0.06	0.09
0.10	0.13
0.06	0.02
0.01	0.09
0.06	0.05
0.08	0.09
0.01	0.01
0.12	0.02
0.00	0.04
0.06	0.00
0.01	0.04
0.02	0.05
0.02	0.04
0.01	0.02
0.05	0.04
0.09	0.07
0.02	0.15
0.06	0.09
0.03	0.00
0.00	0.02
0.04	0.01
0.04	0.07
0.02	0.03
0.11	0.04
0.00	0.01
0.00	0.02
0.06	0.13
0.09	0.02
0.09	0.00
0.14	0.05
0.03	0.01
0.15	0.01
0.10	0.10
0.05	0.04
0.09	0.03
0.09	0.07
0.06	0.11

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.78	0.81
0.98	1.03
0.47	0.49
0.51	0.53
1.36	1.42
1.41	1.48
1.04	1.09
0.77	0.81
0.67	0.70
2.90	3.04
0.92	0.96
1.09	1.15
1.06	1.11
1.38	1.44
1.56	1.64
0.83	0.87
1.15	1.21
0.81	0.85
1.05	1.10
0.80	0.83
0.85	0.89
0.55	0.58
0.66	0.69
1.05	1.10
0.73	0.76
0.56	0.59
0.74	0.77
0.45	0.47
0.89	0.93
0.98	1.02
0.86	0.90
0.71	0.74
0.81	0.85
1.02	1.06
0.64	0.66
0.76	0.79
1.14	1.19
0.95	0.99
0.65	0.68
1.07	1.12
0.75	0.78
0.78	0.81
0.56	0.58
0.93	0.97
0.76	0.79
0.72	0.75
0.73	0.76
1.16	1.20
0.70	0.73
0.68	0.71
1.92	1.99
1.20	1.25
0.59	0.61
0.79	0.82

Antibody Array Assay Results	Assay Data
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Signaling Explorer Antibody Array

	Fold Change between Samples		Average Signal of Replicate Spots	
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
p50 Dynamitin	1.04	p50 Dynamitin	360	297
XPF	1.04	XPF	325	268
HDAC3	1.04	HDAC3	379	312
ACTR3	1.04	ACTR3	184	151
CD14	1.04	CD14	198	163
EPCAM	1.04	EPCAM	119	98
EPHA1	1.04	EPHA1	338	278
STMN4	1.04	STMN4	183	151
CIB1	1.04	CIB1	152	125
HDAC9	1.04	HDAC9	296	243
FABP4	1.04	FABP4	135	111
DNA Polymerase alpha	1.04	DNA Polymerase alpha	222	183
LATH	1.03	LATH	416	342
GPR152	1.03	GPR152	261	215
Cyclin F	1.03	Cyclin F	691	567
PIK3R5	1.03	PIK3R5	201	165
p14 ARF	1.03	p14 ARF	366	300
14-3-3 eta	1.03	14-3-3 eta	229	188
DOK4	1.03	DOK4	192	158
PDGFR alpha	1.03	PDGFR alpha	405	332
ZADH1	1.03	ZADH1	169	139
Ku70	1.03	Ku70	272	223
R-spondin 1	1.03	R-spondin 1	130	107
PDGFR beta	1.03	PDGFR beta	141	116
CDKA2	1.03	CDKA2	227	186
MAP2K2 (MEK2)	1.03	MAP2K2 (MEK2)	133	109
LHR2A	1.03	LHR2A	271	222
PDK2	1.03	PDK2	284	233
DNAJB11	1.03	DNAJB11	256	210
NCOA3	1.03	NCOA3	206	169
BAGE4	1.03	BAGE4	236	193
CNN2	1.03	CNN2	252	206
LILRA2	1.03	LILRA2	192	157
BUB3	1.03	BUB3	235	192
CPB2	1.03	CPB2	235	192
ELOVL1	1.03	ELOVL1	210	172
KLHL3	1.03	KLHL3	207	169
APAF-1-ALT	1.03	APAF-1-ALT	343	280
MAP3KL4	1.03	MAP3KL4	708	578
DGKH	1.03	DGKH	261	213
COX7S/A2	1.03	COX7S/A2	283	231
CAMK5	1.03	CAMK5	228	186
ТВР	1.03	ТВР	227	185
S100 A1	1.03	S100 A1	437	356
CHST6	1.03	CHST6	270	220
GSK3 alpha	1.03	GSK3 alpha	135	110
IL-10	1.02	IL-10	175	142
Keratin 20	1.02	Keratin 20	298	242
LDOC1L	1.02	LDOC1L	300	244
GCNT7	1.02	GCNT7	279	227
CDCA7	1.02	CDCA7	305	248
C1 D7	4.00	mGluR7	375	305
mGluR7	1.02	mgiuk/	3/3	505
BUB1	1.02	BUB1	270	220

Coefficient of Varia	ation for Replicates
Bigger Sample	Smaller Sample
0.00	0.01
0.07	0.10
0.01	0.13
0.04	0.00
0.08	0.12
0.03	0.07
0.02	0.08
0.02	0.01
0.07	0.08
0.01	0.10
0.04	0.18
0.03	0.02
0.29	0.21
0.13	0.08
0.06	0.02
0.06	0.10
0.08	0.04
0.02	0.08
0.02	0.05
0.02	0.02
0.02	0.07
0.05	0.06
0.03	0.02
0.02	0.07
0.00	0.01
0.03	0.06
0.02	0.04
0.07	0.07
0.17	0.03
0.08	0.01
0.02	0.06
0.04	0.11
0.11	0.00
0.07	0.07
0.05	0.05
0.05	0.05
0.05	0.00
0.02	0.00
0.07	0.05
0.13	0.13
0.02	0.12
0.06	0.03
0.07	0.05
0.03	0.01
0.03	0.04
0.01	0.03
0.05	0.01
0.10	0.04
0.02	0.02
0.05	0.02
0.10	0.07
0.08	0.07
0.10	0.04
0.00	0.06

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.27	1.32
1.15	1.19
1.34	1.39
0.65	0.67
0.70	0.72
0.42	0.43
1.19	1.24
0.65	0.67
0.54	0.56
1.04	1.08
0.48	0.49
0.78	0.81
1.47	1.52
0.92	0.95
2.44	2.52
0.71	0.73
1.29	1.33
0.81	0.83
0.68	0.70
1.43	1.47
0.60	0.62
0.96	0.99
0.46	0.47
0.50	0.51
0.80	0.83
0.47	0.48
0.96	0.99
1.00	1.03
0.90	0.93
0.73	0.75
0.83	0.86
0.89	0.92
0.68	0.70
0.83	0.85
0.83	0.85
0.74	0.76
0.73	0.75
1.21	1.25
2.50	2.57
0.92	0.95
1.00	1.03
0.80	0.83
0.80	0.82
1.54	1.58
0.95	0.98
0.48	0.49
0.62	0.63
1.05	1.08
1.06	1.09
0.98	1.01
1.08	1.10
1.32	1.35
0.95	0.98
1.02	1.04

Antibody	Array	Assay	/ Results	Assay	y Data
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	Fold Change between Samples	Wedian Signal	Average Signal of Replicate Spots	
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
ARHGEF12	1.02	ARHGEF12	267	217
RASSF6	1.02	RASSF6	221	180
MMP-1	1.02	MMP-1	421	342
GPRIN1	1.02	GPRIN1	298	242
TNF11	1.02	TNF11	298	242
Hepatitis B Surface Antigen	1.02	Hepatitis B Surface Antigen	168	136
SVOP	1.02	SVOP	168	136
PAR1	1.02	PAR1	593	481
ACVL1	1.02	ACVL1	178	145
Cytochrome P450 27A1	1.02	Cytochrome P450 27A1	332	270
KDR (VEGFR2) SLU7	1.02	KDR (VEGFR2) SLU7	120 258	97 209
	1.02			•
MMP-15	1.02	MMP-15	292	237
SHIP1	1.02	SHIP1	528	429
DOK3	1.02	DOK3	252	205
CEBPE	1.02	СЕВРЕ	533	433
EMR2	1.02	EMR2	188	153
GRK5	1.02	GRK5	207	168
Calcyclin (S100A6)	1.02	Calcyclin (S100A6)	238	193
NSG2	1.02	NSG2	230	186
USP53	1.02	USP53	203	165
FAKD1	1.02	FAKD1	216	175
AP2C	1.02	AP2C	248	201
GPR18	1.02	GPR18	205	166
PARP3	1.02	PARP3	155	126
C9	1.02	C9	533	432
Stefin B	1.02	Stefin B	286	232
NFRKB	1.02	NFRKB	255	206
LW-1	1.02	LW-1	181	147
CRP	1.02	CRP	171	138
HOXB2	1.02	HOXB2	186	151
S100B	1.02	S100B	134	108
SLC4A8/10	1.02	SLC4A8/10	181	146
RSK1 (p90 RSK)	1.02	RSK1 (p90 RSK)	139	112
Collagen VI alpha3	1.02	Collagen VI alpha3	243	197
PLK2	1.02	PLK2	350	283
ZHX2	1.02	ZHX2	248	201
Calnexin	1.02	Calnexin	180	146
IPKA	1.02	IPKA	282	228
ROR1	1.02	ROR1	209	169
Angiopoietin-1	1.02	Angiopoietin-1	151	122
CD154 (sCD40-Ligand)	1.02	CD154 (sCD40-Ligand)	115	93
ATPAF2	1.02	ATPAF2	273	220
CST1	1.02	CST1	197	159
Akt	1.02	Akt	311	251
Septin-2	1.02	Septin-2	253	204
KLKB1 (heavy chain,Cleaved-Arg390)	1.02	KLKB1 (heavy chain,Cleaved-Arg390)	635	512
4-Mar	1.01	4-Mar	201	162
TSH1	1.01	TSH1	278	224
5-HT-2C	1.01	5-HT-2C	226	182
ELOVL3	1.01	ELOVL3		
ELUVL3	1.01	ELUVL3	249	201

Coefficient of Variation for Replicates
0.04         0.21           0.02         0.13           0.02         0.05           0.05         0.11           0.01         0.00           0.06         0.01           0.17         0.29           0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.02         0.13           0.02         0.05           0.05         0.11           0.01         0.00           0.06         0.01           0.17         0.29           0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.02         0.05           0.05         0.11           0.01         0.00           0.06         0.01           0.17         0.29           0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.05         0.11           0.01         0.00           0.06         0.01           0.17         0.29           0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.01         0.00           0.06         0.01           0.17         0.29           0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.06         0.01           0.17         0.29           0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.17         0.29           0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.01         0.06           0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.03         0.11           0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.01         0.09           0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.02         0.08           0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.22         0.08           0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.01         0.02           0.12         0.07           0.03         0.09           0.01         0.02
0.12         0.07           0.03         0.09           0.01         0.02
0.03 0.09 0.01 0.02
0.01 0.02
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0.18 0.04
0.08 0.18
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0.03 0.08
0.09 0.05
0.02 0.00
0.02 0.13
0.23 0.01
0.04 0.04
0.03 0.01
0.08 0.20
0.02 0.05
0.04 0.03
0.20 0.06
0.04 0.05
0.04 0.05
0.03 0.01

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.94	0.97	
0.78	0.80	
1.49	1.52	
1.05	1.08	
1.05	1.08	
0.59	0.61	
0.59	0.61	
2.09	2.14	
0.63	0.64	
1.17 0.42	1.20 0.43	
0.91	0.93	
1.03	1.05	
1.87	1.91	
0.89	0.91	
1.88	1.92	
0.66	0.68	
0.73	0.75	
0.84	0.86	
0.81	0.83	
0.72	0.73	
0.76	0.78	
0.87	0.89	
0.72	0.74	
0.55	0.56	
1.88	1.92	
1.01	1.03	
0.90	0.92	
0.64	0.65	
0.60	0.61	
0.66	0.67	
0.47	0.48	
0.64	0.65	
0.49	0.50	
0.86	0.87	
1.24	1.26	
0.88	0.89	
0.64	0.65	
0.99	1.01	
0.74	0.75	
0.53	0.54	
0.40	0.41	
0.96	0.98	
0.70	0.71	
1.10	1.12	
0.89	0.91	
2.24	2.28	
0.71	0.72	
0.98	1.00	
0.80	0.81	
0.88	0.89	
	2"	

Antibody Array Assay Results
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Signaling Explorer Antibody Array

Protein List  Urocortin  FAM84B  PLAZG4C  HLA-DOA  Histone 1F0  CBR3  C1S (heavy chain,Cleaved-Arg437)  AIFM2  GNL3L  PTK6 (breast tumor kinase)	Fold Change between Samples Smaller Sample/Bigger Sample  1.01 1.01 1.01 1.01 1.01 1.01 1.01 1.	Protein List  Urocortin  FAM84B  PLA2G4C  HLA-DOA  Histone 1F0  CBR3	Average Signal of Bigger Sample  270  257  259  180	Smaller Sample   217   207   209
Urocortin FAM84B PLA2G4C HLA-DOA Histone 1F0 CBR3 C1S (heavy chain,Cleaved-Arg437) AIFM2 GNL3L PTK6 (breast tumor kinase)	1.01 1.01 1.01 1.01 1.01 1.01 1.01	FAM84B PLA2G4C HLA-DOA Histone 1F0	270 257 259 180	217 207
FAM84B PLA2G4C HLA-DOA Histone 1F0 CBR3 C1S (heavy chain, Cleaved-Arg437) AIFM2 GNL3L PTK6 (breast tumor kinase)	1.01 1.01 1.01 1.01 1.01 1.01	FAM84B PLA2G4C HLA-DOA Histone 1F0	257 259 180	207
PLA2G4C HLA-DOA Histone 1F0 CBR3 C1S (heavy chain, Cleaved-Arg437) AIFM2 GNL3L PTK6 (breast tumor kinase)	1.01 1.01 1.01 1.01 1.01	PLA2G4C HLA-DOA Histone 1F0	259 180	
HLA-DOA Histone 1F0 CBR3 C1S (heavy chain,Cleaved-Arg437) AIFM2 GNL3L PTK6 (breast tumor kinase)	1.01 1.01 1.01 1.01	HLA-DOA Histone 1F0	180	209
Histone 1F0 CBR3 C1S (heavy chain,Cleaved-Arg437) AIFM2 GNL3L PTK6 (breast tumor kinase)	1.01 1.01 1.01	Histone 1F0		1 445
CBR3 C1S (heavy chain,Cleaved-Arg437) AIFM2 GNL3L PTK6 (breast tumor kinase)	1.01 1.01		405	145
C1S (heavy chain,Cleaved-Arg437)  AIFM2  GNL3L  PTK6 (breast tumor kinase)	1.01	CBR3	485	390
AIFM2 GNL3L PTK6 (breast tumor kinase)		046 ()	228	184
GNL3L PTK6 (breast tumor kinase)	1.01	C1S (heavy chain,Cleaved-Arg437)	354	285
PTK6 (breast tumor kinase)	1.01	AIFM2	256	206
		GNL3L	159	128
	1.01	PTK6 (breast tumor kinase)	118	95
ZAP70	1.01	ZAP70	120	97
RFPL4A	1.01	RFPL4A	225	181
LPL	1.01	LPL	151	121
FOXB1/2	1.01	FOXB1/2	265	213
DJ-1	1.01	DJ-1	436	350
Cytochrome P450 2W1	1.01	Cytochrome P450 2W1	499	401
SIAH1	1.01	SIAH1	247	198
6-Phosphofructo-2-Kinase	1.01	6-Phosphofructo-2-Kinase	310	249
HER2	1.01	HER2	310	249
DCC	1.01	DCC	219	176
DOK6	1.01	DOK6	290	233
A26C2/3	1.01	A26C2/3	267	214
LIMK1	1.01	LIMK1	236	190
EPN2	1.01	EPN2	264	212
PIGH	1.01	PIGH	264	212
Gamma-glutamyltransferase 4 (heavy ch	1.01	Gamma-glutamyltransferase 4 (heavy chain, Cleaved	251	201
NEGR1	1.01	NEGR1	251	201
CLDN19	1.01	CLDN19	294	236
MYH14	1.01	MYH14	177	142
HMG20B	1.01	HMG20B	190	152
STEA3	1.01	STEA3	270	217
Synuclein-pan	1.01	Synuclein-pan	356	285
Cytochrome P450 7B1	1.01	Cytochrome P450 7B1	182	146
S100Z	1.01	S100Z	398	319
CD44	1.01	CD44	134	107
Mevalonate Kinase	1.01	Mevalonate Kinase	277	222
Histone H3 (Acetyl-Lys27)	1.01	Histone H3 (Acetyl-Lys27)	257	206
CYB5R3	1.01	CYB5R3	304	244
IL-1 alpha	1.01	IL-1 alpha	108	87
BCLW	1.01	BCLW	354	284
PTEN	1.01	PTEN	128	103
CBLN2	1.01	CBLN2	261	209
GSK3 beta	1.01	GSK3 beta	161	129
DNAL1	1.01	DNAL1	238	191
CATL1 (heavy chain,Cleaved-Thr288)	1.01	CATL1 (heavy chain,Cleaved-Thr288)	246	197
TAF6L	1.01	TAF6L	251	201
DCT	1.01	DCT	193	154
ЕРНВ6	1.01	EPHB6	220	176
RABEP1	1.01	RABEP1	240	192
ITGA5 (heavy chain,Cleaved-Phe42)	1.01	ITGA5 (heavy chain,Cleaved-Phe42)	148	118

Selficient of Variation for Replicates	Coefficient of Vani	ation for Doulisates
0.01         0.06           0.14         0.05           0.04         0.21           0.05         0.03           0.02         0.09           0.06         0.03           0.07         0.03           0.09         0.05           0.07         0.03           0.02         0.08           0.02         0.05           0.09         0.14           0.03         0.14           0.00         0.03           0.07         0.08           0.01         0.01           0.02         0.08           0.01         0.01           0.02         0.08           0.03         0.01           0.04         0.11           0.05         0.09           0.18         0.00           0.09         0.18         0.00           0.05         0.11           0.02         0.05           0.07         0.02           0.19         0.05           0.07         0.02           0.19         0.05           0.01         0.06           0.02         0.06 <t< th=""><th></th><th></th></t<>		
0.14         0.05           0.04         0.21           0.05         0.03           0.02         0.09           0.06         0.03           0.07         0.09           0.09         0.05           0.07         0.03           0.02         0.08           0.02         0.05           0.09         0.14           0.03         0.14           0.00         0.10           0.00         0.03           0.07         0.08           0.01         0.01           0.04         0.11           0.05         0.09           0.18         0.00           0.05         0.11           0.02         0.05           0.07         0.02           0.19         0.05           0.07         0.02           0.19         0.05           0.01         0.02           0.02         0.06           0.03         0.01           0.04         0.02           0.05         0.00           0.04         0.02           0.05         0.00           0.01 <th></th> <th>1</th>		1
0.04         0.21           0.05         0.03           0.02         0.09           0.06         0.03           0.06         0.07           0.09         0.05           0.07         0.03           0.02         0.08           0.02         0.05           0.09         0.14           0.03         0.14           0.00         0.03           0.07         0.08           0.01         0.01           0.04         0.11           0.05         0.09           0.18         0.00           0.00         0.03           0.05         0.11           0.02         0.05           0.07         0.02           0.19         0.05           0.07         0.02           0.08         0.01           0.09         0.01           0.05         0.00           0.07         0.02           0.08         0.01           0.09         0.06           0.01         0.05           0.02         0.06           0.03         0.06           0.04 <td></td> <td></td>		
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0.09 0.05 0.07 0.03 0.02 0.08 0.02 0.08 0.02 0.05 0.09 0.14 0.03 0.14 0.00 0.10 0.00 0.03 0.07 0.08 0.01 0.01 0.00 0.01 0.04 0.11 0.05 0.09 0.18 0.00 0.07 0.02 0.19 0.05 0.02 0.06 0.04 0.02 0.05 0.01 0.06 0.01 0.06 0.05 0.01 0.05 0.01 0.06 0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.08 0.01 0.01 0.05 0.00 0.06 0.08 0.01 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.06 0.00 0.01 0.01 0.01 0.04 0.06 0.05 0.00 0.06 0.00 0.06 0.00 0.01 0.01 0.01 0.01 0.01 0.04 0.06 0.06 0.09 0.00 0.06 0.00 0.00 0.01 0.00 0.01 0.01 0.00 0.01 0.06 0.00 0.00 0.01 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.00		
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0.09 0.14 0.03 0.14 0.03 0.14 0.00 0.10 0.00 0.10 0.00 0.03 0.07 0.08 0.01 0.01 0.04 0.11 0.05 0.09 0.18 0.00 0.00 0.03 0.05 0.11 0.02 0.05 0.07 0.02 0.19 0.05 0.02 0.06 0.04 0.02 0.05 0.00 0.03 0.05 0.11 0.05 0.00 0.01 0.05 0.02 0.06 0.04 0.02 0.06 0.04 0.02 0.06 0.01 0.05 0.00 0.06 0.01 0.05 0.00 0.06 0.01 0.05 0.00 0.06 0.08 0.01 0.01 0.01 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.07 0.14 0.05 0.20 0.06 0.00 0.01 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.07 0.14 0.09 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.00 0.01 0.06 0.00 0.00 0.00 0.00 0.01 0.06 0.00 0.00 0.01 0.00 0.00 0.01 0.06 0.00 0.00 0.01		
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0.07         0.08           0.01         0.01           0.04         0.11           0.05         0.09           0.18         0.00           0.00         0.03           0.05         0.11           0.02         0.05           0.07         0.02           0.19         0.05           0.02         0.06           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.02         0.06           0.03         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.05         0.20           0.04         0.06           0.05         0.00           0.01         0.06           0.02         0.07           0.04         0.06           0.05         0.00           0.01         0.06           0.02         0.07           0.04 <td></td> <td></td>		
0.01         0.01           0.04         0.11           0.05         0.09           0.18         0.00           0.00         0.03           0.05         0.11           0.02         0.05           0.07         0.02           0.09         0.06           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.01         0.05           0.02         0.06           0.01         0.05           0.02         0.06           0.03         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.05         0.20           0.04         0.06           0.05         0.00           0.01         0.06           0.02         0.07           0.04         0.06           0.05         0.00           0.06         0.00           0.07 <td></td> <td></td>		
0.04         0.11           0.05         0.09           0.18         0.00           0.00         0.03           0.05         0.11           0.02         0.05           0.07         0.02           0.09         0.06           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.01         0.05           0.02         0.06           0.03         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.02         0.07           0.04         0.06           0.05         0.00           0.01         0.06           0.02         0.07           0.04         0.07           0.05         0.01           0.06         0.00           0.07         0.01           0.08 <td></td> <td></td>		
0.05         0.09           0.18         0.00           0.00         0.03           0.05         0.11           0.02         0.05           0.07         0.02           0.19         0.05           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.00         0.06           0.08         0.01           0.01         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.02         0.07           0.04         0.07           0.02         0.07           0.04         0.09           0.08         0.10           0.09         0.08         0.10           0.05         0.04           0.05         0.04           0.05         0.04		
0.18         0.00           0.00         0.03           0.05         0.11           0.02         0.05           0.07         0.02           0.19         0.05           0.02         0.06           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.00         0.06           0.08         0.01           0.01         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.02         0.07           0.04         0.07           0.02         0.07           0.04         0.09           0.08         0.10           0.09         0.08           0.10         0.01           0.05         0.04           0.05         0.04           0.05         0.04           0.05 <td></td> <td></td>		
0.00 0.03 0.05 0.11 0.02 0.05 0.07 0.02 0.19 0.05 0.00 0.06 0.04 0.02 0.06 0.01 0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.01 0.05 0.00 0.06 0.01 0.05 0.00 0.06 0.08 0.01 0.01 0.01 0.06 0.01 0.01 0.01 0.01 0.01 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.07 0.04 0.06 0.00 0.01		
0.05         0.11           0.02         0.05           0.07         0.02           0.19         0.05           0.02         0.06           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.02         0.06           0.08         0.01           0.01         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.02         0.07           0.04         0.07           0.02         0.07           0.04         0.09           0.08         0.10           0.00         0.11           0.07         0.02           0.05         0.04           0.08         0.10           0.09         0.01		
0.02 0.05 0.07 0.02 0.19 0.05 0.02 0.06 0.04 0.02 0.05 0.00 0.05 0.00 0.01 0.05 0.00 0.06 0.01 0.05 0.00 0.06 0.08 0.01 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.07 0.04 0.06 0.00 0.09 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.00 0.00 0.00 0.00	0.00	0.03
0.07         0.02           0.19         0.05           0.02         0.06           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.07         0.08           0.01         0.05           0.02         0.06           0.08         0.01           0.01         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.02         0.07           0.04         0.07           0.02         0.07           0.04         0.09           0.08         0.10           0.00         0.11           0.07         0.02           0.05         0.04           0.08         0.04		
0.19         0.05           0.02         0.06           0.04         0.02           0.05         0.00           0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.00         0.06           0.08         0.01           0.01         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.02         0.07           0.04         0.09           0.08         0.10           0.00         0.11           0.07         0.02           0.05         0.04           0.05         0.04           0.08         0.10           0.05         0.04		
0.02 0.06 0.04 0.02 0.05 0.00 0.13 0.09 0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.01 0.05 0.01 0.05 0.01 0.06 0.08 0.01 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.06 0.00 0.01 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.09 0.00 0.01 0.06 0.00 0.00 0.01 0.06 0.00 0.01 0.01 0.06 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.00		
0.04 0.02 0.05 0.00 0.13 0.09 0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.01 0.05 0.00 0.06 0.08 0.01 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.07 0.10 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.06 0.01 0.07 0.02 0.07 0.02 0.07 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04	0.19	0.05
0.05 0.00 0.13 0.09 0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.08 0.01 0.04 0.06 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.08 0.01 0.05 0.20 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.07 0.10 0.01 0.06 0.01 0.06 0.00 0.01 0.00 0.01 0.06 0.00 0.01 0.00 0.01 0.06 0.00 0.01 0.00 0.01 0.06 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.00 0.00	0.02	0.06
0.13         0.09           0.06         0.01           0.06         0.05           0.01         0.05           0.00         0.06           0.08         0.01           0.01         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.04         0.07           0.02         0.07           0.04         0.09           0.08         0.10           0.00         0.11           0.07         0.02           0.05         0.04           0.08         0.04	0.04	0.02
0.06 0.01 0.06 0.05 0.01 0.05 0.00 0.06 0.08 0.01 0.01 0.01 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.01 0.01 0.01 0.01 0.01 0.06 0.00 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01 0.00 0.01	0.05	0.00
0.06 0.05 0.01 0.05 0.00 0.06 0.08 0.01 0.01 0.01 0.04 0.06 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.01 0.01 0.01 0.01 0.01 0.01		
0.01 0.05 0.00 0.06 0.08 0.01 0.01 0.01 0.04 0.06 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.06 0.00 0.01 0.06 0.00 0.07 0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.07 0.02 0.07 0.02 0.08 0.10 0.00 0.01	0.06	0.01
0.00 0.06 0.08 0.01 0.01 0.01 0.04 0.06 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.06 0.00 0.01 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.06	0.05
0.08         0.01           0.01         0.01           0.04         0.06           0.07         0.14           0.05         0.20           0.04         0.06           0.06         0.00           0.01         0.06           0.04         0.07           0.02         0.07           0.04         0.09           0.08         0.10           0.07         0.02           0.05         0.04           0.08         0.04	0.01	0.05
0.01 0.01 0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.01 0.06 0.02 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.07 0.02 0.07 0.02 0.07 0.02 0.07 0.02 0.08 0.10 0.09 0.08 0.00 0.11 0.07 0.02 0.05 0.04	0.00	0.06
0.04 0.06 0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.08	0.01
0.07 0.14 0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.00	0.01	0.01
0.05 0.20 0.04 0.06 0.06 0.00 0.01 0.06 0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.07 0.02 0.07 0.02 0.07 0.02 0.08 0.04 0.09 0.08 0.08 0.10 0.09 0.09 0.08 0.00	0.04	0.06
0.04 0.06 0.06 0.00 0.01 0.06 0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.00	0.07	0.14
0.06 0.00 0.01 0.06 0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.07 0.02 0.07 0.02 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.05	0.20
0.01 0.06 0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.04	0.06
0.04 0.07 0.02 0.07 0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.06	0.00
0.02 0.07 0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.01	0.06
0.04 0.09 0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.04	0.07
0.08 0.10 0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.02	0.07
0.00 0.11 0.07 0.02 0.05 0.04 0.08 0.04	0.04	0.09
0.07         0.02           0.05         0.04           0.08         0.04	0.08	0.10
0.05         0.04           0.08         0.04	0.00	0.11
0.08 0.04	0.07	0.02
	0.05	0.04
0.02 0.01	0.08	0.04
	0.02	0.01

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.95	0.97	
0.91	0.92	
0.92	0.93	
0.63	0.64	
1.71	1.74	
0.81	0.82	
1.25	1.27	
0.90	0.92	
0.56	0.57	
0.42	0.42	
0.42	0.43	
0.79	0.80	
0.53	0.54	
0.94	0.95	
1.54	1.56	
1.76	1.78	
0.87	0.88	
1.10	1.11	
1.10	1.11	
0.77	0.78	
1.02	1.03	
0.94	0.95	
0.83	0.84	
0.93	0.94	
0.93	0.94	
0.89	0.89	
0.89	0.89	
1.04	1.05	
0.63	0.63	
0.67	0.68	
0.95	0.96	
1.26	1.27	
0.64	0.65	
1.41	1.42	
0.47	0.48	
0.98	0.99	
0.91	0.91	
1.07	1.08	
0.38	0.38	
1.25	1.26	
0.45	0.46	
0.92	0.93	
0.57	0.57	
0.84	0.85	
0.87	0.87	
0.89	0.89	
0.68	0.69	
0.78	0.78	
0.85	0.85	
0.52	0.53	

Antibody	y Array	/ Assay	y Results	Assay	y Data
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Signaling Explorer Antibody Array

		Median Signal	283	225
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
ULK3	1.01	ULK3	250	200
5-Mar	1.01	5-Mar	235	188
ACTN 1/2/3/4	1.01	ACTN 1/2/3/4	235	188
G3BP2	1.01	G3BP2	319	255
A1BG	1.01	A1BG	159	127
JNKK	1.01	JNKK	241	192
CDCA2	1.01	CDCA2	298	238
Flt3 ligand	1.01	Flt3 ligand	278	222
TOP2A	1.00	TOP2A	302	241
MATK (CTK)	1.00	MATK (CTK)	121	97
Mucin-14	1.00	Mucin-14	249	199
TALL-2	1.00	TALL-2	311	248
HPRT	1.00	HPRT	131	104
CLK2	1.00	CLK2	187	149
LEG9	1.00	LEG9	246	196
MUM1	1.00	MUM1	271	216
SLC24A4	1.00	SLC24A4	180	143
AFP	1.00	AFP	1365	1087
CD10	1.00	CD10	128	102
2-Mar	1.00	2-Mar	451	359
RAB7L1	1.00	RAB7L1	284	226
STAT5A/B	1.00	STAT5A/B	396	315
CD3EAP	1.00	CD3EAP	456	363
EPHB2	1.00	EPHB2	290	231
ATP6V1H	1.00	ATP6V1H	229	182
Keratin 19	1.00	Keratin 19	305	242
CHD4	1.00	CHD4	246	196
Collagen V alpha2	1.00	Collagen V alpha2	239	190
p19 INK4d	1.00	p19 INK4d	270	215
ERAB	1.00	ERAB	501	398
ENDOGL1	1.00	ENDOGL1	241 192	191
SLC5A3 EFNA5	1.00	SLC5A3 EFNA5	221	152 175
LAMA3	1.00	LAMA3	264	210
cTnl (TNNI3)	1.00	cTnl (TNNI3)	145	115
PGP9.5	1.00	PGP9.5	290	230
IL-8	1.00	IL-8	138	109
RHG17	1.00	RHG17	287	228
DFFA	1.00	DFFA	388	308
Myoglobin	1.00	Myoglobin	154	122
STAT5A	1.00	STAT5A	229	181
LDLRAD2	1.00	LDLRAD2	178	141
Osteopontin	1.00	Osteopontin	350	277
PCNA	1.00	PCNA	312	247
DNA-PK	1.00	DNA-PK	436	345
TUBGCP4	1.00	TUBGCP4	268	212
CHST2	1.00	CHST2	323	256
PTTG1	1.00	PTTG1	325	257
AURKB	1.00	AURKB	127	100
IKK-gamma	1.00	IKK-gamma	315	249
PLA2G4E	1.00	PLA2G4E	263	208
ABHD14B	1.00	ABHD14B	186	147
ADCY8	1.00	ADCY8	248	196
Free PSA (KLK3)	1.00	Free PSA (KLK3)	124	98

Coefficient of Varie	ation for Replicates
Bigger Sample	Smaller Sample
0.00	0.08
0.02	0.08
0.02	0.09
0.02	0.12
0.04	0.04
0.01	0.07
0.03	0.04
0.00	0.02
0.05	0.04
0.05	0.04
0.05	0.00
0.13	0.02
0.01	0.03
0.02	0.03
0.14	0.01
0.05	0.15
0.04	0.00
0.07	0.02
0.03	0.12
0.08	0.15
0.07	0.08
0.02	0.04
0.11	0.08
0.07	0.01
0.21	0.02
0.01	0.08
0.02	0.04
0.05 0.04	0.13 0.04
	0.07
0.13 0.04	0.01
0.04	0.11
0.06	0.10
0.04	0.03
0.01	0.04
0.05	0.01
0.04	0.06
0.13	0.05
0.04	0.03
0.01	0.05
0.03	0.01
0.09	0.07
0.07	0.01
0.01	0.04
0.05	0.09
0.13	0.05
0.01	0.04
0.12	0.07
0.04	0.03
0.10	0.03
0.03	0.19
0.10	0.08
0.03	0.01
0.06	0.12

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.88	0.89
0.83	0.83
0.83	0.83
1.13	1.13
0.56	0.57
0.85	0.85
1.05	1.06
0.98	0.99
1.07	1.07
0.43	0.43
0.88	0.88
1.10	1.10
0.46	0.46
0.66	0.66
0.87	0.87
0.96	0.96
0.63	0.64
4.82	4.84
0.45	0.45
1.59	1.60
1.00	1.01
1.40	1.40
1.61	1.61
1.02	1.03
0.81	0.81
1.08	1.08
0.87	0.87
0.84	0.84
0.95	0.95
1.77	1.77
0.85	0.85
0.68	0.68
0.78	0.78
0.93	0.93
0.51	0.51
1.02	1.02
0.49	0.48
1.01	1.01
1.37	1.37
0.54	0.54
0.81	0.81
0.63	0.63
1.24	1.23
1.10	1.10
1.54	1.53
0.95	0.94
1.14	1.14
1.15	1.14
0.45	0.44
1.11	1.11
0.93	0.92
0.66	0.65
0.88	0.87
0.44	0.44

Antibody	/ Arrav	Assay I	Resul	ts

Signaling Explorer Antibody Array

		Median Signal	283	225
Protein List	Fold Change between Samples	Protein List		f Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
ADK	0.99	ADK	391	309
Serpin A5	0.99	Serpin A5	238	188
RASSF2	0.99	RASSF2	923	729
MSH6	0.99	MSH6	281	222
FGF-1	0.99	FGF-1	105	83
Integrin beta5	0.99	Integrin beta5	282	223
Collagen XXV alpha1	0.99	Collagen XXV alpha1	197	155
EFEMP1	0.99	EFEMP1	258	204
NRBF2	0.99	NRBF2	239	189
CER1	0.99	CER1	133	105
SRC	0.99	SRC	130	103
FHIT	0.99	FHIT	397	313
Amylin	0.99	Amylin	376	296
Histone H2B	0.99	Histone H2B	279	220
Cytochrome P450 2A6	0.99	Cytochrome P450 2A6	271	214
SLK	0.99	SLK	219	173
LAMA5	0.99	LAMA5	217	171
CBLN1	0.99	CBLN1	301	237
Collagen XVIII alpha1	0.99	Collagen XVIII alpha1	245	193
CBP (Acetyl-Lys1535)	0.99	CBP (Acetyl-Lys1535)	186	146
MAST3	0.99	MAST3	314	247
RPC8	0.99	RPC8	284	223
MSH2	0.99	MSH2	544	428
Elk1	0.99	Elk1	269	212
CNKR2	0.99	CNKR2	206	162
Collagen IV alpha3 (Cleaved-Pro1426)	0.99	Collagen IV alpha3 (Cleaved-Pro1426)	220	173
GABRA6	0.99	GABRA6	236	185
Caspase 6 (Cleaved-Asp162)	0.99	Caspase 6 (Cleaved-Asp162)	310	244
EGF	0.99	EGF	138	108
HSF2	0.99	HSF2	399	313
Keratin 1 (CK1)	0.99	Keratin 1 (CK1)	124	97
SH-PTP2	0.99	SH-PTP2	394	309
Collagen XIX alpha1	0.99		270	212
SLC17A2	0.99	Collagen XIX alpha1 SLC17A2	175	137
FES SECTIFAL	0.99	FES FES	305	239
SIRPB1	0.99	SIRPB1	384	301
HOXA11/D11	0.99	HOXA11/D11	232	182
Smad4	0.99	Smad4	200	157
DNA Polymerase theta	0.99	DNA Polymerase theta	378	297
Annexin A6	0.99	Annexin A6	404	317
CATD (light chain,Cleaved-Gly65)	0.99	CATD (light chain,Cleaved-Gly65)	230	180
MMP15 (Cleaved-Tyr132)	0.99	MMP15 (Cleaved-Tyr132)	197	155
Collagen IV alpha3	0.99	Collagen IV alpha3	271	213
CDC25C	0.99	CDC25C	162	127
CHST8	0.99	CHST8	236	185
POTE8	0.99	POTE8	317	248
PTH (Parathyroid Hormone )	0.99	PTH (Parathyroid Hormone )	127	100
ERK2	0.99	ERK2	139	109
GATA1	0.99	GATA1	139	109
MARK2	0.99	MARK2	259	203
BRI3B	0.99	BRI3B	305	239
CKI-gamma2	0.99	CKI-gamma2	277	217
PARP (Cleaved-Asp214)	0.99	PARP (Cleaved-Asp214)	417	327
IL-6	0.99	IL-6	129	101
KCNK15	0.99	KCNK15	226	177

0 (0 1 1 1 1)	
	ation for Replicates
Bigger Sample	Smaller Sample
0.00	0.14
0.07	0.05
0.03	0.03
0.00	0.05
0.01	0.04
0.24	0.12
0.01	0.16
0.00	0.02
0.00	0.03
0.03	0.07
0.02	0.02
0.04	0.10
0.08	0.02
0.01	0.02
0.09	0.08
0.06	0.02
0.06	0.07
0.04	0.07
0.03	0.07
0.07	0.03
0.02	0.02
0.17	0.07
0.21	0.09
0.06	0.08
0.05	0.00
0.08	0.09
0.12	0.04
0.04	0.07
0.10	0.01
0.13	0.08
0.01	0.15
0.02	0.04
0.05	0.09
0.08	0.01
0.01	0.07
0.18	0.01
0.07	0.01
0.05	0.00
0.02	0.02
0.04	0.05
0.02	0.07
0.10	0.05
0.01	0.01
0.12	0.14
0.04	0.02
0.04	0.07
0.01	0.11
0.04	0.03
0.04	0.08
0.10	0.09
0.03	0.06
0.05	0.00
0.03	0.01
0.03	0.06
0.08	0.07
·	

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.38	1.37
0.84	0.84
3.26	3.24
0.99	0.99
0.37	0.37
1.00	0.99
0.69	0.69
0.91	0.91
0.84	0.84
0.47	0.46
0.46	0.46
1.40	1.39
1.33	1.32
0.98	0.98
0.96	0.95
0.77	0.77
0.77	0.76
1.06	1.05
0.86	0.86
0.66	0.65
1.11	1.10
1.00	0.99
1.92	1.90
0.95	0.94
0.73	0.72
0.78	0.77
0.83	0.82
1.10	1.08
0.49	0.48
1.41	1.39
0.44	0.43
1.39	1.37
0.95	0.94
0.62	0.61
1.08	1.06
1.36	1.34
0.82	0.81
0.70	0.70
1.34	1.32
1.43	1.41
0.81	0.80
0.70	0.69
0.96	0.95
0.57	0.57
0.83	0.82
1.12	1.10
0.45	0.44
0.49	0.48
0.49	0.48
0.91	0.90
1.08	1.06
0.98	0.96
1.47	1.45
0.46	0.45
0.80	0.79

Antibody	/ Arrav	Assay I	Resul	ts

Signaling Explorer Antibody Array

		ivieaian Signai	283	225
Protein List	Fold Change between Samples	Protein List		f Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
SIX5	0.99	SIX5	184	144
C3AR1	0.99	C3AR1	246	193
CHK1	0.99	CHK1	124	97
Notch 2 (Cleaved-Ala1734)	0.98	Notch 2 (Cleaved-Ala1734)	218	170
CLCC1	0.98	CLCC1	238	186
ALDOB	0.98	ALDOB	215	168
YES1	0.98	YES1	140	109
Septin-1	0.98	Septin-1	343	268
ТОРЗВ	0.98	TOP3B	304	238
CDCA3	0.98	CDCA3	345	270
CBLN3	0.98	CBLN3	270	211
BLCAP	0.98	BLCAP	512	400
JAK3	0.98	JAK3	137	107
STYK1	0.98	STYK1	183	143
PARK7	0.98	PARK7	169	132
Septin-3	0.98	Septin-3	218	170
igE	0.98	IgE	143	112
RPC4	0.98	RPC4	275	214
IKBKB (IKK beta)	0.98	IKBKB (IKK beta)	127	99
RPC1	0.98	RPC1	399	311
MIPT3	0.98	MIPT3	215	168
FADD	0.98	FADD	312	243
TNFL4	0.98	TNFL4	271	211
Collagen IV alpha5	0.98	Collagen IV alpha5	296	230
CSTF2T	0.98	CSTF2T	262	204
ABHD12B	0.98	ABHD12B	228	177
SLC5A6	0.98	SLC5A6	246	191
CLIC3	0.98	CLIC3	252	196
LEG7	0.98	LEG7	288	224
MYST1	0.98	MYST1	131	102
CKI-alpha1/L	0.98	CKI-alpha1/L	272	212
BMX (ETK)	0.98	BMX (ETK)	133	103
CD38	0.98	CD38	256	199
RTN3	0.98	RTN3	265	206
CDH4	0.98	CDH4	316	246
ZP1	0.98	ZP1	204	158
CLIC4	0.98	CLIC4	284	221
ALDH1A2	0.98	ALDH1A2	291	226
Neuropsin (Cleaved-Val33)	0.98	Neuropsin (Cleaved-Val33)	244	189
AGR3	0.98	AGR3	428	332
CDH11	0.98	CDH11	214	166
GPRIN3	0.98	GPRIN3	239	185
CIB2	0.98	CIB2	294	228
TUFM	0.98	TUFM	216	168
C1S	0.98	C1S	232	180
ADRB1	0.98	ADRB1	336	261
RDX	0.98	RDX	296	229
Fibulin 5	0.98	Fibulin 5	136	105
HLAH	0.98	HLAH	136	153
Connexin 43 MEF2C	0.98	Connexin 43 MEF2C	446 193	346 150
	0.98			
COX41	0.97	COX41	310	240
BAGE3	0.97	BAGE3	210	163
PRKY	0.97	PRKY	195 453	151
Ku70/80	0.97	Ku70/80		351
Collagen I alpha2 (Cleaved-Gly1102)	0.97	Collagen I alpha2 (Cleaved-Gly1102)	265	205

Coefficient of Varia	Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample		
0.12 0.02	0.11		
0.02	0.04		
0.04	0.07		
0.00	0.11		
0.02	0.13		
0.05	0.05		
0.00	0.12		
0.06	0.07		
0.07	0.07		
0.15	0.04		
0.02	0.04		
0.07	0.05		
0.03	0.09		
0.08	0.05		
0.02	0.06		
0.01	0.04		
0.06 0.04	0.09		
0.09	0.05		
0.06	0.00		
0.10	0.05		
0.05	0.05		
0.04	0.08		
0.03	0.01		
0.05	0.02		
0.07	0.05		
0.02	0.02		
0.04	0.10		
0.01	0.02		
0.03	0.00		
0.07	0.04		
0.17	0.01		
0.11	0.09 0.01		
0.14	0.05		
0.00	0.07		
0.11	0.01		
0.06	0.10		
0.08	0.03		
0.01	0.09		
0.04	0.05		
0.03	0.09		
0.11	0.10		
0.08	0.14		
0.03	0.10		
0.02	0.08		
0.06	0.09		
0.08	0.02		
0.26	0.02		
0.03	0.07		
0.06	0.01		
0.08	0.08		
0.04	0.06 0.11		
0.08	0.07		
0.07	0.07		

Data Normalized	
Bigger Sample	
0.65	0.64
0.87	0.86
0.44	0.43
0.77	0.76
0.84	0.83
0.76	0.75
0.49	0.48
1.21	1.19
1.07	1.06
1.22	1.20
0.95	0.94
1.81	1.78
0.48	0.48
0.64	0.63
0.60	0.59
0.77	0.76
0.51	0.50
0.97	0.95
0.45	0.44
1.41	1.38
0.76	0.75
1.10	1.08
0.96	0.94
1.04	1.02
0.92	0.91
0.80	0.79
0.87	0.85
0.89	0.87
1.02	1.00
0.46	0.45
0.96	0.94
0.47	0.46
0.90	0.89
0.93	0.91
1.12	1.09
0.72	0.70
1.00	0.98
1.03	1.00
0.86	0.84
1.51	1.48
0.76	0.74
0.84	0.82
1.04	1.01
0.76	0.75
0.82	0.80
1.19	1.16
1.04	1.02
0.48	0.47
0.70	0.68
1.58	1.54
0.68	0.67
1.09	1.07
0.74	0.72
0.69	0.67
1.60	1.56
0.94	0.91

Antibody Array Assay Results	Antibod	v Array	Assav Resu	lts
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Signaling Explorer Antibody Array

		Median Signal	283	225
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
TSH	0.97	TSH	155	120
MARK3	0.97	MARK3	283	219
Thioredoxin (TRX)	0.97	Thioredoxin (TRX)	128	99
AXL	0.97	AXL	139	108
EPHB4	0.97	EPHB4	269	208
SLC9A7	0.97	SLC9A7	320	247
ATF6B	0.97	ATF6B	447	346
Collagen III alpha1 (Cleaved-Gly1221)	0.97	Collagen III alpha1 (Cleaved-Gly1221)	302	233
DAXX	0.97	DAXX	132	102
SLC25A21	0.97	SLC25A21	262	202
CD34	0.97	CD34	130	100
Akt3	0.97	Akt3	119	92
HIPK4	0.97	HIPK4	272	210
IL-2	0.97	IL-2	136	105
MSH3	0.97	MSH3	338	261
USP19	0.97	USP19	180	139
4E-BP1	0.97	4E-BP1	166	128
FA7 (light chain,Cleaved-Arg212)	0.97	FA7 (light chain,Cleaved-Arg212)	273	211
TYRO3	0.97	TYRO3	162	125
Histone H2B (Acetyl-Lys5)	0.97	Histone H2B (Acetyl-Lys5)	373	288
TAF5	0.97	TAF5	299	230
CARD6	0.97	CARD6	436	336
ITK (LYK)	0.97	ITK (LYK)	135	104
CDCA4	0.97	CDCA4	457	352
MPRIP	0.97	MPRIP	309	238
SMF	0.97	SMF	279	215
Caspase 9 (Cleaved-Asp353)	0.97	Caspase 9 (Cleaved-Asp353)	161	124
Nucleophosmin (NPM)	0.97	Nucleophosmin (NPM)	207	159
IGLL1	0.97	IGLL1	185	142
Dipeptidyl-peptidase 1 (heavy chain,Clea		Dipeptidyl-peptidase 1 (heavy chain,Cleaved-Arg394)	284	219
ALDOC	0.97	ALDOC	245	188
BACH1	0.97	BACH1	193	148
COX17	0.97	COX17	266	205
USP32	0.97	USP32	335	258
Dynamin-1	0.97	Dynamin-1	136	105
ERCC6	0.97	ERCC6	386	296
RAB20	0.97	RAB20	373	286
Prostate Stem Cell Antigen	0.97	Prostate Stem Cell Antigen	357	274
SRA	0.97	SRA	179	137
C5orf13	0.97	C5orf13	245	188
CSE1L	0.97	CSE1L	468	359
p53 (Acetyl-Lys386)	0.97	p53 (Acetyl-Lys386)	264	203
LAMB3	0.97	LAMB3	324	249
	0.97	EFNA1		267
EFNA1 HSP10		HSP10	348 412	316
	0.97			
SLC6A6	0.97	SLC6A6	279 129	214
CDKN1B	0.97	CDKN1B		99
APC	0.96	APC	492	377
GATA3	0.96	GATA3	139	107
MEKKK 4	0.96	MEKKK 4	319 241	244 185
AKR1CL1	0.96	AKR1CL1		
RAB6A	0.96	RAB6A	250	191
p18 INK		p18 INK	358	274
	0.96		200	450
ACOT4	0.96	ACOT4	200	153
ACOT4 LAMA1 Transglutaminase 2			200 194 396	153 148 303

Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample	
0.01	0.12	
0.06	0.06	
0.00	0.04	
0.07	0.09	
0.04	0.05	
0.03	0.14	
0.03	0.04	
0.12	0.03	
0.01	0.00	
0.00	0.09	
0.01	0.01	
0.03	0.04	
0.02	0.04	
0.02	0.08	
0.06	0.07	
0.04	0.03	
0.21	0.01	
0.05	0.10	
0.07	0.06	
0.14	0.04	
0.01	0.06	
0.06	0.02	
0.03	0.08	
0.07	0.06	
0.02	0.01	
0.02 0.04	0.02	
	0.10	
0.22 0.10	0.12	
0.10	0.13	
0.04	0.13	
0.05	0.04	
0.00	0.10	
0.10	0.09	
0.19	0.07	
0.01	0.07	
0.01	0.14	
0.06	0.03	
0.07	0.22	
0.06	0.07	
0.17	0.07	
0.01	0.06	
0.02	0.01	
0.05	0.09	
0.00	0.09	
0.05	0.08	
0.02	0.01	
0.06	0.01	
0.03	0.03	
0.05	0.06	
0.16	0.14	
0.04	0.03	
0.06	0.04	
0.00	0.08	
0.09	0.02	
0.02	0.05	

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.55	0.53	
1.00	0.97	
0.45	0.44	
0.49	0.48	
0.95	0.93	
1.13	1.10	
1.58	1.54	
1.07	1.04	
0.47	0.45	
0.92	0.90	
0.46	0.44	
0.42	0.41	
0.96	0.93	
0.48	0.47	
1.19	1.16	
0.63	0.62	
0.59	0.57	
0.96	0.94	
0.57	0.55	
1.32	1.28	
1.05	1.02	
1.54	1.49	
0.48	0.46	
1.61	1.57	
1.09	1.06	
0.98	0.95	
0.57	0.55	
0.73	0.71	
0.65	0.63	
1.00	0.97	
0.86	0.84	
0.68	0.66	
0.94	0.91	
1.18	1.15	
0.48	0.46	
1.36	1.32	
1.32	1.27	
1.26	1.22	
0.63	0.61	
0.87	0.84	
1.65	1.60	
0.93	0.90	
1.14	1.11	
1.23	1.19	
1.45	1.40	
0.98	0.95	
0.45	0.44	
1.74	1.68	
0.49	0.47	
1.13	1.09	
0.85	0.82	
0.88	0.85	
1.27	1.22	
0.71	0.68	
0.68	0.66	
1.40	1.35	

Antibody Array Assay Results
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Signaling Explorer Antibody Array

	Fold Change between Samples		Average Signal of Replicate Spots	
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
ADD3	0.96	ADD3	308	235
ARHGEF3	0.96	ARHGEF3	221	169
Septin-8	0.96	Septin-8	288	220
LAMA4	0.96	LAMA4	352	269
TLE4	0.96	TLE4	440	336
PIGY	0.96	PIGY	231	176
Stefin A	0.96	Stefin A	400	305
EGR1	0.96	EGR1	144	110
HMGB1	0.96	HMGB1	336	256
FGR	0.96	FGR	386	295
p15 INK	0.96	p15 INK	485	370
STK39	0.96	STK39	194	148
CA19-9	0.96	CA19-9	175	134
PRIM1	0.96	PRIM1	337	257
CD69	0.96	CD69	143	109
ADA2L	0.96	ADA2L	279	212
CDH20	0.96	CDH20	293	223
MCL-1	0.96	MCL-1	136	104
Claudin 10	0.96	Claudin 10	414	315
Glucose-6-phosphate isomerase	0.96	Glucose-6-phosphate isomerase	142	108
FGF-2	0.96	FGF-2	109	83
ATP2C1	0.96	ATP2C1	182	138
CPNE8	0.96	CPNE8	359	273
	0.96	Calreticulin	192	146
Calreticulin	0.96		275	209
CATZ (Cleaved-Leu62)	0.96	CATZ (Cleaved-Leu62) ARSA	275	180
ARSA				
DGKK	0.95	DGKK	290	220
BRCA2	0.95	BRCA2	323	245
ARHGEF5	0.95	ARHGEF5	354	268
CRYAB	0.95	CRYAB	139	105
ELOVL5	0.95	ELOVL5	279	212
IFN-gamma	0.95	IFN-gamma	126	96
MAPK9	0.95	МАРК9	322	244
RORA	0.95	RORA	357	271
KCNT1	0.95	KCNT1	332	252
CDKA1	0.95	CDKA1	204	155
p55CDC	0.95	p55CDC	229	173
Caspase 3 (Cleaved-Asp175)	0.95	Caspase 3 (Cleaved-Asp175)	301	228
CDK8	0.95	CDK8	340	257
AKR1CL2	0.95	AKR1CL2	255	193
ST6GAL1	0.95	ST6GAL1	302	229
SERPINB7	0.95	SERPINB7	156	118
GPR175	0.95	GPR175	154	116
Retinoid X Receptor gamma	0.95	Retinoid X Receptor gamma	330	249
Notch 2 (Cleaved-Val1697)	0.95	Notch 2 (Cleaved-Val1697)	235	177
E2F6	0.95	E2F6	495	374
UBAC1	0.95	UBAC1	175	132
CDH8	0.95	CDH8	330	249
TAF15	0.95	TAF15	307	232
MDM4	0.95	MDM4	134	101
UBTD1	0.95	UBTD1	203	153
Cyclin E1	0.95	Cyclin E1	487	367
Histone H3 (Acetyl-Lys9)	0.95	Histone H3 (Acetyl-Lys9)	318	240
MEF2B	0.95	MEF2B	480	362
IVILI 40	0.95	IVILI ZU	480	302

Coefficient of Variation for Replicates		
Bigger Sample	Smaller Sample	
0.06	0.01	
0.02	0.05	
0.07	0.00	
0.01	0.07	
0.13	0.15	
0.04	0.16	
0.12	0.11	
0.04	0.03	
0.06	0.02	
0.02	0.02	
0.00	0.05	
0.00	0.02	
0.15	0.01	
0.12	0.07	
0.03	0.07	
0.03	0.07	
0.00	0.01	
0.10	0.10	
0.01	0.04	
0.02	0.05	
0.06	0.03	
0.00	0.11	
0.12	0.09	
0.06	0.12	
0.03	0.02	
0.07	0.10	
0.01	0.04	
0.08	0.14	
0.02	0.00	
0.03	0.03	
0.07	0.02	
0.07	0.04	
0.06	0.02	
0.04	0.02	
0.05	0.02	
0.01	0.06	
0.08	0.03	
0.03	0.05	
0.02	0.02	
0.02	0.05	
0.04	0.16	
0.01	0.04	
0.00	0.02	
0.01	0.04	
0.13	0.08	
0.01	0.09	
0.05	0.06	
0.00	0.07	
0.00	0.04	
0.03	0.11	
0.12	0.03	
0.08	0.05	
0.00	0.09	
0.03	0.01	
	0.01	

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.09	1.05
0.78	0.75
1.02	0.98
1.24	1.19
1.55	1.49
0.81	0.78
1.41	1.36
0.51	0.49
1.19	1.14
1.36	1.31
1.71	1.65
0.69	0.66
0.62	0.59
1.19	1.14
0.50	0.48
0.98	0.94
1.04	0.99
0.48	0.46
1.46	1.40
0.50	0.48
0.38	0.37
0.64	0.61
1.27	1.21
0.68	0.65
0.97	0.93
0.84	0.80
1.02	0.98
1.14	1.09
1.25	1.19
0.49	0.47
0.99	0.94
0.45	0.42
1.14	1.09
1.26	1.20
1.17	1.12
0.72	0.69
0.81	0.77
1.06	1.01
1.20	1.14
0.90	0.86
1.07	1.02
0.55	0.53
0.54	0.52
1.16	1.11
0.83	0.79
1.75	1.66
0.62	0.59
1.16	1.11
1.08	1.03
0.47	0.45
0.72	0.68
1.72	1.63
1.12	1.07
1.70	1.61

Δnti	hody /	Array A	Assav F	Resul	ts

Signaling Explorer Antibody Array

		ivieaian Signai	283	225
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
BRMS1	0.95	BRMS1	162	122
Cytochrome P450 2E1	0.95	Cytochrome P450 2E1	205	154
ATPG	0.95	ATPG	312	235
Adrenergic Receptor alpha-2A	0.95	Adrenergic Receptor alpha-2A	273	206
eNOS	0.95	eNOS	301	227
MYOM1	0.95	MYOM1	253	190
AKR1B1	0.95	AKR1B1	238	179
Collagen XII alpha1	0.95	Collagen XII alpha1	252	190
PRKAB1	0.95	PRKAB1	288	217
ARHGEF10	0.95	ARHGEF10	250	188
KCND1	0.95	KCND1	358	269
PIAS1	0.95	PIAS1	524	394
ITGA5	0.95	ITGA5	143	107
DDX4	0.95	DDX4	155	116
CSTL1	0.95	CSTL1	235	176
CASP5 (p10,Cleaved-Ser331)	0.94	CASP5 (p10,Cleaved-Ser331)	341	256
IP3KA RCL	0.94 0.94	IP3KA RCL	354 298	266 224
ABCB7	0.94	ABCB7	274	205
RHG22	0.94	RHG22	224	168
SPR1	0.94 0.94	SPR1	319 317	239 238
CD153	0.94	CD153		
Cyclin A1	0.94	Cyclin A1	514 147	385 110
IKBKE (IKK epsilon) RBM26	0.94	IKBKE (IKK epsilon) RBM26	282	211
Total PSA	0.94	Total PSA	133	100
NKX3A	0.94	NKX3A	141	105
RhoH	0.94	RhoH	378	282
Neurogenin-3	0.94	Neurogenin-3	162	121
HEN1/2	0.94	HEN1/2	361	270
GLB1L3	0.94	GLB1L3	320	239
FER	0.94	FER	355	265
ADCY5/6	0.94	ADCY5/6	223	166
QSK	0.94	QSK	332	248
АТР7В	0.94	ATP7B	358	267
PMP22	0.94	PMP22	322	240
GRK6	0.94	GRK6	226	168
EPHB1/2/3	0.94	EPHB1/2/3	324	241
S100A16	0.94	S100A16	243	181
STRAD	0.94	STRAD	300	223
S100A10/ P11	0.94	S100A10/ P11	137	102
CNTD2	0.94	CNTD2	550	409
Cytochrome P450 2U1	0.94	Cytochrome P450 2U1	391	291
LAMB2	0.94	LAMB2	408	303
RED	0.94	RED	271	202
ITGA6 (light chain,Cleaved-Glu942)	0.94	ITGA6 (light chain,Cleaved-Glu942)	265	197
FOXJ3	0.94	FOXJ3	322	239
GRID2	0.94	GRID2	263	196
STK36	0.94	STK36	319	237
CDC6	0.94	CDC6	368	273
UBFD1	0.94	UBFD1	193	143
WNT5A	0.93	WNT5A	130	97
CLASP1	0.93	CLASP1	316	235
CREM	0.93	CREM	392	291
<u>-</u>	5.55			

Coefficient of Vari	ation for Replicates
Bigger Sample	Smaller Sample
0.14	0.00
0.08	0.07
0.09	0.06
0.01	0.01
0.12	0.08
0.04	0.01
0.02	0.06
0.09	0.04
0.06	0.03
0.02	0.01
0.07	0.00
0.01	0.07
0.07	0.00
0.11	0.00
0.05	0.18
0.12	0.12
0.01	0.02
0.10	0.05
0.10	0.11
0.01	0.06
0.08	0.19
0.04	0.04
0.01	0.01
0.03	0.09
0.02	0.06
0.07	0.11
0.01	0.09
0.03	0.06
0.07	0.25
0.08	0.01
0.00	0.02
0.02	0.06
0.08	0.09
0.00	0.05
0.03	0.06
0.25	0.01
0.03	0.08
0.12	0.01
0.04	0.00
0.01	0.02
0.01	0.01
0.04	0.02
0.12	0.08
0.05	0.05
0.05	0.18
0.01	0.05
0.08	0.11
0.09	0.02
0.07	0.07
0.08	0.07
0.08	0.01
0.01	0.10
0.01	0.10
	0.05
0.02	0.25

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.57	0.54
0.72	0.69
1.10	1.04
0.96	0.91
1.06	1.01
0.89	0.85
0.84	0.80
0.89	0.84
1.02	0.96
0.88	0.83
1.26	1.19
1.85	1.75
0.50	0.48
0.55	0.52
0.83	0.78
1.20	1.14
1.25	1.18
1.05	0.99
0.97	0.91
0.79	0.75
1.13	1.06
1.12	1.06
1.82	1.71
0.52	0.49
1.00	0.49
0.47	0.44
0.50	0.47
1.33	1.25
0.57 1.28	0.54 1.20
1.13	
	1.06
1.25 0.79	1.18 0.74
1.17	1.10
1.26	1.19
1.14	1.07
0.80	0.75
1.14	1.07
0.86	0.81
1.06	0.99
0.48	0.45
1.94	1.82
1.38	1.29
1.44	1.35
0.96	0.90
0.94	0.88
1.14	1.06
0.93	0.87
1.13	1.05
1.30	1.21
0.68	0.64
0.46	0.43
1.12	1.04
1.38	1.29

Antibody	Array A	Assav	Resul	ts

Signaling Explorer Antibody Array

		ivieaian Signai	283	225
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
RHG9	0.93	RHG9	227	168
RGS1	0.93	RGS1	319	237
CKI-alpha	0.93	CKI-alpha	271	201
Smad1/5/9	0.93	Smad1/5/9	282	209
LAT3	0.93	LAT3	520	385
RFWD2	0.93	RFWD2	294	218
CD8	0.93	CD8	135	100
CXADR	0.93	CXADR	322	239
ORCTL-2	0.93	ORCTL-2	330	244
Caspase 9 (Cleaved-Asp315)	0.93	Caspase 9 (Cleaved-Asp315)	389	288
SLC6A15	0.93	SLC6A15	362	268
SDCG1	0.93	SDCG1	380	281
CD3E	0.93	CD3E	131	97
MAP4K3	0.93	MAP4K3	202	149
MYBPC3	0.93	MYBPC3	173	128
RAB11FIP2	0.93	RAB11FIP2	312	231
GPR160	0.93	GPR160	266	197
IKK Alpha	0.93	IKK Alpha	130	96
·				
ATF3	0.93	ATF3	325	240
CASP3 (p17,Cleaved-Asp175)	0.93	CASP3 (p17,Cleaved-Asp175)	994	734
MEKKK 1	0.93	MEKKK 1	307	227
Cytochrome P450 39A1	0.93	Cytochrome P450 39A1	307	226
CD45	0.93	CD45	128	94
CDKL3	0.93	CDKL3	217	160
RAB3GAP1	0.93	RAB3GAP1	365	269
MCL1	0.93	MCL1	528	389
SNCA (alpha-synuclein)	0.93	SNCA (alpha-synuclein)	209	154
MYH4	0.93	MYH4	197	145
EGFR	0.93	EGFR	140	103
E2F2	0.93	E2F2	227	167
UPF1	0.93	UPF1	375	276
ATP5G2	0.93	ATP5G2	435	320
SNAP25	0.93	SNAP25	310	228
ALDH1B1	0.93	ALDH1B1	282	207
PIP5K	0.93	PIP5K	312	229
ABL1	0.93	ABL1	402	296
Collagen IV alpha3 (Cleaved-Leu1425)	0.93	Collagen IV alpha3 (Cleaved-Leu1425)	279	205
RAB41	0.92	RAB41	382	281
	0.92		282	207
Collagen IV alpha2 MAPK15	0.92	Collagen IV alpha2 MAPK15	600	440
Cytochrome P450 2S1	0.92	Cytochrome P450 2S1	387	284
S6K-alpha6	0.92	S6K-alpha6	237	174
RBM5	0.92	RBM5	265	194
ENAH	0.92	ENAH	383	281
EPHA7	0.92	ЕРНА7	293	215
ACTL6A	0.92	ACTL6A	249	183
CDC7	0.92	CDC7	275	202
JAK2	0.92	JAK2	137	100
TAF5L	0.92	TAF5L	350	256
CATG (Cleaved-Ile21)	0.92	CATG (Cleaved-Ile21)	342	251
MMP12 (Cleaved-Glu106)	0.92	MMP12 (Cleaved-Glu106)	234	171
Claudin 4	0.92	Claudin 4	458	335
3-Mar	0.92	3-Mar	310	227
ADCK3	0.92	ADCK3	205	150
	0.32	1.00.00	203	130

Coefficient of Vari	ation for Replicates
Bigger Sample	Smaller Sample
0.07	0.03
0.09	0.07
0.06	0.05
0.14	0.12
0.08	0.12
0.03	0.06
0.08	0.03
0.06	0.13
0.07	0.03
0.07	0.04
0.08	0.09
0.19	0.03
0.05	0.04
0.07	0.01
0.23	0.13
0.00	0.04
0.16	0.03
0.02	0.07
0.03	0.00
0.06	0.00
0.02	0.01
0.00	0.03
0.03	0.05
0.10	0.10
0.02	0.09
0.03	0.02
0.05	0.12
0.24	0.02
0.11	0.14
0.11	0.08
0.11	0.04
0.06	0.10
0.03	0.03
0.04	0.05
0.09	0.02
0.03	0.07
0.09	0.01
0.00	0.12
0.02	0.01
0.09	0.19
0.01	0.01
0.06	0.03
0.05	0.09
0.05	0.09
0.02	0.05
0.07	0.01
0.04	0.04
0.08	0.04
0.03	0.06
0.02	0.07
0.03	0.09
0.09	0.05
0.08	0.03
0.01	0.05

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
0.80	0.75
1.13	1.05
0.96	0.89
1.00	0.93
1.84	1.71
1.04	0.97
0.48	0.44
1.14	1.06
1.16	1.09
1.37	1.28
1.28	1.19
1.34	1.25
0.46	0.43
0.71	0.66
0.61	0.57
1.10	1.03
0.94	0.87
0.46	0.43
1.15	1.07
3.51	3.26
1.08	1.01
1.08	1.01
0.45	0.42
0.77	0.71
1.29	1.19
1.86	1.73
0.74	0.68
0.70	0.65
0.49	0.46
0.80	0.74
1.32	1.23
1.54	1.42
1.10	1.01
0.99	0.92
1.10	1.02
1.42	1.31
0.99	0.91
1.35	1.25
1.00	0.92
2.12	1.96
1.37	1.26
0.84	0.77
0.93	0.86
1.35	1.25
1.03	0.95
0.88	0.81
0.97	0.90
0.48	0.44
1.23	1.14
1.21	1.11
0.83	0.76
1.62	1.49
1.09	1.01
0.72	0.67
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Anti	body	/ Array /	Assav	Result
Anti	poav	/ Arrav /	Assav	Kesuit

Signaling Explorer Antibody Array

		ivieaian Signai	283	225
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
COT2	0.92	COT2	352	258
Flt-1 (VEGFR1)	0.92	Flt-1 (VEGFR1)	155	113
ARPP21	0.92	ARPP21	318	233
USP6NL	0.92	USP6NL	190	139
Cytochrome c-type Heme Lyase	0.92	Cytochrome c-type Heme Lyase	485	354
5-HT-4	0.92	5-HT-4	278	203
Cytochrome P450 4Z1	0.92	Cytochrome P450 4Z1	345	252
CST2	0.92	CST2	324	237
ITGAV (heavy chain,Cleaved-Lys889)	0.92	ITGAV (heavy chain,Cleaved-Lys889)	211	154
PE2R4	0.92	PE2R4	159	116
WASF4	0.92	WASF4	335	244
SLC28A2	0.92	SLC28A2	205	150
Histone H3 (Acetyl-Lys18)	0.92	Histone H3 (Acetyl-Lys18)	321	234
Cytochrome P450 2C19	0.92	Cytochrome P450 2C19	435	317
GRAH	0.92	GRAH	339	247
AARSD1	0.92	AARSD1	278	203
ACTN alpha-2/3	0.92	ACTN alpha-2/3	383	279
LEG4	0.92	LEG4	291	212
CSK	0.92	CSK	285	207
Rab25	0.92	Rab25	151	110
USP42	0.92	USP42	206	150
CD19	0.92	CD19	138	100
ARHGEF2	0.92	ARHGEF2	323	235
RAB11FIP3	0.92	RAB11FIP3	295	215
CDKL2	0.92	CDKL2	359	261
Dyskerin	0.91	Dyskerin	359	261
NF-kB p65 (Acetyl-Lys310)	0.91	NF-kB p65 (Acetyl-Lys310)	329	239
14-3-3 zeta	0.91	14-3-3 zeta	307	223
RON	0.91	RON	132	96
HOXA6	0.91	HOXA6	197	143
TP53INP2	0.91	TP53INP2	311	226
IL-1 beta	0.91	IL-1 beta	140	102
SLC30A1	0.91	SLC30A1	240	174
Cytochrome P450 3A4/5	0.91	Cytochrome P450 3A4/5	287	208
C1R (light chain,Cleaved-Ile464)	0.91	C1R (light chain,Cleaved-Ile464)	344	249
ATF7	0.91	ATF7	331	240
FGF18	0.91	FGF18	241	174
ADAR1	0.91	ADAR1	441	319
SLC30A4	0.91	SLC30A4	405	293
Adrenergic Receptor alpha-2B	0.91	Adrenergic Receptor alpha-2B	352	255
PC	0.91	PC	240	174
ERN1 (IRE1)	0.91	ERN1 (IRE1)	1930	1395
ACSL6	0.91	ACSL6	224	162
Cullin 3	0.91	Cullin 3	459	332
ADNP	0.91	ADNP	436	315
KSR2	0.91	KSR2	415	300
C140	0.91	C140	268	193
AVEN	0.91	AVEN	280	202
LRP10	0.91 0.91	LRP10	223	161
FOXA2		FOXA2	179	129
KCNJ9	0.91	KCNJ9	335	241
ME3	0.91	ME3	215	155
ATP5G3	0.91	ATP5G3	373	269
5-HT-1A	0.91	5-HT-1A	328	236

Coefficient of Vari	ation for Replicates
Bigger Sample	Smaller Sample
0.02	0.01
0.00	0.04
0.08	0.09
0.11	0.08
0.04	0.06
0.01	0.02
0.02	0.00
0.02	0.07
0.02	0.11
0.00	0.07
0.07	0.03
0.07	0.00
0.17	0.05
0.04	0.06
0.00	0.03
0.02	0.04
0.12	0.14
0.06	0.05
0.02	0.08
0.11	0.12
0.06	0.07
0.03	0.01
0.08	0.03
0.00	0.08
0.05	0.09
0.03	0.02
0.03	0.02
0.06	0.11
0.02	0.11
0.21	0.01
0.04	0.05
0.03	0.01
0.01	0.10
0.07	0.05
0.13	0.01
0.01	0.01
0.04	0.02
0.04	0.01
0.05	0.12
0.10	0.01
0.02	0.05
0.03	0.34
0.09	0.14
0.04	0.02
0.00	0.05
0.06	0.04
0.03	0.16
0.02	0.03
0.09	0.02
0.01	0.12
0.04	0.07
0.06	0.03
0.11	0.07
0.05	0.04

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.24	1.15
0.55	0.50
1.12	1.03
0.67	0.62
1.71	1.58
0.98	0.90
1.22	1.12
1.14	1.05
0.75	0.69
0.56	0.52
1.18	1.09
0.72	0.67
1.13	1.04
1.54	1.41
1.20	1.10
0.98	0.90
1.35	1.24
1.03	0.94
1.01	0.92
0.53	0.49
0.73	0.67
0.49	0.44
1.14	1.04
1.04	0.95
1.27	1.16
1.27	1.16
1.16	1.06
1.08	0.99
0.46	0.42
0.69	0.63
1.10	1.00
0.49	0.45
0.85	0.77
1.01	0.93
1.22	1.11
1.17	1.07
0.85	0.77
	1.42
1.56 1.43	1.42
1.43	1.13
0.85	0.77
6.82	6.21
0.79	0.72
1.62 1.54	1.47
	1.40
1.47	1.33
0.95	0.86
0.99	0.90
0.79	0.71
0.63	0.57
1.18	1.07
0.76	0.69
1.32	1.19
1.16	1.05

Antibody Array Assay Results	Antibod	v Arrav A	Assav I	Results
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Signaling Explorer Antibody Array

		Median Signal	283	225
Protein List	Fold Change between Samples	Protein List		f Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
AATF	0.91	AATF	430	309
NF-kB p65	0.91	NF-kB p65	335	241
RBAK	0.91	RBAK	330	237
APLP2	0.90	APLP2	228	164
CYTL1	0.90	CYTL1	210	151
IRAK3	0.90	IRAK3	275	197
SLC30A8	0.90	SLC30A8	421	302
SNAI2 (SLUG)	0.90	SNAI2 (SLUG)	145	104
MYOM2	0.90	MYOM2	244	175
VANGL1	0.90	VANGL1	231	166
CD33	0.90	CD33	201	144
SOX2	0.90	SOX2	155	111
MARK4	0.90	MARK4	423	303
ATP5A1	0.90	ATP5A1	305	218
ADCY4	0.90	ADCY4	343	246
UBAP2L	0.90	UBAP2L	189	135
CDH3	0.90	CDH3	427	305
PDRG1	0.90	PDRG1	329	235
ICAM1	0.90	ICAM1	131	94
ATP6V1B1	0.90	ATP6V1B1	285	203
MAP3K9	0.90	MAP3K9	285 466	333
SAR1B	0.90	SAR1B	211	151
EFNB3	0.90	EFNB3	487	347
Cytochrome P450 4X1	0.90	Cytochrome P450 4X1	221	158
Histone H2B (Acetyl-Lys12)	0.90	Histone H2B (Acetyl-Lys12)	457	326
C56D2	0.90	C56D2	429	306
Fos	0.90	Fos	533	379
C9orf89	0.90	C9orf89	304	216
ATF1	0.90	ATF1	397	283
ADCK1	0.90	ADCK1	250	178
CLK1	0.90	CLK1	306	218
MLH1	0.89	MLH1	401	285
UBA5	0.89	UBA5	430	305
LRP3	0.89	LRP3	264	187
Collagen IV alpha6	0.89	Collagen IV alpha6	401	285
Keratin 10	0.89	Keratin 10	389	276
Collagen V alpha1	0.89	Collagen V alpha1	333	236
DDR1	0.89	DDR1	175	124
ATRX	0.89	ATRX	268	190
EPHA6	0.89	EPHA6	563	399
M3K13	0.89	M3K13	320	227
Cytochrome P450 2R1	0.89	Cytochrome P450 2R1	296	210
SLC24A6	0.89	SLC24A6	221	156
CDK2	0.89	CDK2	323	229
MAPK3	0.89	маркз	388	274
CMKLR1	0.89	CMKLR1	426	301
ARFGEF2	0.89	ARFGEF2	417	295
CaMK1-beta	0.89	CaMK1-beta	380	268
STAG3	0.89	STAG3	327	231
Cyclin G	0.89	Cyclin G	1053	742
RAB34	0.89	RAB34	279	197
DLEC1	0.89	DLEC1	279	197
Collagen XI alpha1	0.89	Collagen XI alpha1	350	246
NKX2.5	0.89	NKX2.5	150	106

Coefficient of Varia	ation for Replicates
Bigger Sample	Smaller Sample
0.10	0.05
0.05	0.08
0.00	0.11
0.08	0.00
0.04	0.04
0.06	0.01
0.04	0.10
0.07	0.10
0.12	0.10
0.17	0.04
0.01	0.11
0.03	0.08
0.03	0.09
0.00	0.08
0.02	0.08
0.07	0.01
0.04	0.03
0.02	0.01
0.05	0.07
0.13	0.02
0.08	0.08
0.07	0.03
0.02	0.16
0.03	0.02
0.02	0.12
0.00	0.01
0.13	0.00
0.01	0.01
0.04	0.00
0.03	0.10
0.03	0.02
0.02	0.51
0.02	0.06
0.01	0.16
0.04	0.02
0.02	0.00
0.04	0.08
0.05	0.14
0.03	0.13
0.03	0.02
0.08	0.02
0.02	0.06
0.05	0.10
0.17	0.05
0.09	0.05
0.01	0.00
0.03	0.07
0.02	0.03
0.04	0.06
0.17	0.01
0.13	0.08
0.13	0.07
0.03	0.07
0.08	0.09

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
1.52	1.37	
1.18	1.07	
1.16	1.05	
0.80	0.73	
0.74	0.67	
0.97	0.88	
1.49	1.34	
0.51	0.46	
0.86	0.78	
0.82	0.74	
0.71	0.64	
0.55	0.49	
1.49	1.35	
1.08	0.97	
1.21	1.09	
0.67	0.60	
1.51	1.35	
1.16	1.04	
0.46	0.42	
1.01	0.90	
1.65	1.48	
0.75	0.67	
1.72	1.54	
0.78	0.70	
1.61	1.45	
1.52	1.36	
1.88	1.69	
1.07	0.96	
1.40	1.26	
0.88	0.79	
1.08	0.97	
1.42	1.27	
1.52	1.36	
0.93	0.83	
1.42	1.27	
1.37	1.23	
1.18	1.05	
0.62	0.55	
0.95	0.84	
1.99	1.77	
1.13	1.01	
1.05	0.93	
0.78	0.69	
1.14	1.02	
1.37	1.22	
1.51	1.34	
1.47	1.31	
1.34	1.19	
1.15	1.03	
3.72	3.30	
0.99	0.87	
0.98	0.87	
1.23	1.09	
0.53	0.47	
0.33	0.47	

Antibody	ν Array A	Assay F	Results

Signaling Explorer Antibody Array

		ivieaian Signai	283	223
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
EMR1	0.89	EMR1	251	177
Aggrecan (Cleaved-Asp369)	0.89	Aggrecan (Cleaved-Asp369)	303	213
GRB2	0.89	GRB2	455	320
SESN1	0.88	SESN1	283	199
POLI	0.88	POLI	406	285
MAST4	0.88	MAST4	316	222
Foxp3	0.88	Foxp3	237	166
ARF4	0.88	ARF4	330	231
MMP17 (Cleaved-Gln129)	0.88	MMP17 (Cleaved-Gln129)	258	180
p53	0.88	p53	312	217
MET	0.88	MET	407	284
CA5B	0.88	CA5B	459	319
AMPD1	0.88	AMPD1	248	172
ACBD6	0.88	ACBD6	384	267
MCM5	0.87	MCM5	347	241
WDHD1	0.87	WDHD1	357	248
CaMK2beta/gamma	0.87	CaMK2beta/gamma	370	257
Collagen IV	0.87	Collagen IV	1246	864
SIAH2	0.87	SIAH2	362	251
SPTA2 (Cleaved-Asp1185)	0.87	SPTA2 (Cleaved-Asp1185)	331	230
MYL3	0.87	MYL3	178	123
CHML	0.87	CHML	345	239
S100A3	0.87	S100A3	369	255
	0.87	UBE3B	310	215
UBE3B			338	234
Cytochrome P450 2A13	0.87	Cytochrome P450 2A13		
KCNG3	0.87	KCNG3	456	313
FA12 (heavy chain,Cleaved-Arg372)	0.87	FA12 (heavy chain,Cleaved-Arg372)	524	360
EFNA4	0.86	EFNA4	666	457
ATP5D	0.86	ATP5D	461	317
Cofilin	0.86	Cofilin	395	271
DFF45 (Cleaved-Asp224)	0.86	DFF45 (Cleaved-Asp224)	299	205
PMS2/PMS2CL	0.86	PMS2/PMS2CL	563	385
TNNI3K	0.86	TNNI3K	512	350
POLG2	0.86	POLG2	340	233
ME1	0.86	ME1	293	200
LAMP3	0.86	LAMP3	319	218
AIG1	0.86	AIG1	228	155
ZADH2	0.86	ZADH2	292	199
SHC2	0.86	SHC2	458	312
WEE2	0.86	WEE2	439	299
APOF	0.86	APOF	316	215
MYL2	0.86	MYL2	283	192
FA10 (activated heavy chain, Cleaved-Ile:	0.86	FA10 (activated heavy chain,Cleaved-Ile235)	382	260
Caspase 7 (Cleaved-Asp198)	0.86	Caspase 7 (Cleaved-Asp198)	904	614
Parkin	0.85	Parkin	488	331
Cytochrome P450 2C8/9/18/19	0.85	Cytochrome P450 2C8/9/18/19	416	282
Adrenergic Receptor alpha-2C	0.85	Adrenergic Receptor alpha-2C	298	202
CASP4 (p20,Cleaved-Gln81)	0.85	CASP4 (p20,Cleaved-Gln81)	239	162
CA181	0.85	CA181	353	239
Hexokinase-3	0.85	Hexokinase-3	307	207
STAT1	0.85	STAT1	337	228
Histone H4 (Acetyl-Lys12)	0.85	Histone H4 (Acetyl-Lys12)	583	394
Histone H2A (Acetyl-Lys5)	0.85	Histone H2A (Acetyl-Lys5)	370	250
p16 INK	0.85	p16 INK	427	288
bro use	0.03	PTO HIM	44/	400

Cff'-'	- 1' f P l' 1
	ation for Replicates
Bigger Sample	Smaller Sample
0.01	0.08
0.01	0.07
0.06	0.11
0.13	0.01
0.01	0.01
0.09	0.11
0.00	0.01
0.01	0.01
0.11	0.09
0.01	0.00
0.10	0.09
0.00	0.04
0.07 0.16	0.01
	0.04
0.04	0.49
0.14	0.07
0.07	0.00
0.32	0.02 0.01
0.05	
0.00	0.00 0.15
0.05	0.05
0.03	0.03
0.01	0.03
0.02	0.19
0.02	0.07
0.02	0.06
0.01	0.02
0.07	0.02
0.06	0.07
0.04	0.10
0.08	0.01
0.03	0.10
0.04	0.03
0.10	0.00
0.00	0.01
0.07	0.01
0.02	0.03
0.10	0.05
0.09	0.03
0.09	0.03
0.06	0.12
0.11	0.12
0.19	0.02
0.11	0.04
0.03	0.02
0.09	0.02
0.12	0.02
0.03	0.03
0.06	0.22
0.18	0.01
0.03	0.09
0.27	0.12
0.07	0.15
-	

Data Normalized to Median Signal		
Bigger Sample	Smaller Sample	
0.89	0.79	
1.07	0.95	
1.61	1.42	
1.00	0.88	
1.43	1.27	
1.12	0.99	
0.84	0.74	
1.17	1.03	
0.91	0.80	
1.10	0.97	
1.44	1.26	
1.62	1.42	
0.87	0.77	
1.36	1.19	
1.23	1.07	
1.26	1.10	
1.31	1.14	
4.40	3.84	
1.28	1.12	
1.17	1.02	
0.63	0.55	
1.22	1.06	
1.30	1.13	
1.10	0.95	
1.19	1.04	
1.61	1.39	
1.85	1.60	
2.35	2.03	
1.63	1.41	
1.40	1.21	
1.06	0.91	
1.99	1.71	
1.81	1.56	
1.20	1.03	
1.03	0.89	
1.13	0.97	
0.80	0.69	
1.03	0.88	
1.62	1.39	
1.55	1.33	
1.12	0.96	
1.00	0.85	
1.35	1.15	
3.19	2.73	
1.72	1.47	
1.47	1.25	
1.05	0.90	
0.84	0.72	
1.25	1.06	
1.08	0.92	
1.19	1.01	
2.06	1.75	
1.31	1.11	
1.51	1.28	

Anti	body	/ Array /	Assav	Result
Anti	poav	/ Arrav /	Assav	Kesuit

Signaling Explorer Antibody Array

		Median Signal	283	225
Protein List	Fold Change between Samples	Protein List		of Replicate Spots
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
PAR4 (Cleaved-Gly48)	0.85	PAR4 (Cleaved-Gly48)	380	256
NSG1	0.85	NSG1	308	207
S6K-alpha2	0.85	S6K-alpha2	356	239
SHD	0.85	SHD	326	219
USP36	0.84	USP36	233	156
TAF1A	0.84	TAF1A	302	202
TNF12	0.84	TNF12	454	304
ADPGK	0.84	ADPGK	337	226
p97 MAPK	0.84	p97 MAPK	367	246
Collagen XIV alpha1	0.84	Collagen XIV alpha1	412	275
SOD1	0.84	SOD1	551	368
TACD1	0.84	TACD1	518	345
AASDHPPT	0.84	AASDHPPT	282	188
PARP (Cleaved-Gly215)	0.84	PARP (Cleaved-Gly215)	678	451
GPR150	0.84	GPR150	331	220
COPZ1	0.83	COPZ1	488	324
CATL2 (Cleaved-Leu114)	0.83	CATL2 (Cleaved-Leu114)	271	180
CASP2 (p18,Cleaved-Gly170)	0.83	CASP2 (p18,Cleaved-Gly170)	247	164
CASP8 (Cleaved-Asp384)	0.83	CASP8 (Cleaved-Asp384)	262	173
NCR3	0.83	NCR3	498	329
NOX5	0.83	NOX5	447	295
ABCA8	0.83	ABCA8	292	193
URB1	0.83	URB1	278	183
MYO1D	0.83	MYO1D	332	219
MMP3 (Cleaved-Phe100)	0.83	MMP3 (Cleaved-Phe100)	291	191
GRK3	0.82	GRK3	351	229
Histone H2AX	0.82	Histone H2AX	470	306
Cytochrome P450 2D6	0.82	Cytochrome P450 2D6	366	238
ARSD	0.82	ARSD	222	145
HMGB2	0.82	HMGB2	333	216
CD3	0.82	CD3	181	117
NOX3	0.82	NOX3	349	226
p57KIP2	0.81	p57KIP2	365	235
KCNV2	0.81	KCNV2	434	279
MRP9	0.81	MRP9	392	252
SGOL1	0.81	SGOL1	317	204
Histone H4 (Acetyl-Lys8)	0.81	Histone H4 (Acetyl-Lys8)	343	220
Androgen receptor	0.81	Androgen receptor	341	219
RAB18	0.81	RAB18	341	219
CKLF2	0.80	CKLF2	465	297
UNG	0.80	UNG	397	252
IgM	0.78	IgM	7177	4465
COX2	0.78	COX2	359	222
Collagen I	0.78	Collagen I	427	264
CASP5 (p20,Cleaved-Asp121)	0.78	CASP5 (p20,Cleaved-Asp121)	488	301
NCR1	0.77	NCR1	402	247
TTF2	0.77	TTF2	219	134
ADAM 17 (Cleaved-Arg215)	0.77	ADAM 17 (Cleaved-Arg215)	511	312
SLC39A1	0.77	SLC39A1	426	259
Cadherin-pan	0.77	Cadherin-pan	559	340
PE2R3	0.74	PE2R3	321	189
Cytochrome P450 1A1/2	0.73	Cytochrome P450 1A1/2	603	352
Caspase 9 (Cleaved-Asp330)	0.73	Caspase 9 (Cleaved-Asp330)	468	271
EFNA2 (Cleaved-Asn188)	0.73	EFNA2 (Cleaved-Asn188)	325	188
ELIVAZ (CICAVCU-ASIITOO)	0.73	ELIANE (CICATEA-WILLIAM)	323	100

Coefficient of Varia	ation for Replicates
Bigger Sample	Smaller Sample
0.14	0.05
0.00	0.05
0.01	0.08
0.13	0.02
0.10	0.04
0.11	0.01
0.17	0.02
0.03	0.00
0.01	0.05
0.05	0.13
0.08	0.12
0.01	0.05
0.10	0.09
0.14	0.09
0.10	0.12
0.07	0.09
0.16	0.04
0.07	0.10
0.22	0.07
0.00	0.04
0.07	0.06
0.01	0.06
0.20	0.02
0.09	0.01
0.06	0.02
0.05	0.05
0.03	0.06
0.05	0.08
0.24	0.11
0.18	0.01
0.04	0.07
0.08	0.06
0.00	0.12
0.04	0.02
0.03	0.04
0.07	0.11
0.20	0.05
0.07	0.15
0.10	0.20
0.01	0.05
0.08	0.11
0.07	0.18
0.03	0.30
0.04	0.02
0.10	0.03
0.02	0.09
0.32	0.05
0.23	0.07
0.02	0.09
0.04	0.19
0.20	0.10
0.13	0.04
0.07	0.10
0.02	0.01

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
1.34	1.14
1.09	0.92
1.26	1.06
1.15	0.97
0.82	0.69
1.07	0.90
1.60	1.35
1.19	1.00
1.30	1.09
1.46	1.22
1.95	1.64
1.83	1.54
1.00	0.83
2.40	2.00
1.17	0.98
1.72	1.44
0.96	0.80
0.87	0.73
0.93	0.77
1.76	1.46
1.58	1.31
1.03	0.86
0.98	0.81
1.17	0.97
1.03	0.85
1.24	1.02
1.66	1.36
1.29	1.06
0.78	0.64
1.17	0.96
0.64	0.52
1.23	1.01
1.29	1.05
1.53	1.24
1.38	1.12
1.12	0.91
1.21	0.98
1.20	0.97
1.20	0.97
1.64	1.32
1.40	1.12
25.36	19.86
1.27	0.99
1.51	1.17
1.72	1.34
1.42	1.10
0.77	0.60
1.80	1.39
1.51	1.15
1.97	1.51
1.13	0.84
2.13	1.56
1.65	1.20
1.15	0.84
-	

Antibody Array	Assay Results	Assay Data		
Signaling Explorer Antibody Array		Median Signal	283	225
Description	Fold Change between Samples	Burstalla Hat	Average Signal o	of Replicate Spots
Protein List	Smaller Sample/Bigger Sample	Protein List	Bigger Sample	Smaller Sample
Ferritin	0.73	Ferritin	1476	851
Histone H1 (Acetyl-Lys25)	0.72	Histone H1 (Acetyl-Lys25)	375	213
BLK	0.71	BLK	212	120
14-3-3 beta	0.69	14-3-3 beta	398	219
CASP1 (p20,Cleaved-Asn120)	0.69	CASP1 (p20,Cleaved-Asn120)	589	323
MMP14 (Cleaved-Tyr112)	0.69	MMP14 (Cleaved-Tyr112)	395	216
GPR171	0.68	GPR171	273	148
E-cadherin	0.68	E-cadherin	506	272
ITGA5 (light chain,Cleaved-Glu874)	0.67	ITGA5 (light chain,Cleaved-Glu874)	492	264
MMP27 (Cleaved-Tyr99)	0.67	MMP27 (Cleaved-Tyr99)	772	410
GPR173	0.66	GPR173	394	207
GPR153	0.61	GPR153	783	380
DNAL4	0.61	DNAL4	349	169
MDFI	0.60	MDFI	568	270
Histone H4 (Acetyl-Lys5)	0.55	Histone H4 (Acetyl-Lys5)	335	147
SUMO2/3 (Cleaved-Gly93)	0.54	SUMO2/3 (Cleaved-Gly93)	811	347
	4.20	Average of Frank Contra	112	02
Min	1.20	Average of Empty Spots	112 130	82 110
Max	4.41 1.37	Average of Negative Controls  Average of Positive Markers	2405	2552
Mean	1.37	Average of Fositive Ivial Refs	2403	2552

Coefficient of Variation for Replicates								
Bigger Sample	Smaller Sample							
0.01	0.15							
0.01	0.15							
0.02	0.05							
0.05	0.08							
0.10	0.05							
0.08	0.06							
0.07	0.07							
0.03	0.02							
0.09	0.07							
0.10	0.06							
0.06	0.20							
0.02	0.01							
0.43	0.11							
0.07	0.08							
0.53	0.14							
0.05	0.04							
0.03	0.07							

0.04

0.04

0.08

0.02

Data Normalized	to Median Signal
Bigger Sample	Smaller Sample
5.21	3.79
1.33	0.95
0.75	0.53
1.40	0.97
2.08	1.43
1.39	0.96
0.96	0.66
1.79	1.21
1.74	1.17
2.73	1.82
1.39	0.92
2.77	1.69
1.23	0.75
2.01	1.20
1.18	0.65
2.86	1.54

## Appendix F Pooled-Microarray

Globally

ormalized Me

MED

Normalized Signal %CFC

Globally

Z-ratio

-0.53

-0.38

0.15

NP\_003647

Q8IU85

MAX

>+200%

3433 4055 Log2 (Intensity %Error Range Globally Globally Log2 (Intensity Serial Full Target Antibody Target Phospho Site %Error Range %CFC (Treated Z-score Difference Z-ratio Flag-Control Normalized Control Control Normalized Treated Corrected) -Z score (Control) Block Row Column Refseq Uniprot Link Codes Control (Treated, Control Pan-specific PN001 4F-RP1 S65 Fukaryotic translatio 1183 -0.67 -0 11 -0.41 NP 004086 Q13541 Q13541 0, 0 0, 0 0, 0 0, 0 CN005 4G10 pTyr Y309 Phosphotyrosine (Clor Twinfilin-2 2906 8478 4526 9463 0.06 0.22 N/A N/A PK502 Afir 0.50 NP 009215 1 13538 833 NK001 Abl Pan-specific Abelson proto-oncoge 0, 0 1339 -0.87 -0.66 NP 005148 P00519 P00519 P00519 NK001-2 0.28 NP 005148 1981 1933 -0.23 0.12 PK001 Abl Abelson proto-oncoge -0.06 0.03 NP\_005148 NP\_000655 Y393 Q13085 Q07912 P68133 PN002 S79 Acetyl coenzyme A ca NK002 ACK1 Pan-specific Activated CDC42 kins 2677 2884 -0.20 0.35 NP\_005772 NP\_001091. 1.27 0.95 0.13 CN001 0.26 Pan-specific Actin, alpha skeletal r Adducin a/g P35611 O95831 P54819 PN003-PN00 S662 Adducin alpha (ADD1) 0.0 0.22 0.25 0.04 NP 058432 NN002 NN003 1727 NP\_004199 NP\_001616 AIF AK2 Pan-specific Apoptosis inducing fac -0.45 0.09 0.28 Pan-specific Adenylate kinase 2 P31749 P31749 P31749 NK129-3 Akt1 Pan-Specific RAC-alpha serine/thre 0.0 9868 -31 0.54 0.30 -0.24 -0.86 NP 005154 NK129-5 RAC-alpha serine/thre 0, 0 -0.17 -0.11 NP\_005154 NP\_005154 RAC-alpha serine/thre 0.35 PK517 Akt1 Y326 0.24 -0.39 RAC-alpha serine/thre RAC-alpha serine/thre NP\_005154 NP\_005154 NP\_005154 P31749 P31749 P31749 NK129 AKT1 (PKRa) 0, 0 0, 0 0, 0 18678 642 522 0.90 0.86 -0.04 -0.04 -0.29 PK072-3 Akt1 (PKBa) S473 RAC-alpha serine/thre PK072-5 Akt1 (PKRa) S473 RAC-alpha serine/thre RAC-alpha serine/thre 0, 0 0.07 -0.19 -0.03 -0.69 NP\_005154 NP\_005154 P31749 P31749 PK148 Akt1 (PKBa) -33 -0.86 P31751 P31751 P31751 NK130-4 Akt2 Pan-Specific RAC-heta serine/thren 0, 0 0, 0 0, 0 19180 12930 0.92 0.68 -0.24 0.05 NP\_001617 NP\_001617 Pan-specific Pan-specific NK130-6 Akt2 RAC-heta serine/thre RAC-beta serine/threo 0, 0 0, 0 0, 0 0, 0 NK130-8 Akt2 Pan-Specific RAC-beta serine/threo 43939 0, 0 44572 1.39 0.02 NP 001617 P31751 NK130-9 Akt2 Akt3 ALK Pan-Specific RAC-beta serine/three NK131-3 Pan-Specific RAC-gamma serine/th 0.08 0.29 NP 005456 Q9Y243 NK003 Pan-specific 0.03 AAB71619 Q9UM73 PK520 ALK Y1507 0, 0 AAR71610 Q9UM73 P54646 AMPKa2 PK522 5'-AMP-activated prote 0.53 0.56 0.03 NP 006243.2 2430 P57078 P07355 O95757 PK523 ANKRD3 S438 Ankvrin repeat domain 2630 -0.26 0.00 PN504 NN004 ANXA2 APG1 NP\_001002857. NP\_055093 Y238 Annexin A2 0, 0 0.03 3259 2431 -0.09 -0.26 -0.06 0.23 Pan-specific Hsp 70-related heat sl NN122 APG2 Pan-specific Hsp 70-related heat st 0.0 0.0 275 -0.11 0.49 0.60 BAA75062 P34932 P05067 APP A-Raf 445 2947 Amyloid beta A4 prote 0.60 NP\_000475.1 NK205-2 Pan-specific A-Raf proto-oncogene 0.0 272 -0.15 0.27 0.42 NP 001645. P10398 NK205-4 NK205-5 Pan-Specific A-Raf proto-oncogene Pan-Specific A-Raf proto-oncogene NP\_001645.1 NP\_001645.1 P10398 P10398 P10398 A-Raf A-Raf A-Raf 0, 0 0, 0 0, 0 0.00 12135 -0.06 PK500 Y302 A-Raf proto-oncogene 0.65 -0.23NP 001645. Arrestin b Arrestin b Pan-specific S412 -0.64 -0.30 NN121 -1.26 -0.18 -0.08 NP\_004032 PN133 Arrestin beta 1 NP\_004032 P49407 Apoptosis signal regul Apoptosis signal regul Apoptosis signal regul NP\_005914 NP\_005914 NP\_005914 NK007 ASK1 Pan-specific 0, 0 0, 0 0, 0 8633 0.07 0.27 -1.13 0.38 -0.33 -0.10 Q99683 ASK1 ASK1 Q99683 Q59GL6 NK007-2 PK143 Activating transcription Activating transcription 0, 0 0, 0 0, 0 0, 0 PN115 ATF2 S94/S112 0, 0 2347 -31 -0.07 -0.33 -0.26 -0.94 NP 001871 P15336 ATF2 P15336 7480 13925 AurKA AurKA NK008-3 Pan-Specific Aurora Kinase A (serin 0.52 1.53 0.21 NP\_940835 NP\_940835 O14965 NK008-4 Pan-Specific Aurora Kinase A (serir O14965 O14965 AurKA AurKB Aurora Kinase A (seri 0, 0 32540 27283 1.22 NP\_940835 34058 19213 -30 -0.74 NK193-2 Pan-Specific Aurora Kinase B (serin 0.92 -0.20 NP 004208 Q96GD4 NK103-3 AurKB Pan-Specific Aurora Kingge R (serin 40853 22551 25015 42532 11125 21895 0.04 NP 004208 AurKB AurKB Pan-Specific Aurora Kinase B (serin -0.42 -0.08 NP\_004208 NP\_004208 PK530 S227 Aurora Kinase B (serin Q96GD4 NKUU0-2 AurkC Pan-Specific Aurora Kinasa C (serie 0.0 -25 1.03 0.86 -0.17 -0.61 NP 003151 Q9UQB9 0, 0 P06748 PN008 B23 (NPM T199 B23 (nucleophosmin -0.90 -0.95 -0.06 NP\_002511 PN009 B23 (NPM) T234/237 B23 (nucleophosmin 0.0 -1.55 -0.23 -0.84 NP 002511 P06748 1529 16330 Q16611 Q07812 NN000 NN005 Pan-specific -0.47 0.28 Pan-specific Apoptosis regulator Bi NK257-1 BCKD (BCKDK) Pan-Specific [3-methyl-2-oxobutano 0.77 0.93 0.16 NP 001116429. O14874 NN006-1 Pan-specific B-cell lymphoma prote 0, 0 -0.07 -0.03 -0.27 NP\_000624 231 12691 2220 NN006 Pan-specific B-cell lymphoma prote NP\_000624 P10415 NN007 Bcl-XL Bcl-xS/L Bcr Pan-specific Bcl2-like protein 1 Pan-specific Bcl2-like protein 1 0.68 0.93 0.08 -1.60 0.24 0.39 -0.10 NP\_612815 NP\_612815 NP\_004318.3 Q07817 Q07817 P11274 -0.37 PK164 Y177 Breakpoint cluster regi 281 2174 PK538 Bor Y177 Breakpoint cluster regi BH3 interacting domai 0, 0 3583 -0.32 -0.07 0.25 NP 004318.3 3690 13889 -0.06 0.73 -0.45 -0.60 BLK 16960 11974 PK542 Y188 B lymphoid tyrosine kii -18 -23 -0.12 -0.17 NP 001706.2 P51451 PN013 BI NK Y84 0.65 0.48 NP 037446 O75498 P51813 Bone marrow X protei NP\_001712 -0.76 0, 0 -0.21 PK003 BMX (Etk) Y40 Bone marrow X proteir -1.93 -2.13 NP 001712 P51813 RafB proto-oncogene P15056 P15056 P15056 P15056 P15056 1730 2511 NP\_004324 NP\_004324 NP\_004324 NK156 B-Raf Pan-specific -0.57 -0.71 B-Raf B-Raf NK156-4 Pan-Specific RafB proto-oncogene 36252 8923 -0.16 -0.20 NK156-5 Pan-Specific RafB proto-oncogene 0.29 S446+pS447 RafB proto-oncog 25355 24433 416 PK534 R.Raf 22653 1.08 -n ne -0.23 NP 004324 B-Raf 0, 0 0, 0 0.19 PK535 S729 1.25 NP 004324 RafB proto-oncogene 1.06 -1.22 PN116 BRCA1 S1423 Breast cancer type 1 s -35 -1.27 -0.34 NP 009225 P38398 BRCA1 BRD2 S1497 Breast cancer type 1 s 0.33 NP\_009225 NP\_005095 P38398 P25440 Q8TDC3 0.72 -0.10 Pan-specific PK549 BRSK1 T189 BR serine/threonine-p 0.0 12522 12206 0.68 0.65 -0.03 NP 115806.1 Btk CA9 Pan-specific Bruton's agammaglob 2333 0.65 0.28 NN174 Pan-specific Carbonic anhydrase 9 0,0 -0.02 0.06 KP\_006716930.1 Q16790 PN015 Caldesmor Calnexin S789 Caldesmon Calnexin -1.81 1.20 1.53 -1.84 1.18 1.53 -0.03 -0.03 0.00 -0.13 -0.10 0.00 NP\_004333 NP\_001019820.1 NP\_004334.1 Q05682 P27824 P27797 Pan-specific NN137-1 Pan-specific

SAMPLE DETAILS

NK016-2

CaMK1d

Pan-specific Calcium/calmodulin-de

Sample IDs: Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

Globally

malized Me

Globally Normalized Signal MED MAX %CFC >+200%

Z-ratio

Globally

-0.22

-0.21

AAA60095

P05771-2

Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

Globally

malized Me ormalized Me 3433 4055 Log2 (Intensity Globally %Error Range Log2 (Intensit Serial Full Target Antibody Target Phospho Site %Error Range %CFC (Treated Z-score Difference Z-ratio Flag-Contro Normalized Control Control Z score (Control) Z score (Treated) Block Row Column Refseq Uniprot Link No. Codes Control (Treated, Control NP\_057065.2 -0.54 PK555 NK019-2 CAMK2d Pan-specific Pan-specific Calcium/calmodulin-de 5143 0.12 0 14 0.02 NP 742126 0, 0 0, 0 0, 0 0, 0 0, 0 4362 1520 PK556 CaMK4 T200 Calcium/calmodulin-de 0.08 0.00 0.02 NP\_001735.1 NP\_003647.1 Q16566 NK211 CamKI CaMKK Pan-specific Pan-Specific Calcium/calmodulin-d 2661 -0.53 Q14012 Q8N5S9 0.00 3908 5199 4116 5760 PN505 Cas-L Y166 Enhancer of filamental 0.17 NP 001135865. Q14511 P29466 Caspase 1 Pan-specific 0.34 NP\_001214 NP\_004337 -0.34 0.05 Caspase 3 Pan-specific 0, 0 -0.09 0.02 P42574 Caspase 3 (apopain, c P55212 P55210 P35221 P35222 P35222 P35222 -1.84 NN016 Caspase 6 Pan-specific Caspase 6 (apoptotic NP 001217 NN017-2 Caspase 7 Pan-specific Caspase 7 (ICE-like a 1159 1073 1666 1136 -0.68 0.15 NP\_01218 NP\_001277236. PN162 -0.03 Catenin a S641 Catenin (cadherin-ass 2196 1340 501 100 NN021 Catenin b Pan-specific Catenin (cadherin-ass 0.0 2086 -0.32 -0.39 -0.08 -0.28 NP 001895 S33 Y333 0.27 NP\_001895 NP\_001895 Catenin (cadherin-ass 0.07 PN167 Catenin b Catenin (cadherin-ass 384 119 103 NN021-1 Catenin b1 Pan-Specific Catenin (cadherin-assi 0.0 0.0 -1.31 -1.28 0.03 NP 001895 NN167 0, 0 0.05 NP\_001166366. Q03135 Q03135 Pan-specific NP 001166366. PN147 Caveolin 1 Y14 Caveolin 1 -1.36 Caveolin 2 Caveolin 2 2291 3695 285 853 NP\_001224 NP\_001224 NP\_005179.2 P51636 P51636 P22681 106 NN022-1 0, 0 0, 0 0, 0 1833 -20 -0.29 -0.02 -0.64 -0.53 PN171 c-Cbl Y700 Signal transduction or 0.0 -1.63 -0.15 109 110 NP001 CD45 CD63 Pan-specific Pan-specific Leukocyte common a CF63 Antigen 0, 0 -0.86 -0.17 -1.37 -0.62 NP\_002829 NP\_001244318. P08575 P08962 NN186 -4.97 NK025-5 Cdc2 n34 Pan-specific Cyclin-dependent prot 0, 0 0, 0 0, 0 -0.97 -0.67 0.29 -0.22 -0.27 NP\_001777 NP\_001777 P06493 Pan-specific Pan-Specific Cyclin-dependent prot Cell division cycle 25A P06493 P30304 NK025-6 Cdc2 p34 -0.81 -0.98 CDC25A 114 115 NP038-2 CDC25A Pan-Specific Cell division cycle 25A 39187 0, 0 31088 1.33 1.20 -0.13 -0.23 NP 001780.2 P30304 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 NP038-3 CDC25A Pan-Specific Cell division cycle 25A 8921 1769 -0.84 NP\_001780.2 116 117 NP002 Cdc25B Cdc25B Pan-specific Cell division cycle 25B -0.66 -0.22 -0.09 -0.78 NP\_004349 NP\_004349 P30305 P30305 P30305 NP002-2 Pan-Specific Cell division cycle 25B 0.98 -0.32 118 NP002-3 Cdc25E Pan-Specific Cell division cycle 25B 48033 2485 NP\_004349 2750 119 NP003 Cdc25C Pan-specific Cell division cycle 25C -0.25 -0.23 0.02 NP 001781 P30307 0.25 P30307 P30307 Q14004 NP003-2 Cdc25C Pan-Specific Cell division cycle 25C NP 001781 Cdc25C CDC2L5 NP\_001781 NP\_003709 Pan-Specific 41343 5759 1.36 1.37 0.01 Cell division cycle 250 NK024 Pan-specific Cell division cycle 2-lik 123 NN023 Cdc34 Pan-specific Cell division cycle 34 ( 0.0 763 1059 1784 0.0 572 759 1998 -0.92 -0.24 NP 004350 P49427 P60953 CDC42 Pan-specific Cell division control pri 0, 0 -0.26 125 PK558 CDC7 T376 Cell division cycle 7-re 0.0 0.0 -0.44 0.02 NP 001127891. O00311 NK025-1 NK025-2 CDK1 Pan-specific Pan-specific NP\_001777 NP\_001777 P06493 P06493 P06493 126 127 0, 0 0, 0 0, 0 0.70 -0.06 -0.22 0.11 0.0 NP 001777 PK563 CDK1 Y19 Cyclin-dependent prot 0.43 0.54 CDK1/2 CDK1/2 Cyclin-dependent prot Cyclin-dependent prot NP\_001777 NP\_001777 129 130 PK006 Y14/Y15 1431 1191 -0.16 -0.03 -0.59 P06493 PK007-1 P06493 Cyclin-dependent prot Cyclin-dependent prot Cell division cycle 2-lik 224 131 132 133 PK007-3 CDK1/2 0, 0 0, 0 0, 0 -1.62 -1.47 0.02 -0.29 -0.14 NP\_001777 P06493 CDK1/CDC2 CDK11A P06493 Q9UQ88 PK008-1 T161 -1.04 -0.50 NP\_076916.2 PK565 134 NK026-3 CDK2 Pan-specific Cyclin-dependent prot 0, 0 -2 47 -2 62 -0.15 -0.55 NP 001789 P24941 3432 9381 2743 P24941 CDK2 CDK2 CDK4 CDK4 CDK4 -0.58 136 137 NK026-6 Pan-specific Cyclin-dependent prot -0.16 -0.34 NP\_001789 NP\_001789 P24941 NK026-7 Pan-specific Cyclin-dependent pro 286 1645 -0.54 P24941 P11802 138 0, 0 0.06 0.23 NK027-2 Pan-specific Cyclin-dependent prot -0.78 -0.72 NP 000066 P11802 P11802 Q00535 Q00535 PK560 T172 12242 -0.08 -n 28 NP 000066 CDK5 CDK5 Pan-specific Cyclin-dependent prot 0, 0 0, 0 0, 0 0, 0 33922 17087 26949 4550 -0.13 -0.79 NP\_004926 NP\_004926 NK028-4 Pan-specific Cyclin-dependent prot 143 NK028-5 CDK5 Pan-specific Cyclin-dependent prot 3687 5521 -0.02 0.18 0.20 NP 004926 CDK6 NK029 Pan-specific Cyclin-dependent prot 53698 3031 798 934 0.05 NP\_001250 Q00534 145 NK029-3 CDK6 Pan-specific Cyclin-dependent prot 0.0 -0.13 -0.85 -0.71 -2.59 -0.68 NP 001250 Q00534 PK165 NK030-2 Y13 Pan-specific NP\_001250 NP\_001790 Q00534 P50613 P49336 CDK6 Cyclin-dependent prot Cyclin-dependent prot -0.19 1.17 -0.14 148 NK031-5 CDK8 Pan-specific Cyclin-dependent prot 2257 2287 -0.30 -0.34 -0.04 NP 001252 CDK9 NK032 Cyclin-dependent prot 0, 0 8403 3639 0.33 NP\_001252.1 P50750 4512 4712 -0.67 PK574 Cyclin-dependent prot -0.18 NP\_001252. P50750 151 152 153 PK575 CDK9 Chk1 Chk1 T186 Cyclin-dependent prot Checkpoint protein-sei 0, 0 0, 0 0, 0 10504 10056 0.58 0.53 -0.04 -0.09 0.18 -0.15 -0.34 NP\_001252.1 P50750 O14757 O14757 NP\_001265 NK034-2 Checkpoint protein-sei Pan-specific 154 155 156 157 0, 0 0, 0 0, 0 0, 0 -0.06 -0.24 -0.01 -0.05 PK162 Chk1 Chk1 S280 Checkpoint protein-sei Checkpoint protein-sei 147 15644 2533 0, 0 -1.86 -1 92 NP\_001265 NP\_001265 014757 014757 2692 PK578 Chk1 Chk1 S317 Checkpoint protein-ser -0.24 -0.24 -0.03 -0.19 NP\_001265 NP\_001265 014757 PK579 S345 O14757 O96017 -0.32 159 160 161 162 0, 0 0, 0 0, 0 0, 0 0, 0 243 2431 1674 -1.57 PK119 Chk2 T68 Checkpoint protein-ser 0, 0 -1.66 -0.09 NP 009125 O96017 244 2132 O96017 P48730 PK581 Chk2 CK1d CK1e TES Checkpoint protein-s -0.26 -0.12 0.07 -0.44 Pan-specific 2074 NP\_001884 NP\_001885 NK036 Casein protein-serine NK037-1 Pan-specific Casein protein-serine P49674 P68400 P68400 NK041 CK2a Pan-Specific 0.57 -0 11 -0.41 NP 001887 CK2a 0, 0 164 165 T360/S362 0.00 NP 001887 Casein protein-serine -1.99 -1.99 -1.01 539 NN026 Cofilin Pan-specific Cofilin 1 -29 -0.28 NP 005498 P23528 Cofilin 1 Cofilin 2 821 2030 -0.14 -0.06 0.17 NP\_005498 NP\_068733 P23528 Q9Y281 P17302 168 PN148 Connexin 43 S367 Gap junction alpha-1 0.0 -1.49 -1.31 NP 000156. Cortactin 169 170 PN022-2 Cortactin (amplaxin) (r 6502 18321 6810 16839 NP\_031829 Q14247 Pan-Specific NP\_005195 P41279 NK042 Osaka thyroid oncoger 0.89 -0.05 NK042-2 COT Pan-Specific Osaka thyroid once 0.73 -0.56 0.55 -1.78 -1.52 -0.18 -1.22 -0.23 -0.66 NP\_005195 NP\_000954 NP\_004725 P41279 P35354 Osaka thyroid oncogei Cyclo-oxygenase 2 (pr 1436 NN027 -0.82 015075 NK043 Pan-specific Serine/threonine-prote cPKC ?II

SAMPLE DETAILS

174

NK134-2

Pan-specific Protein-serine kinase (

Sample IDs:

Globally Normalized Signal

Z-ratio

SAMPLE DETAILS

Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

Sample IDs:

						Normalized Median				Normalized Median												
						3433 Globally		Log2 (Intensity		4055 Globally	%Error Range	Log2 (Intensity										
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Normalized - Control	%Error Range Control	Corrected) - Control	Flag-Treated	Normalized - Treated	Treated	Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link
175	PN023	CREB1		cAMP response eleme	0, 0	377	10	5	0, 0	311	13	5	-18	-1.32	-1.52	-0.20	-0.71	1	6	9	NP_004370	P16220
176	PN024 NN182	CREB1 CrkL (32H4)		cAMP response eleme	0, 0	18492 11600	10	11	0, 0	9990 10671	13	10	-46	0.90	0.53	-0.37 -0.06	-1.33 -0.23	5	6	9	NP_004370 NP_005198.1	P16220 P46109
178	NN149-1	Crystallin aB		Crystallin alpha B (hea	0, 0	20231	7	11	0, 0	19215	3	11	-o -5	0.95	0.92	-0.03	-0.12	5	6	10	NP_005196.1	P02511
179	NN149-2	Crystallin aB	Pan-specific	Crystallin alpha B (hea	0, 0	2391	5	8	0, 0	2674	18	8	12	-0.27	-0.25	0.02	0.08	9	6	10	NP_001876	P02511
180 181	PN025 PN110	Crystallin aB Crystallin aB	S19 S45	Crystallin alpha B (hea Crystallin alpha B (hea	0, 0	23305 16114	32 25	11	0, 0	19310 10532	39 12	11	-17 -35	1.03	0.92	-0.11 -0.26	-0.40 -0.93	13	6	9	NP_001876 NP_001876	P02511 P02511
182	NK234-3	CSF1R		Macrophage colony-st	0, 0	52530	52	12	0, 0	47202	41	12	-35	1.49	1.45	-0.26	-0.93	13	6	10	NP_001275634.1	P02511 1 P07333
183	PK587	CSF1R	Y699	Macrophage colony-st	0, 0	3593	54	8	0, 0	4522	39	9	26	-0.04	0.06	0.10	0.36	1	6	11	NP_001275634.1	P07333
184 185	NK044 NK044-2	Csk Csk	Pan-specific	C-terminus of Src tyror	1, 0 0, 0	16491 1963	14	11	1, 0	3129 2012	12	8	-81	0.83 -0.38	-0.15 -0.42	-0.99 -0.03	-3.58 -0.13	5	6	11	NP_004374 NP_004374	P41240 P41240
186	NN028	Cvclin A	Pan-specific		0, 0	32054	21	12	0, 0	29325	21	12	-9	1.21	1.17	-0.05	-0.13	13	6	11	NP_004374 NP_003905	P78396
187	NN029	Cyclin B1		Cyclin B1	0, 0	1627	49	7	0, 0	3071	10	8	89	-0.49	-0.17	0.32	1.17	5	7	1	NP_114172	P14635
188 189	PN190 NN030-1	Cyclin B1 Cyclin D1	S147 Pan-specific	Cyclin B1 Cyclin D1 (PRAD1)	0, 0	1529 20429	28	7	0, 0	1352 12767	14 24	7	-12 -38	-0.52 0.96	-0.65 0.68	-0.13 -0.28	-0.46 -1.01	1	7	1	NP_114172 NP_444284	P14635 P24385
190	NN031	Cyclin E			0, 0	3347	74	8	0, 0	12676	215	10	279	-0.08	0.67	0.75	2.71	4	7	2	NP_444204 NP_001229	P24385 P24864
191	PN191	Cyclin E	T395	Cyclin E1	0, 0	1512	0	7	0, 0	1953	29	8	29	-0.53	-0.43	0.10	0.35	13	7	1	NP_001229	P24864
192	NN032	Cyclin G1	Pan-specific	Cyclin G1	0, 0	4039	14	9	0, 0	7605 18996	175	10	88	0.03	0.37	0.34	1.23	8 12	7	2	NP_004051	P51959
193 194	NN033 PN026	CytoC Dab1	Pan-specific Y198	Cytochrome C Disabled homolog 1	0, 0	2605 386	10	5	0, 0	18996 510	85 115	6	32	-0.22 -1.31	0.91 -1.23	1.13 0.08	0.30	16	7	2	NP_061820 NP_066566	P99999 075553
195	NN034	DAXX	Pan-specific	Death-associated prote	0, 0	5658	96	9	0, 0	3984	139	9	-30	0.22	-0.01	-0.24	-0.85	4	7	3	NP_001341	Q9UER7
196	PK591	DDR1		Epithelial discoidin dor	0, 0	4449 3807	102	9	0, 0	4257 7605	43	9	-4 100	0.09	0.03	-0.06	-0.21	8	7	3	NP_001189450.1	Q08345
197	NK219 NK048	DGKZ DNAPK		Diacylglycerol kinase z DNA-activated protein	0, 0	514	21	9	0, 0	7605 650	20	10	27	0.00 -1.15	0.37 -1.08	0.37	0.23	12	7	3	NP_963290 NP_008835	Q13574 P78527
199	PK595	DNAPK	T2609	DNA-activated protein-	0, 0	2320	39	8	0, 0	2853	28	8	23	-0.29	-0.21	0.08	0.28	4	7	4	NP_008835	P78527
200	PN027	Dok2		Docking protein 2	0, 0	5057	30	9	0, 0	4141	22	9	-18	0.16	0.01	-0.15	-0.54	12	7	4	NP_034201	<u>060496</u>
201 202	PN027-2 NK050	Dok2 DRAK2		Docking protein 2 DAP kinase-related ap	0, 0	8250 9602	38	10	0, 0	5295 11036	15 25	9	-36 15	0.44	0.16	-0.28 0.06	-1.02 0.24	16	7	4	NP_034201 NP_004217	O60496 O94768
203	NP006-2	DUSP1 (MKP1)	Pan-Specific	MAP kinase phosphat	0, 0	52371	4	12	0, 0	57511	11	13	10	1.49	1.57	0.07	0.26	4	7	5	NP 004408.1	P28562
204	NP006-3	DUSP1 (MKP1)		MAP kinase phosphat	0, 0	62341	13	13	0, 0	67111	7	13	8	1.59	1.66	0.06	0.23	8	7	5	NP_004408.1	P28562
205 206	NP047-2 NP045-2	DUSP10 DUSP11		Dual specificity protein  Phosphatidylinositol-3	0, 0	9001 18395	83	10	0, 0	5604 13081	39 22	9	-38 -29	0.49	0.19	-0.30 -0.21	-1.08 -0.74	12	7	5	NP_009138.1 NP_001558.3	Q9Y6W6 Q15357
207	NP045-3	DUSP11		Phosphatidylinositol-3	0, 0	12848	16	10	0, 0	12344	3	10	-4	0.69	0.66	-0.04	-0.13	4	7	6	NP 001558.3	O15357
208	NP046-2	DUSP12	Pan-Specific	Dual specificity protein	0, 0	17597	21	11	0, 0	6642	49	9	-62	0.87	0.29	-0.58	-2.10	8	7	6	NP_009171.1	Q9UNI6
209 210	NP046-3 NP008-2	DUSP12 DUSP2		Dual specificity protein  Dual specificity protein	0, 0	20860	27	11	0, 0	12860	22	10	-38 47	0.97	0.68	-0.29 0.12	-1.04 0.42	12 16	7	6	NP_009171.1 NP_004409.1	Q9UNI6 Q05923
211	NP008-4	DUSP2		Dual specificity protein	0, 0	88425	8	13	0, 0	87376	3	13	-1	1.79	1.81	0.02	0.07	4	7	7	NP 004409.1	Q05923
212	NP030-2	DUSP3		Dual specificity protein	0, 0	70094	12	13	0, 0	70605	11	13	1	1.66	1.69	0.03	0.10	8	7	7	NP_004081.1	P51452
213 214	NP030-3 NP030-4	DUSP3 DUSP3	Pan-Specific	Dual specificity protein Dual specificity protein	0, 0	13683 29820	15	10	0, 0	7118 26743	29	10	-48 -10	0.73	0.33	-0.40 -0.06	-1.43 -0.21	12 16	7	7	NP_004081.1 NP_004081.1	P51452 P51452
215	NP007-3	DUSP4		Dual specificity protein	0, 0	51925	13	12	0, 0	54063	0	12	4	1.49	1.53	0.04	0.15	3	7	2	NP 001385.1	Q13115
216	NP007-4	DUSP4		Dual specificity protein	0, 0	54019	4	12	0, 0	63054	12	13	17	1.51	1.62	0.11	0.39	7	7	2	NP_001385.1	Q13115
217 218	NP039-2 NP040-1	DUSP5 DUSP6		Dual specificity protein  Dual specificity protein	0, 0	18447 50481	39	11	0, 0	32764 51767	73	12	78	0.90	1.23 1.50	0.34	1.21 0.11	11	7	2	NP_004410.3 NP_001937.2	Q16690 Q16828
219	NP040-1	DUSP6		Dual specificity protein	0, 0	20708	29	11	0, 0	12832	11	10	-38	0.96	0.68	-0.28	-1.03	3	7	3	NP_001937.2	Q16828
220	NP040-3	DUSP6		Dual specificity protein	0, 0	15026	18	11	0, 0	16153	15	11	8	0.78	0.81	0.03	0.12	7	7	3	NP_001937.2	Q16828
221	NP041-1 NP041-2	DUSP7 DUSP7		Dual specificity protein  Dual specificity protein	0, 0	17620 36261	30 23	11	0, 0	14386 33773	16	11	-18	0.87 1.28	0.75 1.25	-0.12 -0.03	-0.45 -0.12	11 15	7	3	NP_001938.2 NP_001938.2	Q16829 Q16829
223	NP041-2 NP041-3	DUSP7		Dual specificity protein	0, 0	34924	23	12	0, 0	29910	49	12	-14	1.26	1.18	-0.03	-0.12	3	7	4	NP_001938.2	Q16829
224	NP042-3	DUSP8	Pan-Specific	Dual specificity protein	0, 0	26583	3	11	0, 0	22231	3	11	-16	1.11	1.00	-0.10	-0.37	7	7	4	NP_004411.2	Q13202
225 226	NP043-2 PN509	DUSP9 eFF1A1		Dual specificity protein	0, 0	30618	49	12	0, 0	26332	24 33	11	-14	1.19	1.10	-0.08 0.01	-0.30 0.02	11 15	7	4	NP_001386.1 NP_001393.1	Q99956 P68104
227	NN175	EFNA5	Pan-Specific	Elongation factor 1-alp Ephrin-A5	0, 0	2440 324	35	5	0, 0	2663 229	26	5	-29	-1.41	-0.25	-0.29	-1.05	3	7	5	NP_001393.1	P52803
228	NK052-1	EGFR	Pan-specific	Epidermal growth factor	0, 0	21806	27	11	0, 0	15781	12	11	-28	0.99	0.80	-0.19	-0.69	11	7	7	NP_005219	P00533
229 230	NK052-4 NK052-5	EGFR EGFR		Epidermal growth factor	0, 0	49060 54753	9	12	0, 0	51119 54645	10 17	12	4	1.46	1.50	0.04	0.14	3 11	7	7	NP_005219 NP_005219	P00533 P00533
231	NK052-6	EGFR		Epidermal growth factor	0, 0	44239	16	12	0, 0	45427	12	12	3	1.40	1.43	0.02	0.06	15	7	6	NP_005219 NP_005219	P00533
232	PK121	EGFR	T693	Epidermal growth facto	0, 0	753	40	6	0, 0	1209	160	7	61	-0.93	-0.72	0.21	0.77	11	7	5	NP_005219	P00533
233	PK122-1 PK123	EGFR EGFR	Y1068 Y1110	Epidermal growth factor	0, 0	588 1229	9	6 7	0, 0	665 1278	12 10	6	13	-1.07 -0.65	-1.07 -0.68	0.00	0.00 -0.13	7 15	7	6	NP_005219 NP_005219	P00533 P00533
235	PK010	EGFR	Y1148	Epidermal growth factor	0, 0	1480	2	7	0, 0	1316	28	7	-11	-0.54	-0.67	-0.12	-0.45	3	7	6	NP_005219	P00533
236	PK010-2	EGFR	Y1148	Epidermal growth factor	0, 0	958	1	7	0, 0	1305	66	7	36	-0.79	-0.67	0.12	0.43	7	7	7	NP_005219	P00533
237 238	PK011-1 PK603	EGFR EGFR	Y1197 Y998	Epidermal growth factor	0, 0	476 3589	0 84	6	0, 0	678 3756	233	6	42	-1.19 -0.04	-1.06 -0.05	0.13 -0.01	0.48 -0.04	7 15	7	5	NP_005219 NP_005219	P00533 P00533
239	NN038-1	elF2a		Eukaryotic translation	0, 0	36	187	2	0, 0	41	110	2	14	-2.66	-2.71	-0.05	-0.19	2	7	2	NP_004085	P05198
240	PN028-1	elF2a	S52	Eukaryotic translation	0, 0	427	39	5	0, 0	393	49	5	-8	-1.25	-1.38	-0.13	-0.47	6	7	2	NP_004085	P05198
241 242	PN028-2 PN172	elF2a elF4B	S52 S422	Eukaryotic translation Eukaryotic translation	0, 0	213 306	20 43	4	0, 0	369 262	61	5	73 -14	-1.65 -1.44	-1.42 -1.62	0.23 -0.18	0.84 -0.64	10 14	7	2	NP_004085 NP_001287750.1	P05198 P23588
242	NN039-1	elF4B elF4E		Eukaryotic translation	0, 0	851	61	6	0, 0	339	21	5	-14 -60	-1.44	-1.62	-0.18	-0.64	10	7	3	NP_001287750.1	P23588 P06730
244	PN030-1	elF4E	S209	Eukaryotic translation	0, 0	15184	32	11	0, 0	12265	10	10	-19	0.79	0.65	-0.13	-0.49	2	7	3	NP_001959	P06730
245 246	PN030-2 PN031	elF4E elF4G	S209 S1108	Eukaryotic translation Eukaryotic translation	0, 0	366 5431	46	5	0, 0	251 4411	46	5	-31 -19	-1.34 0.20	-1.64 0.05	-0.31 -0.15	-1.10 -0.55	6	7	3	NP_001959 NP_004944	P06730 Q04637
246	PN031 PN193	elF4G elF4G	S1108 S1232	Eukaryotic translation	0, 0	304	7	5	0, 0	784	68	6	158	-1.45	-0.97	-0.15	1.71	2	7	4	NP_004944 NP_004944	Q04637 Q04637
248	NN168	Elk 1	Pan-specific	ETS domain-containin	0, 0	129	21	4	0, 0	131	49	4	2	-1.94	-2.03	-0.09	-0.34	6	7	4	NP_001107595.1	P19419
249 250	PN149 PN170	Elk1	S383 S389	ETS domain-containin	0, 0	780 397	9	6	0, 0	628 359	6 51	6	-19 -10	-0.91 -1.29	-1.10 -1.43	-0.20 -0.14	-0.71 -0.51	10	7	4	NP_001107595.1	
250	NN170	Epcam		Epithelial cell adhesion	0, 0	243	47	5	0, 0	359	6	5	35	-1.29 -1.57	-1.43 -1.49	-0.14	0.31	2	7	5	NP_001107595.1 NP_002345.2	P19419 P16422
252	NK053	EphA1	Pan-specific	Ephrin type-A receptor	0, 0	754	77	6	0, 0	1013	24	7	34	-0.93	-0.82	0.11	0.38	6	7	5	NP_005223	P21709
253 254	PN173 PK134	Ephrin-B2 ERB2	Y316 T686	EPH-related receptor t ErbB2 (Neu) receptor-	0, 0	526 51204	7 41	6	0, 0	561 52514	20	6	7	-1.13 1.48	-1.17 1.51	-0.04 0.03	-0.14 0.11	10 14	7	5	NP_004084.1 NP_004439	P52799 P04626
254	NK054-2	ErbB2		ErbB2 (Neu) receptor-	0, 0	2281	21	8	0, 0	11089	65	10	386	-0.30	0.59	0.03	3.22	2	7	6	NP_004439 NP_004439	P04626
256	NK054-4	ErbB2	Pan-Specific	ErbB2 (Neu) receptor-	0, 0	39981	10	12	0, 0	36890	20	12	-8	1.34	1.30	-0.04	-0.13	6	7	6	NP_004439	P04626
257	NK054-5	ErbB2		ErbB2 (Neu) receptor-	0, 0	31474	0	12	0, 0	31783 12271	14	12	1	1.20	1.21	0.01	0.04	10	7	6	NP_004439	P04626
258 259	PK013-1 NK231-2	ErbB2 ErbB3	Y1248 Pan-Specific	ErbB2 (Neu) receptor- Tyrosine kinase-type c	0, 0	14948 54019	53	11	0, 0	12271 57961	51 2	10	-18 7	0.78 1.51	0.65 1.57	-0.13 0.06	-0.45 0.21	14	7	7	NP_004439 NP_001005915.1	P04626 P21860
260	NK231-3	ErbB3	Pan-Specific	Tyrosine kinase-type c	0, 0	39244	13	12	0, 0	40848	10	12	4	1.33	1.36	0.03	0.13	6	7	7	NP_001005915.1	P21860
261	PK163	ErbB3	Y1328	Tyrosine kinase-type c	0, 0	1207	10	7	0, 0	988	33	7	-18	-0.66	-0.84	-0.18	-0.64	10	7	7	NP_001005915.1	P21860

Globally

Z-ratio <-1.5 0

SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger

Treated ID: Pooled Samples Smaller

Globally

						Globally Normalized Median 3433				Normalized Median 4055		<-1.5				>+1.5						
Serial No.	Antibody Codes	Target Protein Name		Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link
262	NK235-1	ErbB4		Receptor tyrosine-prot	0, 0	34166	37	12	0, 0	27892	44	11	-18	1.25	1.14	-0.11	-0.40	14	7	7	NP_001036064.1	Q15303
263 264	NK235-3 NK055-1	ErbB4 ERK1		Receptor tyrosine-prot Extracellular regulated	0, 0	41147 52427	23 21	12 12	0, 0	40594 40302	20 13	12 12	-1 -23	1.36	1.36 1.35	0.00 -0.14	0.01 -0.50	1 13	7	2	NP_001036064.1 36142.1, NP_002	Q15303 P27361
265	NK055-2	ERK1		Extracellular regulated	0, 0	29454	20	11	0, 0	17327	23	11	-41	1.16	0.86	-0.31	-1.12	1	7	3	36142.1, NP 002	P27361
266	NK055-3	ERK1	Pan-Specific	Extracellular regulated	0, 0	46086	15	12	0, 0	41950	3	12	-9	1.42	1.38	-0.04	-0.15	5	7	3	36142.1, NP_002	P27361
267 268	NK055-NK056 PK867	ERK1/2 FRK1	Pan-specific S74	Extracellular regulated Extracellular regulated	0, 0	6240 3714	13	9	0, 0	5738 3144	8	9	-8 -15	0.28	0.20	-0.08 -0.13	-0.27 -0.49	9	7	3	36142.1, NP_002	P27361
268	PK867 PK621	ERK1		Extracellular regulated	0, 0	3714 4763	75	9	0, 0	3144 6553	115	9	-15 38	0.12	0.28	-0.13 0.16	0.57	13	7	3	36142.1, NP_002	P27361 P27361
270	PK865	ERK1	T207	Extracellular regulated	0, 0	841	20	6	0, 0	1619	366	7	92	-0.86	-0.54	0.32	1.16	1	7	4	36142.1, NP_002	P27361
271	PK864	ERK1	Y204	Extracellular regulated	0, 0	623	59	6	0, 0	808	91	6	30	-1.04	-0.96	0.08	0.30	5	7	4	36142.1, NP_002	P27361
272	PK866 NK055-NK056-2	ERK1 ERK1/2		Extracellular regulated Extracellular regulated	0, 1	2066 15721	167	8	0, 1	2245 14372	19	8 11	9	-0.35 0.81	-0.35 0.75	0.00	0.00 -0.22	5	7	5	36142.1, NP_002	P27361 P27361
	PK170-PK171	ERK1/2	T202	Extracellular regulated	0, 0	590	7	6	0, 0	653	9	6	11	-1.07	-1.08	-0.01	-0.05	13	7	4	AAA36142.1	P27361
275	PK168-PK169	ERK1/2	Y204	Extracellular regulated	0, 0	429	1	5	0, 0	501	10	6	17	-1.25	-1.24	0.01	0.04	9	7	4	AAA36142.1	P27361
276	NK056-3 NK056-4	ERK2 ERK2	Pan-Specific	Extracellular regulated Extracellular regulated	0, 0	29404	28 26	11	0, 0	30322 87853	29	12	3 22	1.16	1.19	0.02 0.14	0.08	5	7	5	NP_002736 NP_002736	P28482 P28482
278	NK057-2	ERK3		Extracellular regulated	0, 0	3780	31	9	0, 0	4739	35	9	25	-0.01	0.09	0.10	0.35	1	7	6	NP 002739	Q16659
279	NK058	ERK3		Extracellular regulated	0, 0	1238	89	7	0, 0	1662	57	7	34	-0.64	-0.53	0.12	0.42	13	7	5	NP_002738	P31152
280 281	PK624 NK206-3	ERK4 ERK5	S186 Pan-specific	Extracellular regulated	0, 0	21771 1943	137	11	0, 0	21036 2970	134	11	-3 53	0.99	0.97	-0.02 0.20	-0.08 0.73	5	7	6	NP_001278968.1 NP 620602	P31152 Q13164
282	NK206-3 NK206-4	ERK5		Extracellular regulated Extracellular regulated	0, 0	50763	17	12	0, 0	39565	21	12	-22	1.48	1.34	-0.13	-0.47	9	7	6	NP_620602	Q13164
283	NK206-5	ERK5		Extracellular regulated	0, 0	36137	30	12	0, 0	29762	13	12	-18	1.28	1.18	-0.11	-0.38	13	7	6	NP_620602	Q13164
284	PK016-3	ERK5		Extracellular regulated	0, 0	1968	125	8	0, 0	813	20	6	-59	-0.38	-0.95	-0.57	-2.07	1	7	7	NP_620602	Q13164
285 286	PK625 PK626	ERK5 ERK5	T219+Y221 Y221	Extracellular regulated Extracellular regulated	0, 0	10932	40 31	10	0, 0	9780	3 20	10	-11 7	0.60 1.63	0.52	-0.08 0.06	-0.29 0.21	9	7	7	NP_002740.2 NP_002740.2	Q13164 Q13164
287		strongen Recept		Estrogen receptor alph	0, 0	906	10	6	0, 0	1697	83	7	87	-0.82	-0.52	0.06	1.11	4	7	8	NP_000116.2	P03372
288	PN174	Ezrin	T567	Cytovillin 2	0,0	181	24	4	0, 0	290	27	5	60	-1.74	-1.56	0.18	0.66	8	7	8	NP_001104547.1	P15311
289	PN175 NK060	Ezrin	Y353	Cytovillin 2	0, 0	2692	24	8	0, 0	4399 1212	44	9	63	-0.20 -0.61	0.05	0.25	0.90	12	7	8	NP_001104547.1	P15311 Q05397
290	PK020	FAK	Pan-specific S722	Focal adhesion proteir Focal adhesion proteir	0, 0	1313 451	88	5	0, 0	916	28	7	-8 103	-0.61	-0.72 -0.88	-0.10 0.34	-0.38 1.23	4	7	9	NP_005598 NP_005598	Q05397 Q05397
292	PK020-3	FAK	S722	Focal adhesion proteir	0, 0	1817	68	7	0, 0	2060	60	8	13	-0.43	-0.40	0.02	0.08	16	7	9	NP_005598	Q05397
293	PK021	FAK	S732	Focal adhesion proteir	0, 0	1006	10	7	0, 0	1097	59	7	9	-0.76	-0.77	-0.01	-0.04	8	7	9	NP_005598	Q05397
294	PK024 PK017	FAK FAK	S910 Y397	Focal adhesion protein	0, 0	1215 24181	6	7	0, 0	2736 20821	152	8	125 -14	-0.66 1.05	-0.23 0.96	0.42	1.52 -0.32	12	7	9	NP_005598 NP_005598	Q05397 Q05397
296	PK017-1	FAK	Y397	Focal adhesion proteir	0, 0	4037	2	9	0, 0	4674	4	9	16	0.03	0.08	0.05	0.19	16	7	8	NP_005598	Q05397
297	PK151	FAK		Focal adhesion proteir	0, 0	335	105	5	0, 0	379	11	5	13	-1.39	-1.40	-0.01	-0.04	4	7	10	NP_005598	Q05397
298 299	PK629 NN042	FAK FAS	Y577 Pan-specific	Focal adhesion proteir Tumor necrosis factor	0, 0	4124 183	47	9	0, 0	5852 1964	49	9	42	0.04 -1.74	0.21 -0.43	0.17 1.31	0.62	16	7	10	NP_005598 NP_003789	Q05397 P25445
300	NN042	FasL		Tumor necrosis factor	0, 0	996	20	7	0, 0	492	53	6	-51	-0.77	-0.43	-0.48	-1.74	8	7	11	NP_003789	P48023
301	NK061	Fes	Pan-specific	Fes/Fps protein-tyrosir	0, 0	1511	20	7	0, 0	2478	16	8	64	-0.53	-0.29	0.24	0.86	12	7	11	NP_001996	P07332
302	NK062-3	FGFR1		Fibroblast growth facto	0, 0	26969	6	- 11	0, 0	27575 15594	14	11	2	1.11	1.13	0.02	0.06	16	7	- 11	NP_001167534.1	P11362
303 304	PK634 NK063-2	FGFR1 FGFR2	Y653+Y654 Pan-Specific	Fibroblast growth factor	0, 0	21244 43727	155	11	0, 0	15594 47368	16	11	-27 8	0.98	0.79	-0.18 0.06	-0.67 0.22	16	8	1 1	NP_001167534.1 NP_000132.3	P11362 P21802
305	NK063-3	FGFR2		Fibroblast growth facto	0, 0	55021	1	12	0, 0	58747	12	13	7	1.52	1.58	0.06	0.20	8	8	1	NP 000132.3	P21802
306	NK063-4	FGFR2		Fibroblast growth facto	0, 0	18736	17	11	0, 0	8393	9	10	-55	0.91	0.43	-0.48	-1.73	12	8	1	NP_000132.3	P21802
307 308	NK236-2 NK236-3	FGFR3		Fibroblast growth factor	0, 0	39353 14632	14	12	0, 0	34671 8522	4	12	-12 -42	1.33	1.27	-0.06 -0.33	-0.23 -1.10	4	8	2	NP_000133.1 NP_000133.1	P22607 P22607
309	PK637	FGFR3		Fibroblast growth facto	0, 0	15424	88	11	0, 0	12115	0	10	-21	0.80	0.64	-0.33	-0.54	12	8	2	NP_000133.1	P22607
310	NN172	FHL2	Pan-Specific	Four and a half LIM do	0, 0	416	33	5	0, 0	851	64	6	104	-1.27	-0.92	0.34	1.24	16	8	2	NP_001034581.1	Q14192
311	PN194 PN195	FKHR FKHR	S256	Forkhead box protein	0, 0	295	14	5	0, 0	406	75	5	38 51	-1.46	-1.36	0.10	0.37	3	7	8	NP_002006.2	Q12778
312 313	PN195 NK240-1	FRHR Flt3	S319 Pan-Specific	Forkhead box protein ( Receptor-type tyrosine	0, 0	137 31802	36 14	4	0, 0	207 52667	20 173	4 12	66	-1.90 1.21	-1.76 1.51	0.14	0.52	11	7	8	NP_002006.2 NP_004110.2	Q12778 P36888
314	NN044	Fos	Pan-specific	Fos-c FBJ murine oste	0, 0	13610	8	10	0, 0	4612	26	9	-66	0.72	0.07	-0.65	-2.35	3	7	9	NP_005243	P01100
315	PN033	Fos	T232	Fos-c FBJ murine oste	0, 0	61	18	3	0, 0	96	10	3	58	-2.37	-2.22	0.15	0.54 -3.07	15	7	8	NP_005243	P01100
316 317	PK641 PN146	FRK FRS2	Y387 Y349	Tyrosine-protein kinas Fibroblast growth facto	0, 0	21573 5683	59 55	11	0, 0	5144 3629	344 28	9	-76 -36	0.99	0.14 -0.07	-0.85 -0.29	-3.07 -1.06	7	7	9	NP_002022.1 NP_001036020.1	P42685 Q8WU20
318	NK065	Fyn		Fyn proto-oncogene-e	0, 0	1056	53	7	0, 0	2427	18	8	130	-0.73	-0.07	0.43	1.56	15	7	9	NP 002028	P06241
319	PN192	Gab1	Y627	GRB2-associated bind	0, 0	1293	20	7	0, 0	1782	10	8	38	-0.62	-0.49	0.13	0.48	3	7	10	NP_002030.2	Q13480
320 321	NN163 PN196	Gab1 GADD 100 (CHOP) GATA1	Pan-specific S142	DNA damage-inducibl	0, 0	2028	14 33	8	0, 0	5989	36	9	195	-0.36 -1.29	0.23 -1.36	0.59	2.14 -0.26	7	7	10	NP 002040.1	P35639 P15976
321	NK066	GCK	Pan-specific	Erythroid transcription Germinal centre protei	0, 0	5447	100	9	0, 0	4859	57	9	-11	-1.29	-1.36 0.10	-0.07	-0.26	11	7	10	NP_002040.1	Q12851
323	PN034	GFAP	S8	Glial fibrillary acidic pro	0, 0	1837	13	7	0, 0	2366	2	8	29	-0.42	-0.32	0.10	0.36	3	7	- 11	NP_002046	P14136
324	PN178	GluR1	S849	Glutamate receptor 1	0, 0	1006	22	7	0, 0	1086	6	7	8	-0.76	-0.78	-0.02	-0.06	7	7	11	NP_000818.2	P42261
325 326	NN045 NK067	GNB2L1 GRK2	Pan-specific Pan-specific	Guanine nucleotide-bi G protein-coupled rece	0, 0	1872 4272	49	8 9	0, 0	2512 7934	30 23	8	34 86	-0.41 0.06	-0.28 0.39	0.12 0.33	0.45	11	7 8	11	NP_006089 NP_001610	P63244 P25098
327	PK025	GRK2	S670	G protein-coupled rece	0, 0	29415	22	11	0, 0	27339	21	11	-7	1.16	1.13	-0.04	-0.14	15	7	11	NP_001610	P25098
328	NN046	GroEL		GroEL homolog (may	0, 0	2332	33	8	0, 0	2143	0	8	-8	-0.28	-0.38	-0.10	-0.35	7	8	1	NP_002147	P10809
329	NN047 NN048	Grp75		Glucose regulated pro	0, 0	46515	4	12	0, 0	38870	15	12	-16	1.43	1.33	-0.09	-0.33	11	8	1	NP_004125	P38646 P11021
330 331	NN048 NN048-2	Grp78 Grp78	Pan-specific Pan-specific	Glucose regulated pro Glucose regulated pro	0, 0	22229 24068	48	11	0, 0	23039 22876	19	11	-5	1.00 1.05	1.02 1.02	0.02	0.08 -0.10	15 3	8	2	NP_005338 NP_005338	P11021
332	NN049	Grp94	Pan-specific	Glucose regulated pro	0, 0	30517	2	12	0, 0	26165	2	11	-14	1.18	1.10	-0.08	-0.31	7	8	2	NP_003290	P14625
333	PK648	GSK3a		Glycogen synthase-se	0, 0	7188	75	9	0, 0	6956	69	9	-3	0.36	0.32	-0.04	-0.15	15	8	2	NP_063937	P49840
334 335	PK650 NK069-NK070-2	GSK3a/b	Y284+Y285 Pan-specific	Glycogen synthase-se Glycogen synthase-se	0, 0	2257 5108	77 44	8	0, 0	2064 3169	10 32	8	-9 -38	-0.30 0.16	-0.40 -0.15	-0.10 -0.31	-0.36 -1.13	11	7	2 8	NP_063937 NP_063937	P49840 P49840
336	1	GSK3a/b		Glycogen synthase-se	0, 0	668	48	6	0, 0	445	22	6	-33	-1.00	-1.31	-0.31	-1.13	6	7	8	NP_063937	P49840
337	PK651	GTF2F1	S385+T389	General transcription f	0, 0	8700	75	10	0, 0	6392	41	9	-27	0.47	0.27	-0.20	-0.73	10	7	8	NP_002087.2	P35269
338	NK071 NN169	Haspin		Haploid germ cell-spec	0, 0	1199	140	7	0, 0	2004	74	8	67	-0.66	-0.42	0.24	0.89 -0.54	14	7	8	NP_114171	Q8TF76
339	PINT/9-PINTOU-	HDAC4/5/9		Histone deacetylase 4 Histone deacetylase 4	0, 0	102 549	13 18	3	0, 0	95 881	24 146	3	-6 60	-2.07 -1.11	-2.22 -0.90	-0.15 0.20	-0.54 0.74	6	7	9	NP_006028.2 NP_006028.2	P56524 P56524
341	PN181 PN188	HDAC5	S498	Histone deacetylase 5	0, 0	908	119	6	0, 0	404	17	5	-55	-0.82	-1.36	-0.54	-1.96	10	7	9	NP_001015053.1	Q9UQL6
342	NN050	hHR23B	Pan-specific	UV excison repair prot	0, 0	339	19	5	0, 0	236	41	5	-30	-1.38	-1.68	-0.30	-1.08	14	7	9	NP_002865	P54727
343 344	NN051 PN036	Hip Histone H2A.X	Pan-specific S139	Hsp70/Hsc70 interacti Histone H2A variant X	0, 0	22028 941	11 20	11	0, 0	28099 948	28 32	11	28	1.00	1.14	0.14	0.52 -0.21	2	7	10	NP_003923 NP_002096	P50502 P16104
344	PN036 PN037	Histone H2A.X Histone H2B	S139 S14	Histone H2A variant X Histone H2B	0, 0	941 26959	20 35	11	0, 0	948 23529	32 29	11	-13	-0.80 1.11	-0.86 1.04	-0.06 -0.08	-0.21 -0.28	10	7	10	NP_002096 NP_778225	P16104 P33778
346	PN038	Histone H3	S10	Histone H3.3	0, 0	20682	62	11	0, 0	27358	103	11	32	0.96	1.13	0.16	0.59	14	7	10	NP_003521	P84243
347	PN039 PN100	Histone H3 Histone H3	S28 T11	Histone H3.3 Histone H3.3	0, 0	16196 1645	10	11	0, 0	16885 1213	4	11	4	0.82	0.84	0.02 -0.23	0.06	2	7	11	NP_003521	P84243 P84243
348	PN100	Histone H3	111	nistone H3.3	υ, 0	1645	16	7	0, 0	1213	10	7	-26	-0.48	-0.71	-0.23	-0.84	б	7	- 11	NP_003521	P84243

Globally Normalized Signal MED

Globally

Z-ratio

MAX

>+200%

malized Me ormalized Me 3433 4055 Log2 (Intensity %Error Range Globally Log2 (Intensit Serial Full Target Antibody Target Phospho Site %Error Range %CFC (Treated Z-score Difference Z-ratio Flag-Contro Normalized Control Corrected) Z score (Control) Block Row Column Refseq Uniprot Link No. Codes Control ated, Control NP\_00352 Histone H3.3 350 351 PN101-2 Histone H3 Т3 Histone H3 3 -0.02 NP 003521 P84243 P09601 Heme oxygenase 19163 20709 17993 19407 352 353 354 355 356 NN053 HO2 Pan-specific Heme oxygenase 2 0.92 -0.04 -0.26 0.17 NP\_002125 NP\_009112 P30519 NK072 Hpk1 Hsc70 Pan-specific Pan-specific -32 -0.94 Q92918 P11142 1142 NN054-2 Hsc70 Pan-specific Heat shock 70 kDa pro 20551 611 2380 19543 0, 0 0.96 0.90 -0.06 -0.23 -0.84 NP 006588 P11142 NNOSS HSF4 Pan-specific Heat shock transcript -0.23 0.20 0.00 NP 001529 Q9ULV5 Q92598 P04792 P04792 P04792 P04792 P04792 P25685 P25685 P29043 P10809 357 358 NN062 Hsp105 -0.27 0.93 Pan-specific Heat shock 105 kDa p NP\_006635 NP\_001531 NN152-1 Hsp25 Pan-specific Heat shock 27 kDa pr 0.93 359 360 361 PN042-3 Hsp25 Hsp27 S82 Heat shock 27 kDa pr -0.47 -0.44 0.02 NP\_001531 NP\_001531 Heat shock 27 kDa pro 0.35 PN040-2 S15 PN041 Hsp27 S78 Heat shock 27 kDa pro 1.08 -0.08 -0.29 NP 001531 Hsp27 Hsp40 Hsp40 Hsp47 Hsp60 PN042-1 NN057-2 NP\_001531 NP\_006136 Heat shock 27 kDa pro -0.15 0.09 Pan-specific DnaJ homolog, subfar -0.15 364 365 366 NN057-3 Pan-specific DnaJ homolog, subfar 0, 0 0, 0 0, 0 0.0 0.79 0.74 -0.04 NP 006136 NN058 Heat shock 47 kDa pro 0, 0 0.55 NP\_001226 NP\_002147 Pan-specific 0.47 -0.04 NN059-1 Pan-specific Heat shock 60 kDa pro Hsp60 Hsp60 Pan-specific Heat shock 60 kDa pro Pan-specific Heat shock 60 kDa pro NP\_002147 NP\_002147 NP\_002147 NP\_005336 P10809 P10809 P08107 367 368 369 NN059-2 1.64 -1.61 0.04 -0.08 0.86 0.14 -0.27 NN060-2 Hsp70 Pan-specific Heat shock 70 kDa pro -0.90 -0.04 3.1z 0.55 370 371 NN060-3 Hsp70 Hsp90 Pan-specific Heat shock 70 kDa pro Pan-specific Heat shock 90 kDa pro 32166 1.07 1.22 0.15 0.53 NP\_005336 NP\_005339 P08107 P07900 NN061 372 373 374 -0.03 0.22 0.22 P07900 P08238 P07900 NN061-16 Hsn90 alnha Pan-specific Heat shock 90 kDa pri Pan-specific Heat shock 90 kDa pri 0, 0 0, 0 0, 0 18853 27928 8453 18690 0.90 -0.01 NP\_005339 NP\_031381 hsp90 beta Hsp90a NN165-1 Pan-specific Heat shock 90 kDa pro 375 376 377 378 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 -0.14 0.30 0.61 0.21 -0.52 NN165 Hsp90b Pan-specific Heat shock 90 kDa pro 0.37 0.23 NP 031381 P08238 PN176 S254 Heat shock 90 kDa pr P08238 O95351 1979 NN063 HspBP1 Pan-specific Hsp70 binding protein -0.43 0.17 NP\_036399 NP\_004208 Q96GD4 P42858 NK193 Pan-specific Aurora Kinase B (serin -0.04 PN103 Huntingt S421 Huntington's disease 0, 0 -0.58 0.01 NP 002102 2169 380 381 NN064-2 IKB-a Pan-specific Inhibitor of NF-kappa-I 2370 -0.32 -0.32 0.02 NP 065390 P25963 NN130 Pan-specific Acidic leucine-rich nuc 15192 -0.08 NP 006296 (2HAZA) (DHADII) IAP1 382 21401 1497 18313 2128 NP\_003002 NP\_001156 Pan-specific Protein SET 0, 0 0.89 -0.09 0.15 Cellular inhibitor of ap-NN025 Pan-specific Q13490 Q9UPZ9 P08069 384 PK655 ICK Y156+T157 Intestinal cell (MAK-lik 0.0 0.42 0.62 0.20 0.74 NP 055735.1 385 IGF1R IGF1R Y1165/Y1166 288 1117 -0.08 0.36 Insulin-like growth fact NP\_000866 PK152 Y1280 Insulin-like growth fact 2263 -0.70 -0.35 NP 000866 P08069 PK658 NK075-6 IGF1R IKD KIIIddi Alaba IkBa Y1346 Pan-specific Insulin-like growth fact Inhibitor of NF-kappa-2470 5788 1752 NP\_000866 NP\_001269 P08069 O15111 P25963 387 388 389 0, 0 0, 0 0, 0 2676 6343 0.00 NP 065390 NN064 Pan-specific Inhibitor of NF-kappa-0.0 2005 -0.45-0.42 0.03 Inhibitor of NF-kappa-I Inhibitor of NF-kappa-I NP\_065390 NP\_002494 390 391 PN164 lkBa lkBb Y42 931 1216 1194 -0.81 0.08 0.30 0.37 P25963 Pan-specific Q15653 NF-kappa-B inhibitor e Inhibitor of NF-kappa-I Inhibitor of NF-kappa-I 392 393 394 395 396 397 398 PN168 IkBe IKKa IKKa S22 0, 0 0, 0 0, 0 1816 966 8566 2020 2457 10877 -0.43 -0.79 -0.41 -0.30 0.01 NP\_004547.2 NP\_001269 00022 NK075-2 NK075-3 Pan-specific Pan-specific 015111 015111 0.12 NP\_001269 PK154 IKKa T23 Inhibitor of NF-kanna-0, 0 0, 0 -1.39 -1.28 0.11 NP 001269 015111 IKKg/NEMO ILK1 ILK1 0, 0 0, 0 0, 0 0, 0 2096 908 2329 931 NK078-2 Pan-specific Integrin-linked protein-2350 1144 -0.34 -0.82 -0.32 -0.75 0.02 0.07 0.26 0.29 NP\_001547 NP\_001547 O14920 PK662 Y351 Integrin-linked protein O14920 P06213 P06213 399 400 401 PK663 2887 498 -0.28 -0.81 NK079 Pan-specific Insulin receptor beta c 0, 0 -1.24 -0.43 NP 000199 Integrin a4 0.00 0.90 -0.05 0.26 P13612 P05556 P06213 P06213 P51617 PN043 5088 Integrin alpha 4 (VLA4 NP\_000876 402 403 Integrin b1 S785 Integrin beta 1 (fibrone 2556 1220 389 972 0.25 NP\_002202 NP\_000199 0.02 -0.67 PK032-1 Y972 Insulin receptor -0.65 404 405 PK033 IR/IGE1R Y1162/Y1163 Insulin receptor / Insul 0, 0 -1 31 -1 23 0.07 NP 000866 IRAK1 0, 0 3001 0.60 NK080-2 Pan-specific Interleukin 1 receptor-NP\_001560 -0.21 -0.38 406 407 408 NK081 IRAK2 Pan-specific Interleukin 1 receptor-0.0 0.02 -0.04 -0.06 NP 001561.3 O43187 -0.10 0.53 0.21 PK665 PN117 IRAK4 IRS1 NP\_001107654. NP\_005535 Q9NWZ3 P35568 T345+S346 0, 0 0, 0 0, 0 14288 1742 Insulin receptor substi 409 410 411 PN118 IRS1 S639 Insulin receptor substr 0.0 -1.55 NP 005535 P35568 4947 1582 PN046-2 IRS1 Y1179 Insulin receptor substr 0, 0 0.22 -0.11 -0.30 -0.38 NP\_005535 P35568 P35568 P23458 P23458 O60674 PN045 Y612 NP\_005535 Insulin receptor substr 412 413 414 NK084-5 JAK1 JAK1 JAK2 Pan-Specific Janus protein-tyrosine Janus protein-tyrosine Janus protein-tyrosine 1.65 -1.46 -1.01 1.72 -1.25 -0.84 0.07 0.21 0.17 0.24 0.78 0.61 NP\_002218 NP\_002218 NP\_004963 Y1022 NK085 Pan-specific 415 416 417 418 JAK2 JAK2 JAK2 JAK2 0, 0 0, 0 0, 0 0, 0 0, 0 0.41 0.30 -0.16 0.05 NK085-2 Pan-Specific Janus protein-tyrosine Pan-Specific Janus protein-tyrosine 0, 0 1.68 1.79 1.60 0.11 NP\_004963 NP\_004963 O60674 O60674 0, 0 NK085-4 Pan-Specific Janus protein-tyrosine Y1007/1008 Janus protein-tyrosine -0.04 0.01 NP\_004963 NP\_004963 060674 PK034-2 0.26 0.28 O60674 O60674 0.45 JAK2 JAK3 420 421 0, 0 NK086 Pan-specific Janus protein-tyrosine 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0.61 0.78 NP 000206 P52333 P52333 P52333 P52333 P52333 P45983 JAK3 JAK3 JAK3 NK086-2 Pan-Specific Janus protein-tyrosin 26754 47345 34106 20067 44898 40973 -0.60 NP\_000206 NK086-3 422 423 424 -0.02 0.12 Pan-Specific Janus protein-tyrosine NP\_000206 NP\_000206 NK086-4 Pan-Specific Janus protein-tyrosine PK660 JAK3 V080+V081 Janus protein-tyrosine -0.53 -0.27 NP 000206 425 426 11391 1059 842 -0.07 PK035-1 T183/Y185 0.62 0.55 NP 002741 Jun N-terminus proteir 232 913 697 -0.54 P45983 P45983 P45983 PK035-2 JNK T183/Y185 Jun N-terminus protei -0.73 -0.15 NP 002741 427 428 429 430 431 PK035-4 NK217-2 T183/Y185 -0.86 1.25 -0.64 -0.55 NP\_002741 Pan-Specific NK217 INK1 (MAPK p49 Pan-specific Jun N-terminus protei 0.0 356 3050 -1.47 -1.44 0.03 0.10 NP 620637. P45983 1832 NK088-2 JNK2 JNK2 0, 0 -0.42 1.53 0.25 0.91 NP\_002741 P45983 P45984 P53779 P05412 P05412 NK189-2 0,0 NP\_002744 Pan-Specific Jun N-terminus proteir 432 433 434 NK197-2 JNK3 Jun Pan-Specific Jun N-terminus proteir Pan-specific Jun proto-oncogene-e 1.54 -1.68 -1.51 0.10 -0.19 -0.13 NP\_002744.1 NP\_002219 NP\_002219 -0.67 PN154 S243 Jun proto-oncogene-e -0.46 435 PN048-1 Jun S73 0.90 NP\_002219 P05412

SAMPLE DETAILS

Treated ID: Pooled Samples Smaller

Globally

Sample IDs: Control ID: Pooled Samples Larger

Globally

uin MED MAX

%CFC <-80%

Globally Normalized Signal

0

>+200%

NP\_002749.2

Z-ratio <-1.5 0

malized Me ormalized Me 3433 4055 Log2 (Intensity %Error Range Globally Globally Log2 (Intensit Serial Full Target Antibody Target Phospho Site %Error Range %CFC (Treated Z-score Difference Z-ratio Flag-Contro Normalized Control Control Normalized Treated Corrected) -Treated Z score (Control) Z score (Treated) Block Column Refseq Uniprot Link No. Codes Control (Treated, Control) NP\_002219 Jun proto-oncogene-e P05412 437 PN163 T91 Jun proto-oncogene-e Jun proto-oncogene-e 1795 -1 05 -0.48 0.57 NP 002219 P05412 P05412 Y170 -0.16 0.59 0.07 -0.58 KAP L Rece VD10 Kit 0, 0 0, 0 0, 0 0, 0 439 440 NP004 Pan-specific Cyclin-dependent kina 1202 1985 0, 0 -0.66 -0.07 NP\_005183 NP\_006792.1 Q1666 3610 2444 NN153 Pan-specific Pan-Specific ER lumen protein reta -0.37 P24390 P10721 0.18 442 443 PK036 Y703 Mast/stem cell growth 0, 0 0.42 0.34 -0.09 NP 006566 P10721 P10721 P10721 PK150 Y721 0, 0 0.11 -0.08 0.35 0.40 NP 006566 PK037 Y730 7955 878 1406 1113 437 1396 0.42 NP\_006566 NP\_006566 Mast/stem cell growth 7226 1768 P10721 Q8IVT5 Q13043 P10586 P06239 P06239 PK038 Y936 Mast/stem cell growth 446 447 NKU0U\*5 Krs-1 Pan-specific 0, 0 1921 3174 0.13 AAC50354 NK113-3 Krs-2 NP\_006273 Pan-specific Mammalian STE20-lik 448 NP005 LAR Pan-specific LCA antigen-related (L 0.0 -1.24 -1.62 -0.38 NP 002831 NK092-2 NK092-3 -0.13 -0.20 -0.47 -0.71 NP\_005347 Pan-specific Lymphocyte-specific p Pan-specific Lymphocyte-specific p P06239 P06239 P06239 451 PK039 Lck S158 Lymphocyte-specific p 0.0 0.08 0.19 0.10 NP 005347 452 453 Lck 0, 0 0.37 -0.05 0.00 NP\_005347 NP\_005347 Lymphocyte-specific p 0.32 PK149 Y394 Lymphocyte-specific p 454 455 456 457 458 Lck LIMK1 LIMK1/2 NP\_005347 NP\_005347 NP\_002305 NP\_002305 P06239 P53667 P53667 PK041 Y505 0, 0 0, 1 0, 0 -1.20 -0.10 0.19 -0.42 -0.51 -1.85 -0.70 PK042-PK144 Y507/T508 LIM domain kinase 1 0.00 -0.19 NK227-2 LKB1 LKB1 Pan-Specific Serine/threonine-prote Pan-Specific Serine/threonine-prote 0, 0 1.67 0.09 0.32 0.03 0.04 NP\_000446.1 Q15831 Q15831 NK227-3 47898 1348 1678 560 1445 459 460 NK227-4 LKB1 Pan-Specific Serine/threonine-prote 0, 0 0, 0 0, 0 1.45 0.07 0.01 NP 000446. Q15831 P07948 P49137 NK095 Pan-specific NP 002341 Mitogen-activated prot 3115 1120 Mitogen-activated prot Mitogen-activated prot 0, 0 0, 0 0, 0 0, 0 462 463 PK044 MAPKAPK2 T222 0, 0 -1.10 -0.76 0.34 NP 004750 P49137 MAPKAPK2 T334 -0.22 -0.06 0.35 NP\_004750 NP\_003659.2 464 465 466 PK693 MAPKAPK5 MAP kinase-activated 16465 135 36305 2271 T186 0.83 -0.23 Q8IW41 P29966 Q9P0L2 PN050-1 MARCKS S152/S156 Myristoylated alanine-r MAP/microtubule affin NP 002347 PK694 MARK T215 0, 0 -0.13 -0.09 NP 001273053.1 -0.47 -0.34 467 468 2092 NN067 Mcl1 Pan-specific Myeloid cell leukemia -0.30 -0.39 NP 068779 Q07820 PN169 MDM2 S166 Double minute 2 0.20 0.22 0.01 0.04 NP 001138809. 469 470 MEF-2 MEK1 MEK1 0, 0 0.30 NP\_057216.2 NP\_002746 Pan-specific Myelin expression fact MAPK/ERK protein-se 3542 639 20145 36866 6276 618 14186 38143 0.26 1.09 -0.33 NK099-1 Pan-specific -0.09 Q02750 471 NK099-3 Pan-Specific MAPK/ERK protein-se 0.0 -30 0.95 0.74 -0.21 -0.76 NP 002746 Q02750 Q02750 472 MEK1 MEK1 MAPK/ERK protein-se Pan-Specific 0.03 NP\_002746 473 NK099-8 Pan-Specific MAPK/ERK protein-se 0.10 NP 002746 Q02750 NP\_002746 NP\_002746 NP\_002746 NP\_002746 MEK1 MEK1 MEK1 Pan-Specific MAPK/ERK protein-se S292 MAPK/ERK protein-se Q02750 Q02750 Q02750 474 475 NK099-9 0, 0 0, 0 0, 0 -0.51 -0.63 476 15786 12678 -0.14 PK047-2 S298 MAPK/ERK protein-se 0.81 0.67 -0.50 477 478 MEK1 MEK1 MAPK/ERK protein-se NP\_002746 NP\_002746 PK046-1 T292 16950 5174 12969 3896 0.85 0.69 -0.16 -0.20 -0.59 -0.71 Q02750 MAPK/ERK protein-se PK048-1 Q02750 MEK1 MEK1 7 D22/AIDA MEK2 Q02750 P06748 P36507 479 480 481 PK048-2 T386 MAPK/FRK protein-se 0, 0 0, 0 0, 0 1.02 0.89 -0.13 -0.08 -0.46 -0.31 NP\_002746 B23 (nucleophosmin, MAPK/ERK protein-se PK045-PN00 S217+S221 516 27207 0.42 AAH00471 NK100-1 Pan-specific 482 483 484 485 0.27 0.26 -0.85 P36507 P36507 NK100-4 MFK2 Pan-Specific MAPK/FRK protein-se 0, 0 1.05 1 12 0.07 AAH00471 MAPK/ERK protein-se 0.07 -0.24 0.22 Pan-Specific MAPK/ERK protein-se 30589 2252 NK100-6 MEK2 20318 3563 -34 0.95 AAH00471. P36507 PK049 MFK2 T394 MAPK/FRK protein-se -0.30 AAH00471 P36507 P36507 486 487 PK049-2 MEK2 human MAPK/ERK protein-se 0, 0 0, 0 0, 0 0, 0 0, 0 -0.03 -0.16 AAH00471. -0.59 PK050 MEK2 mouse T394 MAPK/ERK protein-se -22 0.46 0.29 NP 075627 P36507 1437 P46734 P46734 NK101 MEK3 Pan-specific MAPK/FRK protein-es 1432 -0.21 -0.31 NP 659732 MEK-3 MEK3/6 Pan-specific MAPK/ERK protein-se -0.09 0.36 NP\_659732 NP\_002747 0.59 -1.33 0.50 -0.97 P46734 P46734 P46734 PK051 S189 + S207 MAPK/ERK protein-se 0, 0 491 PK051-2 MEK3/6 MARK/FRK protein-se 0.63 0.47 -0.16 -0.58 NP 002747 Pan-specific 492 -0.28 NP\_659731 NK102 MEK3b MAPK/ERK protein-se -1.62 493 NK103 MEK4 Pan-specific MAPK/ERK protein-se 0.0 1881 -0.52 0.06 NP 003001 P45985 MEK4 MEK4 Pan-Specific S257/T261 MAPK/ERK protein-se MAPK/ERK protein-se -0.69 -0.33 NP\_003001 NP\_003001 NP\_660143 P45985 P45985 NK103-2 0, 0 0, 0 0, 0 5822 9055 719 32257 33123 -0.19 -0.09 0.36 496 497 498 NK104 MEK5 Pan-specific MAPK/ERK protein-se 0.0 1488 27936 35075 -0.95 -0.59 NK104-3 NK104-4 MEK5 MEK5 Pan-Specific MAPK/ERK protein-se Pan-Specific MAPK/ERK protein-se NP\_660143 NP\_660143 0, 0 -0.08 0.04 -0.28 0.15 -0.14 Q13163 Q13163 499 500 501 NK104-5 MEK5-3 Pan-Specific MAPK/ERK protein-se -0.04 0.37 0.42 NP\_660143 NP\_002749 NP\_005034 NK105-1 MEK6 MEK7 MAPK/ERK protei P52564 O14733 945 1251 1835 6755 Pan-specific MAPK/ERK protein-se 2139 NK106-2 0, 0 0, 0 0, 0 0, 0 0, 0 -0.07 0.04 -0.57 0.03 NK107-4 MFKK-1 Pan-specific MAPK/ERK kinase kin 0, 0 1231 2147 -0.64 -0.71 -0.38 -0.24 0.15 XP 042066 502 503 504 505 506 507 508 MEKK2 MAPK/ERK kinase kir Q9Y2U5 Pan-Specific MAPK/ERK kinase kin 0.32 NK107-3 MEKK-N7 2679 -0.25 1.40 XP 042066 Q13233 NK229-2 MELK Pan-Specific Maternal embryonic le NP 001243614 Q14680 Q14680 -0.06 0.02 NP\_001243614. 0, 0 NK110-2 Pan-Specific Hepatocyte growth fac 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 1.54 1.56 NP 000236.2 P08581 P08581 P08581 P08581 P08581 P08581 NK110-3 Pan-Specific Hepatocyte growth fac -0.22 -0.25 0.08 -0.80 NP\_000236.2 Met PK706 509 510 Hepatocyte growth fac -0.90 NP\_000236.2 NP\_000236.2 PK707 T1355+Y1356 Hepatocyte growth fac PK054-2 Y1003 Hepatocyte growth fac 0.25 -0.12 NP 000236 1230/Y1234/Y125Hepatocyte growth fac -0.20 -0.72 512 513 PK055-1 -0.89 NP 000236 -1.09 P46734 P46734 P46734 NK101-4 MKK3 Pan-Specific MAPK/ERK protein-se 0.0 0.25 NP 002747 514 515 516 NK101-5 NK101-6 MKK3 MKK3 Pan-Specific Pan-Specific MAPK/ERK protein-se MAPK/ERK protein-se -0.03 0.16 NP\_002747 PK051-4 MKK3 S189 MAPK/ERK protein-se 0.0 -1.41 -0.45 NP 002747 P46734 P46734 MKK3 MKK3 MAPK/ERK protein-se 517 518 0, 0 25364 5441 -0.03 0.02 -0.09 0.07 P46734 P45985 P45985 P45985 PK714 0,0 NP\_002747.2 Y230 MAPK/ERK protein-se 519 520 521 NK103-4 MKK4 MKK4 MKK4 Pan-Specific MAPK/ERK protein-se Pan-Specific MAPK/ERK protein-se MAPK/ERK protein-se 0, 0 0, 0 0, 0 40044 48053 1.39 1.91 1.60 0.05 0.47 0.15 NP\_003001 NP\_003001 NP\_003001 NK103-5 NK103-6

SAMPLE DETAILS

Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

Globally

Sample IDs: Control ID: Pool

522

NK105-3

MKK6

Pan-Specific MAPK/ERK protein-se

Globally Normalized Signal MED

<-80%

Z-ratio <1.5 0 >>

						Normalized Median				Normalized Median	1											
						3433 Globally		Log2 (Intensity		4055 Globally	%Error Range	Log2 (Intensity										
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Normalized -	%Error Range Control	Corrected) -	Flag-Treated	Normalized -	Treated	Corrected) -	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link
						Control 19095	Control	Control		Treated 10684		Treated	-44				(Treated, Control)				ND COORIO	
523 524	NK105-4 NK105-5	MKK6 MKK6		MAPK/ERK protein-se MAPK/ERK protein-se	0, 0	23613	5	11	0, 0	10684 58953	318	10	-44 150	0.92	0.57 1.58	-0.35 0.54	-1.25 1.96	7	9	3	NP_002749.2 NP_002749.2	P52564 P52564
525	NK106-4	MKK7	Pan-Specific	MAPK/ERK protein-se	0, 0	29591	4	11	0, 0	31714	6	12	7	1.17	1.21	0.05	0.17	11	9	3	NP_005034	O14733
526 527	NK106-5 NP006	MKK7 MKP1		MAPK/ERK protein-se MAP kinase phosphat	0, 0	47893 3039	1 80	12	0, 0	63818 9918	18 347	13	33	1.44	1.63 0.53	0.18	0.67	15	9	3	NP_005034 NP_004408	O14733 P28562
528	NP006	MKP2		MAP kinase phosphat	0, 0	751	63	6	0, 0	308	17	5	-59	-0.13	-1.52	-0.59	-2.15	6	8	9	NP 001385	Q13115
529	PN051-1	MLC	S19	Myosin regulatory light	0, 0	10364	12	10	0, 0	9858	22	10	-5	0.57	0.52	-0.05	-0.16	10	8	9	NP_291024	P19105
530 531	NK208 PK056	MLK3 MLK3	Pan-specific	Mixed-lineage protein- Mixed-lineage protein-	0, 0	728 23403	1 20	6	0, 0	1317 23567	133	7	81	-0.95 1.03	-0.67 1.04	0.28	1.02 0.02	2	8	10	NP_002410 NP_002410	Q16584 Q16584
532	NN132	mMOB1		Preimplantation proteil	0, 0	12644	16	10	0, 0	9653	2	10	-24	0.68	0.51	-0.17	-0.62	6	8	10	NP_056202	Q9Y3A3
533	PK057	Mnk1		MAP kinase-interacting	0, 0	123	13	4	0, 0	140	8	4	14	-1.96	-1.99	-0.03	-0.10	10	8	10	NP_003675	Q9BUB5
534 535	NK111 NN069	Mnk2 MSH2		MAP kinase-interacting DNA mismatch repair	0, 0	689 1583	38 15	6	0, 0	1250 1117	1	7	81 -29	-0.98 -0.50	-0.70 -0.76	0.28 -0.26	1.02 -0.94	14	8	10	NP_060042 NP_000242	Q9HBH9 P43246
536	PK058	Msk1	S376	Mitogen & stress-activ	0, 0	490	5	6	0, 0	624	10	6	28	-1.17	-1.11	0.07	0.24	6	8	11	NP 004746	075582
537	NK113-1	MST1		Mammalian STE20-lik	0, 0	891	34	6	0, 0	1230	10	7	38	-0.83	-0.71	0.13	0.46	10	8	11	NP_006273	Q13043
538 539	NK113-2 NK114	MST1 MST2		Mammalian STE20-lik Mammalian STE20-lik	0, 0	544 51468	24 13	6	0, 0	440	34	5	-19 28	-1.11 1.48	-1.31 1.65	-0.20 0.16	-0.72 0.59	14	8	11	NP_006273 NP_006272	Q13043 Q13188
540	NK115	MST3		Mammalian STE20-lik	0, 0	205	20	4	0, 0	186	26	4	-9	-1.67	-1.82	-0.15	-0.55	6	9	1	NP_003567	Q9Y6E0
541	PK727	MST3	T184	Mammalian STE20-lik	0, 0	7502	146	10	0, 0	5590	162	9	-25	0.38	0.19	-0.20	-0.71	10	9	1	NP_001027467.2	Q9Y6E0
542 543	PK728 NK116-3	MST3 mTOR	T190	Mammalian STE20-lik Mammalian target of ri	0, 0	9530 11333	237 26	10	0, 0	6026 9598	219 46	9	-37 -15	0.52	0.23	-0.29 -0.11	-1.04 -0.41	14	9	1	NP_001027467.2 NP_004949	Q9Y6E0 P42345
544	NK116-4	mTOR		Mammalian target of ri	0, 0	43575	17	12	0, 0	50454	22	12	16	1.39	1.49	0.10	0.36	2	9	2	NP_004949	P42345
545	PK116	mTOR (FRAP)	S2448	Mammalian target of ra	0, 0	1110	3	7	0, 0	1035	17	7	-7	-0.71	-0.81	-0.10	-0.37	10	9	2	NP_004949	P42345
546 547	PN186 PN199	Myc Mvc	S373 T58	Myc proto-oncogene p Myc proto-oncogene p	0, 0	853 1856	12 44	6	0, 0	690 2376	4	6	-19 28	-0.86 -0.41	-1.05 -0.32	-0.19 0.10	-0.69 0.35	14	9	2	NP_002458.2 NP_002458.2	P01106 P01106
547	PN199 PN182	MyoD	S200	Myc proto-oncogene p Myoblast determinatio	0, 0	208	8	4	0, 0	409	62	5	96	-0.41	-0.32 -1.36	0.10	1.10	6	9	3	NP_002458.2 NP_002469.2	P15172
549	PN052	MYPT1	T696	Myosin phosphatase t	0, 0	1920	198	8	0, 0	724	1	6	-62	-0.39	-1.02	-0.63	-2.26	10	9	3	NP_446342	O14974
550 551	NK117-3 NK117-4	Nek2 Nek2		NIMA (never-in-mitosis NIMA (never-in-mitosis	0, 0	4832 925	948	9	0, 0	1478 1613	57 23	7	-69	0.13 -0.81	-0.60 -0.55	-0.73 0.26	-2.65	14	9	3	NP_002488 NP_002488	P51955 P51955
551	NK117-4 NK117-5	Nek2 Nek2		NIMA (never-in-mitosis	0, 0	925 5929	60	9	0, 0	1613 4446	23 35	9	-25	-0.81 0.25	-0.55	-0.20	-0.71	5	8	9	NP_002488 NP_002488	P51955 P51955
553	PK732	Nek2	S171	NIMA (never-in-mitosis	0, 0	56565	28	12	0, 0	63682	37	13	13	1.54	1.63	0.09	0.32	9	8	9	NP_002488	P51955
554	NK119	Nek7	Pan-specific	NIMA (never-in-mitosis	0, 0	2005	57	8	0, 0	2906	29	8	45	-0.37	-0.20	0.17	0.62	13	8	9	NP_598001	Q8TDX7
555 556	NN070 NN071	NFkappaB p50 NFkappaB p65		NF-kappa-B p50 nucle NF-kappa-B p65 nucle	0, 0	494 1086	27 12	6 7	0, 0	882 1193	6	6 7	79	-1.17 -0.72	-0.90 -0.72	0.27 -0.01	0.96 -0.02	- 1	8	10	NP_003989 NP_003989	P19838 Q04206
557	PN156	NFKB p65		NF-kappa-B p65 nucle	0, 0	2392	188	8	0, 0	1499	45	7	-37	-0.27	-0.59	-0.32	-1.16	9	8	10	NP_003989	Q04206
558	PN157	NFKB p65 NFKB p05 (Rei		NF-kappa-B p65 nucle	0, 0	6614	77	9	0, 0	3643	21	9	-45	0.31	-0.07	-0.38	-1.37	13	8	10	NP_003989	Q04206
559 560	PN053-1 NK207	NIK		NF-kappa-B p65 nucle NF-kappa beta-inducir	0, 0	12512 3765	105 45	10	0, 0	8220 2821	59 202	10	-34 -25	0.68	0.42	-0.26 -0.21	-0.94 -0.75	- 1	8	11	NP_003989 NP_003945.2	Q04206 Q99558
561	NK212	Nlk	Pan-specific	Serine/threonine prote	0, 0	1310	22	7	0, 0	2081	30	8	59	-0.61	-0.40	0.22	0.78	9	8	11	NP_057315.3	Q9UBE8
562	PN055-1	NMDAR1	S896	N-methyl-D-aspartate	0, 0	1238	299	7	0, 0	683	13	6	-45	-0.64	-1.05	-0.41	-1.48	13	8	11	NP_000823	Q05586
563 564	PN054 NN074	NMDAR2B NME7	Y1472 Pan-enecific	N-methyl-D-aspartate Nucleotide diphosphat	0, 0	113 2870	53 44	3 8	0, 0	138 2672	32 90	4 8	-7	-2.01 -0.16	-2.00 -0.25	0.01 -0.08	0.05 -0.30	- 1	9	1	NP_000825 NP_037462	Q13224 Q9Y5B8
565	NN075	NT5E		Ecto-5'-nucleotidase (	0, 0	7027	29	9	0, 0	7337	17	10	4	0.35	0.35	0.00	0.01	9	9	1	NP_002517	P21589
566	NN083	p107		Retinoblastoma (Rb) p	0, 0	1880	31	8	0, 0	2447	34	8	30	-0.41	-0.30	0.11	0.38	13	9	1	NP_P28749	P28749
567 568	NN077 NN078	p18 INK4c p21 CDKI1		p18 INK4c cyclin-depe cyclin-dependent kinar	0, 0	4985 3070	36	9	0, 0	2961 4189	28	8	-41 20	0.15 -0.13	-0.19 0.02	-0.34 0.14	-1.22 0.52	1	9	2	NP_523240 NP 000380	P42773 P38936
569	NN080	p27 Kip1		p27 cyclin-dependent	0, 0	2964	17	8	0, 0	3785	21	9	28	-0.15	-0.04	0.10	0.38	9	9	2	NP 004055	P46527
570	NN081-NN12			CDK5 regulatory subu	0, 0	5417	22	9	0, 0	23896	72	11	341	0.20	1.05	0.85	3.07	13	9	2	NP_003876.1	Q15078
571 572	NK120-5 NK059-1	p38 (1727) p36 y		Mitogen-activated prot Mitogen-activated prot	0, 0	17270	7	11	0, 0	15395 553	5 26	11	-11 86	0.86	0.79	-0.07 0.28	-0.27 1.01	- 1	9	3	NP_001306 NP_002960	Q16539 P53778
573	NK120-2	'Esselfinaka'		Mitogen-activated prot	0, 0	11559	13	10	0, 0	11800	0	10	2	0.63	0.63	0.00	0.00	9	9	3	NP_001306	Q16539
574	NK120-4	p38a MAPK		Mitogen-activated prot	0, 0	1542	42	7	0, 0	1550	9	7	0	-0.52	-0.57	-0.05	-0.19	16	9	4	NP_001306	Q16539
575 576	NK120-8 PK060-1	p38a MAPK p38a MAPK	Pan-Specific	Mitogen-activated prot Mitogen-activated prot	0, 0	29606 2844	9	12	0, 0	28172 3349	53	11	-5 10	1.17	1.14	-0.02 0.05	-0.09 0.20	13	9	4	NP_001306 NP_001306	Q16539 Q16539
577	PK060-3	p38a MAPK		Mitogen-activated prot	0, 0	1372	12	7	0, 0	900	17	7	-34	-0.59	-0.89	-0.31	-1.10	12	9	4	NP_001306	Q16539
578	PK739	p38a MAPK		Mitogen-activated prot	0, 0	28537	63	11	0, 0	27169	77	11	-5	1.15	1.12	-0.02	-0.09	4	9	4	NP_001306	Q16539
579 580	NK248-1 NK248-2	p38b p38b		Mitogen-activated prot Mitogen-activated prot	0, 0	14748 25383	8 11	10	0, 0	12341 24992	21	10	-16	0.77	0.66	-0.11 -0.01	-0.41 -0.03	12	9	5	NP_002742.3 NP_002742.3	Q15759 Q15759
581	NK248-3	p38b		Mitogen-activated prot	0, 0	14603	82	10	0, 0	13685	160	10	-6	0.76	0.72	-0.05	-0.17	8	9	5	NP_002742.3	Q15759
582	PK741	p38b		Mitogen-activated prot	0, 0	7976	46	10	0, 0	7716	38	10	-3	0.42	0.38	-0.04	-0.15	16	9	5	NP_002742.3	Q15759
583 584	NK121-2 NK121-3	p38d p38d		Mitogen-activated prot Mitogen-activated prot	0, 0	34764 48229	23	12 12	0, 0	35116 47532	10	12	-1	1.26 1.45	1.27 1.45	0.01	0.05 0.02	8	9	6	NP_002745 NP_002745	O15264 O15264
585	NK121-4	p38d		Mitogen-activated prot	0, 0	29301	3	11	0, 0	32651	7	12	11	1.16	1.23	0.07	0.25	12	9	6	NP_002745	O15264
586 587	PK743	p38d		Mitogen-activated prot	0, 0	14535	67	10	0, 0	11175 18136	67	10	-23	0.76	0.60	-0.16	-0.59	16	9	6	NP_002745.1	O15264
587 588	NK059-3 NK059-4	p38g p38g		Mitogen-activated prot Mitogen-activated prot	0, 0	25353 35497	15	11	0, 0	18136 32664	25	11	-28 -8	1.08	0.88 1.23	-0.20 -0.04	-0.71 -0.15	8	9	7	NP_002960 NP_002960	P53778 P53778
589	NK059-5	p38g		Mitogen-activated prot	0, 0	19438	17	11	0, 0	19664	12	11	1	0.93	0.93	0.00	0.01	12	9	7	NP_002960	P53778
590	NN082	p53	Pan-specific	Tumor suppressor pro	0, 0	1156	6	7	0, 0	732	11	6	-37	-0.68	-1.01	-0.33	-1.19	16	9	8	NP_000537	P04637
591 592	PN158	p53 p53	S33 S37	Tumor suppressor pro Tumor suppressor pro	0, 0	232 3628	5	5	0, 0	461 4346	35	6	99 20	-1.60 -0.03	-1.29 0.04	0.31	1.14 0.25	4 8	9	8 8	NP_000537 NP_000537	P04637 P04637
592	PN057-2	p53	S392	Tumor suppressor pro	0, 0	970	9	7	0, 0	1026	26	7	6	-0.03	-0.81	-0.03	-0.11	16	9	7	NP_000537	P04637
594	PN160	p53	S6	Tumor suppressor pro	0, 0	512	0	6	0, 0	890	55	7	74	-1.15	-0.90	0.25	0.91	12	9	8	NP_000537	P04637
595 596	PK166 PK156	p70 S6K p70 S6K	S411 S424	Ribosomal protein S6 Ribosomal protein S6	0, 0	1733 272	18	7	0, 0	1458 179	27	7	-16 -34	-0.45 -1.51	-0.61 -1.85	-0.15 -0.34	-0.56 -1.21	12	9	9	NP_003152 NP_003152	P23443 P23443
596	PK156 PK146	p70 S6K p70 S6K		Ribosomal protein S6	0, 0	107	7	3	0, 0	123	24	4	14	-1.51	-1.85	-0.03	-1.21 -0.10	4	9	9	NP_003152 NP_003152	P23443 P23443
598	NK223	p70 S6Ka	Pan-specific	Ribosomal protein S6	0, 0	6946	314	9	0, 0	3703	15	9	-47	0.34	-0.06	-0.40	-1.43	16	9	9	NP_003152	P23443
599 600	PK145 NN123	p70-S6K p73	T229	Ribosomal protein S6	0, 0	1179 42293	3	7	0, 0	2202 36125	70	8	87	-0.67 1.37	-0.36 1.29	0.31 -0.08	1.12 -0.29	3	9	4	NP_003152 NP_005418	P23443 O15350
601	PK157	p90 RSK	Pan-specific S352	Tumor suppressor pro Ribosomal S6 protein-	0, 0	1650	1	7	0, 0	1799	5	8	-15 9	-0.48	-0.48	0.00	0.00	11	9	4	NP 002944	Q15350 Q15418
602	PK158	p90 RSK	T348	Ribosomal S6 protein-	0, 0	400	29	5	0, 0	2020	9	8	405	-1.29	-0.41	0.88	3.17	15	9	4	NP_002944	Q15418
603 604	PN187 NP008	p95 NBS1 PAC1	S343	Nijmegen breakage sy Dual specificity MAP k	0, 0	215 2424	21	4	0, 0	948 8844	541 95	7	340	-1.64 -0.26	-0.86 0.46	0.78 0.72	2.83	3	9	5	NP_002476.2 NP_004409	O60934 Q05923
605	NN084	PACSIN1		Protein kinase C + cas	0, 0	2424	6	8	0, 0	3243	18	8	36	-0.26	-0.13	0.72	0.50	11	9	5	NP_004409 NP_065855	Q05923 Q9BY11
606	NK122-4	PAK a	Pan-specific	p21-activated kinase 1	0, 0	993	17	7	0, 0	4055	80	9	308	-0.77	0.00	0.77	2.78	15	9	5	NP_002567	Q13153
607 608	NK122 PK130	PAK1 PAK1		p21-activated kinase 1 p21-activated kinase 1	0, 0	2774 1343	240	8	0, 0	1037 1514	51	7	-63 13	-0.18 -0.60	-0.81 -0.58	-0.62 0.01	-2.26 0.05	7	9	6	NP_002567 NP_002567	Q13153 Q13153
609	PK130 PK061	PAK1 PAK1/2/3	3144/3141/313	p21-activated kinase 1	0, 0	1343 863	14	6	0, 0	1514 997	10	7	16	-0.60	-0.58 -0.83	0.01	0.05	11	9	6	NP_002567 NP_002567	Q13153 Q13153

SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

Globally

Normalized Signal

MED MAX

>+200%

NP\_110395

Z-ratio

Globally

%CFC

Globally Globally malized Me ormalized Me 3433 4055 Log2 (Intensity Globally %Error Range Log2 (Intensit Serial Antibody Target Phospho Site Full Target %Error Range %CFC (Treated Z-score Difference Z-ratio Flag-Contro Normalized Control Control Corrected) -Treated Z score (Control) Z score (Treated) Block Row Column Refseq Uniprot Link No. Codes Control (Treated, Control 610 NP\_002569 NK123 Pan-specific p21-activated kinase 075914 611 PK752 PAK4 S474 n21-activated kinase 24523 0.94 1.06 0.12 NP 001014831 Pan-specific 1573 0, 0 0, 0 0, 0 0, 0 613 614 NN085-1 PARP1 Pan-specific Poly [ADP-ribose] poly 0, 0 1.50 0.19 NP\_001609 NP\_002850 P09874 NN086 Paxillin Paxillin 1 Pan-specific P49023 P49023 616 617 PN059 Paxillin 1 Y31 Paxillin 1 1925 2067 -0.39 -0.40 -0.01 NP 002850 P49023 Q00536 Q00537 NK125 PCTK1 Pan-specific PCTAIRE-1 protein-se 3655 4256 46010 36176 8417 -0.31 NP 148978 3370 4423 41257 -0.01 -0.05 PCTK2 618 619 PK756 S180 Cell division protein kir NP 001163935. -0.04 -0.18 Pan-Specific NK242-1 **PDGFRA** Platelet-derived growt NP 006197. P16234 Platelet-derived growt NK242-2 PDGFRA Pan-Specific 0, 0 43015 11757 NP\_006197.1 P16234 P16234 0.18 PK757 PDGFRa S847+pY849 Platelet-derived growtl 0.0 -0.41 P16234 P16234 P16234 622 PK063 PDGFRa Y754 Platelet-derived growth 8031 6863 0.42 0.31 -0.11 NP 006197.1 PDGFRa PDGFRa 11262 2225 NP\_006197. NP\_006197. Platelet-derived growth 7580 2659 0.39 0.21 -0.54 PK759 Platelet-derived growth P09619 P09619 P09619 625 NK243-1 PDGFRB Pan-Specific Platelet-derived growth 0.0 0.0 -25 0.16 -0.04 -0.20 -0.71 NP 002600.1 NK243-3 PDGFRB Platelet-derived growt 0, 0 9409 2812 0.42 NP\_002600.1 NP\_032835 Pan-Specific 0.35 Platelet-derived growth PK065 PDGFRb Y716 3560 -0.18 -0.08 Pan-specific Pan-specific 21298 2874 46345 19230 39205 -0.02 NP\_000909.2 NP\_002604 628 629 NN141-1 Protein disulfide-isome 0, 0 0, 0 0, 0 0.98 -0.01 0.63 0.12 21505 890 38600 21817 34975 43078 1040 39129 NK126-2 PDK1 PDK1 0.43 NN179-1 Pan-Specific Pyruvate dehydrogena NP 001265478. Q15118 631 NN179-2 PDK1 PDK2 Pan-Specific Pyruvate dehydrogena Pan-Specific Pyruvate dehydrogena 0, 0 0.99 0.92 -0.08 NP 001265478. Q15118 Q15119 -0.35 633 634 NN180-2 PDK2 PDK3 Pan-Specific Pyruvate dehydrogena 0, 0 0, 0 0, 0 35866 1193 45253 1 29 -0.10 0.02 NP 002602 Q15119 Q15120 Q15120 NN181-1 Pan-Specific NP 001135858 Pan-Specific Pyruvate dehydrogena NP\_001135858. 0, 0 0, 0 0, 0 0, 0 38417 636 637 NN178-2 PDK4 Pan-Specific [Pyruvate dehydrogen 1.32 -0.01 NP 002603.1 Q16654 NN178-3 Pan-Specific 37281 2029 0.36 638 639 PED15 (PEA15) 1772 PN061 S116 Phosphoprotein-enrich -0.49 0.05 -0.13 -0.25 NP\_003759 NP\_071404 Q15121 Q9H230 P27986 NN088 PERP Pan-specific p53-induced protein P 4437 -32 -0.91 NNOSC Pan-specific Phosphatidylinositol 3 0, 0 1355 2401 0, 0 597 2315 -0.54 -0.07 -1.96 -0.24 -0.39 PITSLRE NK213 Pan-specific PITSLRE serine/threo -0.27 -0.33 NP 001278274.1 P21127 642 P17612 P17612 NK127-1 PKA Pan-specific cAMP-dependent prot -0.11 NP 002721 0, 0 -0.16 0.23 NP\_002721 NP\_002722 cAMP-dependent prot 6167 3065 7780 1893 PK068 PKA Cb S338 cAMP-dependent prot P22694 645 PK069 S98 cAMP-dependent prot 156 11474 1074 753 5228 0.0 -1.83 -1.80 0.03 0.09 NP 523671 P13861 P31751 PKB2-PCT -0.26 0.53 -0.95 Pan-Specific RAC-beta serine/threo NP\_001617 NK218 PKC h Pan-specific Protein kinase C eta tv 0.0 2908 813 -0.73 -0.20 NP 006246.2 P24723 NK132 PK073 PKCa PKCa PKCb Pan-specific S657 NP\_002728 NP\_002728 P17252 P17252 P05771 648 649 650 0, 0 0, 0 0, 0 -0.02 0.06 0.01 NP 002729 NK133-2 Pan-Specific Protein-serine kinase 0.58 0.59 PKCb 2 PKCb1 2893 1219 2962 2104 651 652 PK076-2 T641 -0.03 0.26 -0.10 NP\_002729 P05771 NK133 Pan-specific NP\_002729 P05771 Protein-serine kinase -0.61 PKCb1/2 PKCd PKCd Protein-serine kinase ( Protein-serine kinase ( Protein-serine kinase ( 653 654 655 PK075-2 T500 0, 0 0, 0 0, 0 3016 8896 -20 -0.01 0.27 -1.18 -0.17 0.19 -0.03 NP\_002729 NP\_006245 P05771 NK135 NP\_006245 PK079-1 2583 -1.15 -0.29 -0.47 656 657 PK080 PKCd S664 Protein-serine kinase 0, 0 1625 -37 -0.22 -0.54 -0.32 NP 006245 Q05655 -0.08 -0.13 0.42 9700 16568 0, 0 0, 0 0, 0 0, 0 20526 1798 1526 1114 658 659 PK077-2 PKCd Y311 Protein-serine kinase 0.83 NP\_006245 Q05655 NK136 PKCe PKCe Pan-specific Protein-serine kinase -0.43 -0 O NP 005391 Q02156 Q02156 660 661 NK136-2 2074 NP\_005391 PK081-1 S729 Protein-serine kinase 0, 0 -0.70 -0.78 -0.08 -0.29 NP 005391 Q02156 PK081-2 PKC. \$720 Protein-cerine kingee -0 17 -0.62 NP 005301 663 664 PKCg PKCg 2155 NP\_002730 Pan-specific T514 Protein-serine kinase 0.26 -0.38 P05129 P05129 P05129 PK082-1 Protein-serine kinase 0.20 NP 002730 665 PK082-2 PKCa T514 Protein-cerine kingee 17795 15132 0.88 0.78 -n 1n -0.36 NP 002730 PKCg 0, 0 PK083 Protein-serine kinase -0.09 NP\_002730 PK084 PKCa T674 Protein-serine kinase 0.0 10573 0.58 0.42 -0.16 -0.56 NP 002730 P05129 PK085 NK138-1 NP\_006246 NP\_002731 P24723 P41743 668 669 670 0, 0 0, 0 0, 0 11523 4027 Pan-specifi PK087 PKCI T555/T563 Protein-serine kinase 1513 1091 0.0 1379 1045 -0.53 -0.64 -0.11 -0.39 NP 002731 P41743 PKCm (PKD) PKCm (PKD) 671 672 PK092 S738/S742 Protein-serine kinase 0, 0 -0.09 -0.29 NP\_002733 Q15139 -35 PK093-1 4353 2836 -0.21 Q15139 S916 Protein-serine kinase NP\_002733 673 674 675 NK140 PKCt Pan-specific Protein-serine kinase Protein-serine kinase 2357 2463 1555 939 -0.28 -1.21 -1.04 -0.02 0.64 0.18 -0.07 NP\_006248 NP\_006248 NP\_006248 Q04759 PK089-1 PK090-1 Q04759 Q04759 460 618 PKCt S695 Protein-serine kinase 0, 0 0, 0 0, 0 0, 0 NK141 PKC<sub>7</sub> Pan-specific Protein-serine kinase Protein-serine kinase 1273 1114 0, 0 1161 -0.63 -0.74 -0.76 -0.11 -0.41 NP 002735 Q05513 676 677 678 679 680 681 682 PKD (PKCm) Pan-specific -0.05 -0.18 0.06 Q15139 -0.18 -0.65 NK143 PKG1 Pan-specific cGMP-dependent prot -1.36 -1.54 NP 006249 Q13976 298 5729 NK203 PKG1h-NT Pan-Specific cGMP-dependent pro 0.20 NP 006249 P14619 Q16512 Pan-specific 1803 PKR1 0, 0 0, 0 0, 0 0, 0 0, 0 0.34 2.21 -0.18 0.34 0.57 NK144-1 Pan-specific Double stranded RNA 0, 0 -1.88 NP 002750 P19525 P19525 P16885 PK132 PKP1 T446 Double-stranded RNA -0.67 NP\_002750 683 684 685 1384 NN156 PLC R(PLCg2) 2701 -0.24 -0.87 NP\_002652.2 NP\_877963.1 Pan-specific 1-phosphatidylinositol-PN165 PLCg1 P19174 P19174 P16885 PN144 PLCa1 V783 -1.87 0.06 NP 877963.1 0, 0 -0.17 -0.62 686 687 PN143 PLCg2 Y753 NP\_002652.2 1-phosphatidylinositol-NP009-2 PP1/Ca (PP1a) Pan-specific Protein-serine phosph 0.68 -0.10 -0.35 NP 002699 P62136 NP010 NP011 PP1/Cb (PP1b) Pan-specific P62140 P36873 Q15172 Protein-serine phosph Pan-specific 690 NP033 PP2A B' (B56) Pan-specific Protein-serine phosph 0.0 16412 20642 0.83 0.13 0.47 NP 001186685. 691 692 PP2A/Aa/b Protein-serine phosph 40495 49423 -0.12 -0.21 PP2A/Bb 0,0 0, 0 1.53 -0.06 NP035 Pan-specific Protein-serine phosph NP\_001258828. Q00005 693 694 695 NP032 PP2A/Bn2 Pan-specific Pan-specific Protein-serine phosph 1.53 -1.30 1.07 0.02 -0.29 -0.16 NP\_001193923.1 NP\_002706 NP\_000935 Q9Y2T4 P67775 Q08209 0.06 -1.06 -0.57 NP013-NP014 PP2A/Ca NP015 PP2B/Aa Pan-specific Protein-serine phosph

SAMPLE DETAILS

696

NP018

PP2Cd

Pan-specific Protein-serine phosph

Sample IDs: Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

Globally Normalized Signal MED %CFC

Z-ratio

Globally

MAX

>+200%

malized Me ormalized Me 3433 4055 Globally Normalized Control Log2 (Intensity %Error Range Globally Log2 (Intensit Serial Antibody Target Phospho Site Full Target %Error Range %CFC (Treated Z-score Difference Z-ratio Flag-Contro Control Normalized Treated Z score (Control) Z score (Treated) Block Row Column Refseq Uniprot Link No. Codes Control ated, Control PP4/A'2 Pan-specific NP\_005125 Protein-serine phospi Q8TF05 698 NP020 PP4C (X/C) Pan-specific Protein-serine phosp 1 28 -0.06 -0.22 NP 00271 P60510 P60510 Pan-specific 0, 0 0, 0 0, 0 0, 0 0, 0 -0.16 -0.45 -0.14 -0.22 -0.58 NP021 PP5/PPT Pan-specific Protein-serine phosph 0, 0 NP 006238 P53041 700 701 702 703 704 705 706 707 PN532 PPP1R11 Y64 3083 1545 -0.57 NP 068778. O60927 PRAS40 NP\_115751 Q96B36 NK149 PRK2 Pan-specific Protein kinase C-relate 17130 1256 -30 0.86 0.64 -0.79 NP 006247 Q16513 NK 140-2 Pan-specific 2329 46545 43360 43481 44350 NP\_006247 Q16513 P78527 NK048-4 0.02 0.00 NP\_001075109. Pan-Specific DNA-activated protein-47335 35148 PRKDC (DNAPK) Pan-Specific P78527 P78527 P78527 NK048-5 DNA-activated protein NP 001075109. NK048-6 PRKDC (DNAPK) Pan-Specific PRKDC (DNAPK) Pan-Specific DNA-activated protein 0, 0 NP 001075109. NK048-7 NP\_001075109. DNA-activated protein 2062 463 3358 0.0 709 NK151 PRKWNK4 Progesterone Pan-specific Putative protein-serine 2850 550 3306 -0.35 -0.21 0.14 NP 115763 NP\_000917 NP\_003904.3 Progesterone receptor 0.02 PRP4K Q13523 P78352 P60484 P60484 PK786 Protein-serine kinase 1937 25090 14249 712 NN142 PSD-95 Pan-specific Disks large homolog 4 0.0 0.0 -1.44 -0.44 1.00 1.11 0.23 NP 001356. 713 714 PTEN 0, 0 0, 0 NP\_000305 NP\_000305.3 Pan-specific Phosphatidylinositol-0.52 0.74 NP023-3 Pan-Specific Phosphatidylinositol-3 PTEN PTEN PTEN Pan-Specific Phosphatidylinositol-3 380/S382/S385Phosphatidylinositol-3 NP\_000305.3 NP\_000305 NP\_000305 P60484 P60484 P60484 NP023-5 0, 0 0, 0 0, 0 35773 2750 257 -0.03 -0.13 0.09 0, 0 0, 0 0, 0 -0.12 -0.48 0.32 S380/S382/S385 2356 PP006 Phosphatidylinositol-3 -1.54 Phosphatidylinositol-3
Phosphatidylinositol-3
Phosphatidylinositol-3
Protein-tyrosine phosp 718 719 PP006-1 PTEN PTP1B 0, 0 713 1112 755 1215 -0.96 -0.99 -0.04 -0.01 NP 000305 P60484 P18031 NP\_002818 720 721 722 NP025 PTP1C Pan-specific Protein-tyrosine phosp 0, 0 0, 0 0, 0 1225 2148 16379 -0.65 -1 21 -0.55 -0.36 -0.13 NP\_002822 NP\_002825 P29350 Q06124 Q16825 NP026 PTP1D/SHP2 -1.29 -0.47 Pan-specific Protein-tyrosine phosp 723 724 725 726 727 NP027 PTP-PEST Pan-specific Protein tyrosine phosp 4726 0, 0 7382 0.12 0.35 0.23 NP\_001124480.1 Q05209 N/A 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 PG001 PYK 8650 1855 -0.16 0.09 -0.08 -0.58 2338 NP 004094 NK154 Pyk2 PYK2 Pan-specific Protein-tyrosine kinase -0.41 -1.37 -0.33 0.31 344 28208 784 1041 148 NP 004094 PK097-3 Y579 Protein-tyrosine kinase Q14289 PG005 PYKSD8 Rac1 рТуг -0.15 -0.26 -0.55 -0.95 N/A 1.14 NP\_001782 728 729 NN092-1 Pan-specific Ras-related C3 botulin -28 P63000 P63000 O75943 P04049 PN063 Rac1/cdc42 S71 Ras-related C3 botuling 890 -0.74 -0.90 -0.56 NP 008839 730 731 -0.09 -0.33 -0.30 NP\_579921 NP\_002871 Rad17 homolog -1.95 -1.82 PK098 S259 Raf1 proto-oncogene-732 NK155-4 Raf-1 Pan-specific Rad17 homolog 0.0 3382 0.0 1418 34069 -0.07 -0.62 -0.55 NP 002871 P04049 P04049 NK155-5 26125 0.16 733 734 Pan-Specific Raf1 proto-oncogene-NP\_002871 NK155-6 Raf-1 Pan-Specific Raf1 proto-oncogene-0.0 14130 1039 2094 6493 0.75 0.28 NP 002871 P04049 NN093 PN113 Pan-specific S608 NP\_000312 NP\_000312 P06400 P06400 P06400 735 736 737 0, 0 0, 0 0, 0 0, 0 -0.37 -0.55 PN066 S612 Retinoblastoma-assoc -22 0.94 0.79 -0.15 NP 000312 738 739 NP\_000312 NP\_000312 PN067 S780 0, 0 3365 0.05 P06400 65-6471 1518 9358 -0.41 PN131-1 P06400 Retinoblastoma-assoc Retinoblastoma-assoc Retinoblastoma-assoc PN068 \$807 0, 0 0, 0 0, 0 6569 1685 7428 0.28 -0.02 0.01 -0.15 0.06 NP\_000312 NP\_000312 P06400 P06400 P06400 PN069 S807+S811 NP\_000312 743 744 745 746 914 9549 P06400 P06400 PN070 Rb T821 Retinoblastoma-assoc 0, 0 0, 0 -28 -0.82 -1 08 -0.26 -0.03 -0.93 NP 000312 0, 0 0, 0 0, 0 0, 0 NN170 Pan-specific Transcription factor Re -2.08 -0.03 -0.64 NP\_006500.2 Q01201 PN151 RelB S552 Transcription factor Re 1299 -0.62 NP 006500 2 Q01201 P07949 NK244-1 Proto-oncogene tyrosi 1.20 0.11 31360 31968 1827 1305 748 749 NK244-2 Pan-Specific Proto-oncogene tyrosii 0, 0 40109 1201 890 1.35 NP 065681 P07949 -1.08 NP\_003812 NP\_003795 NP\_005397 NK157 PIP2/PICK Pan-specific -n 3n RIPK ROCK-I/ROKb Pan-specific -32 -33 -0.61 -0.20 -0.28 -0.28 -1.03 -1.00 Receptor-interacting p NK160 Pan-specific RhoA protein-serine ki 2715 860 1527 1826 Q13464 075116 075116 752 NK150-1 P∩K∘ Pan-specific Physesociated protein 0, 0 -0.85 -n 83 0.02 NP 004841 753 754 2483 -0.52 0.84 NK159-2 ROKa Pan-specific Rho-associated protein -0.29 0.23 NP\_004841 NK161-2 Ron Pan-Specific Macrophage-stimulating 0.0 18415 -23 1.05 0.89 -0.15 NP 002438 Q04912 Pan-Specific Y1238 NP\_002438 NP\_002438 Q04912 Q04912 NK161-3 Macrophage-stimulati 0, 0 0, 0 0, 0 PK800 Macrophage-stimulati NK161 RONa Pan-specific Macrophage-stimulating 1627 42826 0.0 935 41795 -0.49 -0.87 -0.38 NP 002438 Q04912 758 759 NK163-3 Pan-Specific 0, 0 0.00 -0.01 0.45 NP\_002935 P08922 NK163-4 Pan-Specific P08922 Orosomucoid 1 recept 2411 2381 1331 NP\_002935 760 761 762 NK164 RSK1 Pan-specific Ribosomal S6 protein 2991 4142 -0.26 -0.27 -0.60 0.08 0.28 -0.11 0.30 NP\_002944 NP\_002944 NP\_002944 PK099 RSK1/2 RSK1/2 S221/S227 S363/S369 Ribosomal S6 protein-Ribosomal S6 protein-Q15418 Q15418 -0.39 PK100 763 764 765 766 767 0, 0 0, 0 0, 0 0, 0 1818 1218 457 584 0.00 -0.26 0.03 0.22 PK100-2 RSK1/2 S363/S369 Ribosomal S6 protein-S380/S386 Ribosomal S6 protein-0, 0 1967 872 -0.43 -0.43 NP 002944 Q15418 Q15418 Q15418 RSK1/2 PK102 RSK1/2/3 T573 Ribosomal S6 protein--1.21 -1.07 NP\_002944 NP\_001001 PN073 S235 40S ribosomal protei 966 Ribosomal protein S6 -0.09 0.01 768 769 770 771 SAPKb-NT 0, 0 0, 0 0, 0 0, 0 NK197 Pan-Specific Jun N-terminus proteir 0, 0 1.27 1.28 NP 002744.1 P53779 Pan-specific Y239?Y240 Q13033 P29353 NN133 SG2NA Striatin-3 935 -0.26 -0.17 -0.15 -0.96 XP 005267626 NP\_003020 NP\_003020 Shc1 Shc1 SH2 domain-containin 0.55 -1.57 -0.62 PN161 Y349 SH2 domain-containing -0.53 P29353 Q92835 Q15357 772 NP044-2 SHIP1 Pan-Specific Phosphatidylinositol-3 0.23 -n 58 VP 001017015 1 773 774 SHIP2 NP045-1 Pan-Specific 0, 0 24773 0.05 NP\_001558.3 Phosphatidylinositol-3 NP026-2 SHP2 Pan-specific Protein-tyrosine phosp 0.28 -0.02 NP 002825 Q06124 775 776 777 PP004 NK249-1 S576 Protein-tyrosine phosp 2021 -0.19 -0.22 -0.68 -0.79 NP\_002825 NP\_056006. Q06124 Q9H0K1 Q9H0K1 Pan-Specific NK249-2 SIK2 Pan-Specific Serine/threonine-prote 0.0 16001 13461 0.82 -0.11 NP 056006.1 23858 25731 778 779 NK249-3 SIK2 SIK3 Serine/threonine-prote 19136 20910 -0.13 -0.12 NP\_056006.1 NP\_001268677. NK250-1 Pan-Specific Serine/threonine-prote 0,0 Q9Y2K2 NK250-3 SIK3 Pan-Specific Serine/threonine-prote Pan-specific Second mitochondria-S465 Mothers against decar 0, 0 0, 0 0, 0 -32 1.12 -1.08 -1.24 0.90 -1.25 -0.22 -0.17 0.05 -0.81 NP\_001268677.1 NP\_620308 Q9Y2K2 Q9NR28 NN095 PN183 Smad1 NP\_001003688. 783 PN184 Smad2 S467 Mothers against decar -1.08 0.01 NP\_001003652

SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

Globally

\_ ...

Globally

Z-ratio <-1.5 0

Sample IDs: Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

SAMPLE DETAILS

Globally

						Globally Normalized Median 3433				Normalized Median 4055		<-1.5		U		>+1.5						
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link
784 785	PN185 NN096	Smad2 Smad2/3		Mothers against decar SMA- and mothers ag	0, 0	2075 1586	15 80	8	0, 0	4174 643	47 62	9	101 -59	-0.35 -0.50	0.02 -1.09	0.36 -0.59	1.32 -2 12	12 16	10	9	NP_001003652 NP_005892	Q15796 Q15796
786	PN125	SMC1		Structural maintenanc	0, 0	18598	23	11	0, 0	14092	9	10	-24	0.90	0.73	-0.17	-0.61	4	10	10	NP_006297.2.	Q14683
787	NK233-1	SMG1	Pan-Specific	Lambda/iota protein ki	0, 0	68702	2	13	0, 0	58670	1	13	-15	1.65	1.58	-0.07	-0.26	8	10	10	NP 055907.3	Q96Q15
788 789	NK233-3 PN197	SMG1 NCA (a-Synucle		Lambda/iota protein ki Alpha-synuclein	0, 0	43423 501	2	12	0, 0	43552 755	12	12	0 51	1.39	1.40 -1.00	0.01 0.17	0.05 0.60	12	10	10	NP_055907.3 NP_000336.1	Q96Q15 P37840
789	PN197 NK251-1	NCA (a-Synucie SNF1IK		Alpha-synuciein Serine/threonine-prote	0, 0	44022	89	12	0, 0	755 49477	12	12	12	-1.16 1.39	-1.00	0.17	0.30	11	10	10	NP_000336.1	P57059
791	NK146-2	Snk		Polo-like protein kinas	0, 0	1972	4	8	0, 0	3886	50	9	97	-0.38	-0.03	0.35	1.27	3	10	5	NP 006613	Q9NYY3
792	NN145	SOCS2	Pan-specific	Suppressor of cytokine	0, 0	3565	107	8	0, 0	6744	606	9	89	-0.04	0.30	0.34	1.23	7	10	5	NP_003868.1	O14508
793	NN097	SOCS4	Pan-specific	Suppressor of cytokine	0, 0	8428	20 39	10	0, 0	2971 521	7	8	-65 -30	0.45	-0.19	-0.64	-2.30 -1.00	11 15	10	5	NP_543143	Q8WXH5
794 795	NN098 NN099	SOD (Cu/Zn) SODD		Superoxide dismutase Silencer of death doma	0, 0	740 7386	39 18	9	0, 0	3076	0	8	-30 -58	-0.94 0.37	-1.21 -0.17	-0.28 -0.54	-1.00 -1.96	15	10	6	NP_000445 NP_004865	Q6ND84 O95429
796	PN077	SOX9		SRY (sex determining	0, 0	3396	1	8	0, 0	4101	39	9	21	-0.07	0.00	0.07	0.27	7	10	6	NP 000337	P48436
797	NN100	SPHK1	Pan-specific	Sphingosine kinase 1	0, 0	2382	28	8	0, 0	3136	17	8	32	-0.27	-0.15	0.12	0.42	11	10	6	NP_892010	Q9NYA1
798 799	NN101 NK172-2	SPHK2	Pan-specific	Sphingosine kinase 2	0, 0	3001 59224	16	8	0, 0	4466 68613	11	9	49	-0.14 1.56	0.06 1.67	0.19 0.11	0.70	15	10 10	6	NP_064511	Q9NRA0
800	NK172-2 NK172-3	Src Src		Src proto-oncogene-er Src proto-oncogene-er	0, 0	1499	18 20	13	0, 0	11653	12 64	13	16	-0.54	0.62	1.16	0.38	11	10	8	NP_005408 NP_005408	P12931 P12931
801	NK172-3	Src		Src proto-oncogene-er	0, 0	736	17	6	0.0	2552	26	8	246	-0.94	-0.28	0.67	4.19 2.41	15	10	7	NP 005408	P12931
802	PK107	Src	Y418	Src proto-oncogene-er	0, 0	1658	42	7	0, 0	1495	40	7	-10	-0.48	-0.59	-0.11	-0.41	3	10	7	NP_005408	P12931
803	PK108	Src	Y529	Src proto-oncogene-er	0, 0	1192	60	7	0, 0	1246	3	7	5	-0.67	-0.70	-0.03	-0.12	7	10	7	NP_005408	P12931
	N102-NN124 N078-PN135	STAT1 STAT1		Signal transducer and Signal transducer and	0, 0	2586	122 19	8	0, 0	2510 758	49 24	8	-3	-0.22 -0.93	-0.29 -0.99	-0.06 -0.06	-0.22 -0.22	11	10 10	8	NP_009330 NP_009330	P42224 P42224
	N079-PN136	STAT1		Signal transducer and	0, 0	1557	51	7	0, 0	3044	3	8	95	-0.93	-0.99	0.34	1 24	15	10	8	NP_009330	P42224
807	NN103	STAT2	Pan-specific	Signal transducer and	0, 0	4211	1	9	0, 0	3775	13	9	-10	0.05	-0.04	-0.10	-0.36	3	10	9	NP_005410	P52630
808	PN080	STAT2	Y689	Signal transducer and	0, 0	229	119	4	0, 0	133	45	4	-42	-1.61	-2.02	-0.42	-1.50	7	10	9	NP_005410	P52630
809 810	NN104 PN082-1	STAT3 STAT3	Pan-specific Y704	Signal transducer and Signal transducer and	0, 0	2818	85 20	8	0, 0	4707 5576	88	9	67 -17	-0.18 0.32	0.09	0.26 -0.13	0.95 -0.48	15 11	10 10	9	NP_003141 NP_003141	P40763 P40763
811	NN117	STAT4		Signal transducer and	0, 0	1838	46	7	0, 0	1511	5	7	-17	-0.42	-0.59	-0.13	-0.46	3	10	10	NP_003141	Q14765
812	PN083-1	STAT5		Signal transducer and	0, 0	1332	243	7	0, 0	811	19	6	-39	-0.60	-0.95	-0.35	-1.27	7	10	10	NP_003143	P42229
813	NN105	STAT5A		Signal transducer and	0, 0	3822	57	9	0, 0	2716	1	8	-29	0.00	-0.24	-0.24	-0.86	11	10	10	NP_003143	P42229
814	PN119 NN106	STAT5A STAT5B	S780	Signal transducer and	0, 0	743 741	26	6	0, 0	1003 1992	48 57	7	35	-0.94 -0.94	-0.83 -0.42	0.11 0.52	0.39	15	10 10	10	NP_003143	P42229 P51692
815 816	NN106 NN107	STAT5B STAT6		Signal transducer and Signal transducer and	0, 0	741 1176	5	6	0, 0	1992 1714	57 50	8 7	169 46	-0.94 -0.67	-0.42 -0.51	0.52	0.59	2	10	5	NP_036580 NP_003144	P51692 P42226
817	NN108	STI1		Stress induced phospi	0.0	572	25	6	0.0	353	32	5	-38	-1.09	-1.44	-0.36	-1.30	10	10	5	NP 006810	P31948
818	NN134	Striatin	Pan-specific	Striatin	1, 0	12578	4	10	1, 0	12598	33	10	0	0.68	0.67	-0.01	-0.04	14	10	5	NP_003153.2	O43815
819	NK174	Syk		Spleen protein-tyrosin	0, 0	9998	12	10	0, 0	8751	6	10	-12	0.55	0.45	-0.10	-0.34	10	10	6	NP_003168	P43405
820 821	PK159 PK821	Syk Syk	Y323 Y323	Spleen protein-tyrosing Spleen protein-tyrosing	0, 0	690 3844	9	6	0, 0	217 7664	10	4	-69	-0.98 0.00	-1.73 0.37	-0.75 0.37	-2.73	6	10	6	NP_003168 NP_003168	P43405 P43405
821	NN171	Syk Synapsin 1		Synapsin 1 isoform la	0, 0	3844	934	5	0, 0	275	308	10	-30	-1.30	-1.59	-0.29	-1.06	14	10	6	NP_003168 NP_008881	P17600
823	PN111	Synapsin 1		Synapsin 1 isoform la	0, 0	180	43	4	0, 0	307	64	5	71	-1.75	-1.53	0.22	0.79	2	10	7	NP_008881	P17600
824	NK175-5	TAK1		TGF-beta-activated pn	0, 0	2031	212	8	0, 0	1961	64	8	-3	-0.36	-0.43	-0.07	-0.25	6	10	7	NP_663306	O43318
825	PN085	Tau		Microtubule-associated	0, 0	2602	18	8	0, 0	2229	10	8	-14	-0.22	-0.36	-0.13	-0.49	10	10	7	NP_005901	P10636
826 827	PN086 PN091	Tau Tau		Microtubule-associated Microtubule-associated	0, 0	1162 706	23	7	0, 0	1387 657	20 33	7	19	-0.68 -0.97	-0.64 -1.08	0.04 -0.11	0.16 -0.40	14	10	7	NP_005901 NP_005901	P10636
828	PN091	Tau		Microtubule-associated	0, 0	1273	28	7	0, 0	989	5	7	-7	-0.63	-0.84	-0.11	-0.40	10	10	8	NP_005901	P10636
829	PN107	Tau		Microtubule-associated	0, 0	2092	14	8	0, 0	2188	5	8	5	-0.35	-0.37	-0.02	-0.08	14	10	8	NP_005901	P10636
830	PN090	Tau		Microtubule-associated	0, 0	982	30	7	0, 0	948	15	7	-3	-0.78	-0.86	-0.08	-0.30	2	10	8	NP_005901	P10636
831	PN090-2	Tau		Microtubule-associated	0, 0	627	0	6	0, 0	645 491	15	6	3	-1.03	-1.09	-0.06	-0.20	2	10	9	NP_005901	P10636
832 833	PN121 PN122	Tau Tau		Microtubule-associated Microtubule-associated	0, 0	540 328	30	5	0, 0	491 324	35 9	5	-9 -1	-1.12 -1.40	-1.25 -1.50	-0.13 -0.09	-0.47 -0.34	10	10	9	NP_005901 NP_005901	P10636 P10636
834	NK220-2	TBK1		Serine/threonine-prote	0, 0	2246	35	8	0, 0	2612	13	8	16	-0.30	-0.26	0.04	0.15	14	10	9	NP_037386	Q9UHD2
835	PK828	TBK1		Serine/threonine-prote	0, 0	32295	21	12	0, 0	31054	20	12	-4	1.22	1.20	-0.02	-0.06	2	10	10	NP_037386	Q9UHD2
836	PK829 NN110	TEC	Y519	Tyrosine-protein kinas	0, 0	20981 2110	88	11	0, 0	27145 1449	305 22	11	29	0.97	1.12	0.15	0.55 -0.98	6 10	10	10	NP_003206.2	P42680 Q15628
837 838	NN110 NN111	TRADD Trail	Pan-specific Pan-specific	Tumor necrosis factor Tumor necrosis factor-	0, 0	1370	14	7	0, 0	1131	5	7	-31 -17	-0.34 -0.59	-0.61 -0.76	-0.27 -0.17	-0.98	10	10	10	NP_003789 NP_003801	950591
839	NK178	TrkA		Nerve growth factor (N	0, 0	309	41	5	0, 0	491	50	6	59	-1.44	-1.25	0.19	0.68	1	10	5	NP_002520	P04629
840	NK179	TrkB		BNDF/NT3/4/5 recepto	0, 0	1766	20	7	0, 0	2271	10	8	29	-0.44	-0.34	0.10	0.35	5	10	5	NP_006171	Q16620
841	PK160 NK180	TrkB TTK		BNDF/NT3/4/5 recepti	0, 0	2410	19	8	0, 0	3314 4760	36	8	38 62	-0.26 -0.15	-0.12 0.09	0.14 0.24	0.52	9	10	5	NP_006171 AAA61239.1	Q16620 P33981
842	NK180 CN002	Tubulin	Pan-specific Pan-specific	Dual specificity protein Tubulin	0, 0	2936 9350	20	10	0, 0	7143	16	10	-24	-0.15 0.51	0.09	-0.18	-0.64	13	10	6	NP 001061.2	P33981 P23258
844	NK181	Tyk2		Protein-tyrosine kinase	0, 0	841	38	6	0, 0	1413	0	7	68	-0.87	-0.62	0.24	0.87	1	10	7	NP 003322	P29597
845	NK181-2	Tyk2		Protein-tyrosine kinase	0, 0	601	15	6	0, 0	2342	29	8	290	-1.06	-0.33	0.73	2.65	5	10	7	NP_003322	P29597
846	NK181-3	TYK2		Protein-tyrosine kinase	0, 0	35198	4	12	0, 0	33060	32	12	-6	1.27	1.24	-0.03	-0.10	5	10	6	NP_003322	P29597
847 848	NK181-4 NK181-5	TYK2 TYK2		Protein-tyrosine kinase Protein-tyrosine kinase	0, 0	27758 61721	3	11	0, 0	16504 69214	4 8	11	-41 12	1.13 1.59	0.83 1.67	-0.30 0.09	-1.10 0.32	13	10	6	NP_003322 NP_003322	P29597 P29597
849	NK183-1	Tyro10		Neurotrophic receptor-	0, 0	1251	39	7	0, 0	900	7	7	-28	-0.64	-0.89	-0.25	-0.91	9	10	7	NP_006173	Q16832
850	PN093-1	Hudrondoon	S40	Tyrosine hydroxylase it	0, 0	124	33	4	0, 0	126	29	4	2	-1.96	-2.05	-0.09	-0.34	13	10	7	NP_954986	P07101
851	PN543	VAV1	Y826	Vav 1 guanine nucleot	0, 0	2062	3	8	0, 0	2932	10	8	42	-0.35	-0.19	0.16	0.58	1	10	8	NP_001245135.1	P15498
852 853	NN176 PK161	VEGF-C VEGFR2	Pan-Specific Y1059	Vascular endothelial g Vascular endothelial g	0, 0	2273 1437	14 198	8	0, 0	2327 1017	20	8	2 -29	-0.30 -0.56	-0.33 -0.82	-0.03 -0.26	-0.12 -0.94	5	10	8	NP_005420.1 NP_002244	P49767 P35968
854	PK161 PK133	VEGFR2 VEGFR2		Vascular endothelial g	0, 0	176	198	4	0, 0	259	19 40	5	-29 47	-0.56	-0.82	0.13	-0.94	13	10	8	NP_002244	P35968
855	NK226-2	VGFR1		Vascular endothelial g	0, 0	39758	8	12	0, 0	42781	23	12	8	1.34	1.39	0.05	0.20	1	10	9	NP_001153392.1	P17948
856	NK245-2	VGFR2		Vascular endothelial g	0, 0	26516	14	11	0, 0	28323	21	11	7	1.10	1.15	0.04	0.15	5	10	9	NP_002244	P35968
857 858	NK245-3 NK064-2	VGFR2 VGFR3		Vascular endothelial g	0, 0	40208 31067	16	12	0, 0	35924 33237	19 21	12	-11	1.34	1.29 1.24	-0.06 0.05	-0.20 0.17	9	10	9	NP_002244 NP_002011.2	P35968 P35916
859	NK064-2 NK064-3	VGFR3		Vascular endothelial g Vascular endothelial g	0, 0	51360	2	12	0, 0	50985	4	12	-1	1.19	1.24	0.05	0.17	13	10	10	NP_002011.2 NP_002011.2	P35916 P35916
860	NP030	VHR		Dual specificity protein	0, 0	374	0	5	0, 0	290	28	5	-22	-1.33	-1.56	-0.23	-0.84	5	10	10	NP_004081	P51452
861	PN544	VIM	Y117	Vimentin	0, 0	2755	11	8	0, 0	3349	5	8	22	-0.19	-0.11	0.07	0.26	9	10	10	NP_003371.2	P08670
862	PN094	Vimentin		Vimentin	0, 0	418	107	5	0, 0	310	14	5	-26	-1.26	-1.52	-0.26	-0.93	13	10	10	NP_003371.2	P08670
863 864	NK185 NP037	Wee1 Wip1		Wee1 protein-tyrosine Protein phosphatase 1	0, 0	24973 719	9	11	0, 0	20468 1024	6	11	-18 42	1.07	0.95 -0.81	-0.12 0.14	-0.42 0.51	4	10	11	NP_003381 NP_003611.1	P30291 O15297
	NP037 NK252-1	Wip1 WNK1		Protein phosphatase 1 Serine/threonine-prote	0, 0	719 34773	9	12	0, 0	1024 29639	1	12	42 -15	-0.95 1.26	-0.81 1.17	-0.09	0.51 -0.31	12	10	11	NP_003611.1 NP_001171914.1	Q9H4A3
		WNK1		Serine/threonine-prote	0, 0	11128	80	10	0, 0	10618	5	10	-5	0.61	0.57	-0.04	-0.15	3	10	11	NP_001171914.1	Q9H4A3
865 866	PK855									10182												Q9Y3S1
865 866 867	NK253-3	WNK2	Pan-Specific	Serine/threonine-prote	0, 0	17409	3	11	0, 0		2	10	-42	0.86	0.54	-0.32	-1.17	7	10	11	NP_001269323.1	
865 866			Pan-Specific Pan-Specific	Serine/threonine-prote Serine/threonine-prote Serine/threonine-prote	0, 0 0, 0 0, 0	17409 33310 36382	3 10	11 12 12	0, 0	10182 32698 30674	3	10 12 12	-42 -2 -16	0.86 1.23 1.29	0.54 1.23 1.19	-0.32 0.00 -0.09	-1.17 -0.01 -0.33	7 11 15	10 10	11	NP_001269323.1 NP_001002838.1 NP_001002838.1	Q9BYP7 Q9BYP7

SAMPLE DETAILS
Sample IDs: Control ID: Pooled Samples Larger

Treated ID: Pooled Samples Smaller

| Company | Comp

						Normalized Median				Normalized Median												
						3433				4055												
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link
871	NK186-2	Yes	Pan-specific	Yamaguchi sarcoma p	0, 0	251	21	5	0, 0	319	58	5	27	-1.55	-1.50	0.05	0.18	6	10	11	NP_005424	P07947
872	NK214	YSK1	Pan-specific	Serine/threonine-prote	0, 0	6380	10	9	0, 0	11299	2	10	77	0.29	0.60	0.31	1.13	10	10	11	NP_006365.2	O00506
873	NK256-2	YSK4	Pan-Specific	SPS1/STE20-related (	0, 0	18243	25	11	0, 0	17363	20	11	-5	0.89	0.86	-0.03	-0.12	14	10	11	NP_001018054.1	Q56UN5
874	NK187	ZAP70	Pan-specific	Zeta-chain (TCR) asso	0, 0	1058	44	7	0, 0	2329	21	8	120	-0.73	-0.33	0.40	1.47	5	10	11	NP_003168	P43403
875	NK187-2	ZAP70	Pan-specific	Zeta-chain (TCR) asso	0, 0	1595	1	7	0, 0	2581	35	8	62	-0.50	-0.27	0.23	0.84	1	10	11	NP_003168	P43403
876	NK188-1	ZIPK	Pan-specific	ZIP kinase (death asso	0, 0	3626	35	8	0, 0	6255	13	9	73	-0.03	0.25	0.29	1.03	13	10	11	NP_001339	O43293
877	NK188-2	ZIPK	Pan-specific	ZIP kinase (death asso	0, 0	3799	15	9	0, 0	4003	20	9	5	0.00	-0.01	-0.01	-0.02	9	10	11	NP_001339	O43293

## Appendix G Individual Microarray

Storage   Authority   Target Protein   Protein Storage   Flags   Flags   Flags   Protein   Pro		Chalchy   Committee   Commit	2278 (Globally mornalized
150   PM007	6660 6660 6660 6660 6660 6660 6660 666	Patient 6 Patient 7 Patient 6 Patient 7 Patien	2006  800  800  800  800  800  800  800
1985   PROST   CAST	6660 6660 6660 6660 6660 6660 6660 666	971   971	5347 8019 8019 3020
Mode	4949 4949 4949 4949 4949 4949 4949 494	6007 1 60	8019 3620 3695 3690 3690 3690 3690 2209 2247 9947 2947 2947 490 750 3750 3752 3752 3752 3752 3752 3752 3752 3752
March   Marc	1997 2007 1007 1008 1009 1009 1009 1009 1009 1009 1009	2003 - 20	2209 2209 2347 990 828 651 459 651 459 759 357 348 447 214 556 5338 234 457 243 338 250 124 150 168 1127 108 1140 100 1140 207 107 282 245 995 838
Mate   Part	1018 1102 2660 2660 2670 2670 2670 2670 2670 26	1900   19	990 828 828 828 990 990 990 990 990 990 990 990 990 99
Mate   Part	1102 1002 1002 1002 1002 1002 1002 1002	1005   10	828 651 490 750 972 350 972 357 348 447 214 457 234 457 243 380 332 243 380 130 140 140 100 100 100 100 100 100 100 10
1985   Price	1042 1043 807 407 373 808 973 984 984 984 985 989 989 989 989 989 989 989 989 989	1105 1105 1105 1105 1105 1105 1105 1105	490 750 7750 972 972 350 357 348 447 214 447 214 555 338 234 457 243 380 332 124 260 130 130 130 146 100 146 100 147 267 245 995 838
March   Marc	1013 007 419 449 449 449 208 444 332 227 602 228 447 602 259 251 251 251 251 251 251 251 251	692 621 714 714 661 661 377 662 328 334 331 331 331 355 160 96 96 96 102 363 100 96 102 102 103 103 103 103 103 103 103 103 103 103	972 350 357 348 447 214 447 214 457 238 239 234 457 243 380 332 124 260 130 188 127 100 140 100 140 207 107 282 245 995 838
March   Marc	469 469 373 286 469 373 286 569 477 285 579 579 579 579 579 579 579 579 579 57	692 621 714 714 661 661 377 662 328 334 331 331 331 355 160 96 96 96 102 363 100 96 102 102 103 103 103 103 103 103 103 103 103 103	348 447 214 214 555 338 234 457 243 380 332 124 280 130 188 146 100 140 207 107 282 245 995 838
ST   No. 18	286 644 332 477 602 225 500 225 500 225 500 225 500 227 119 154 119 137 137 137 137 137 137 137 149 159 166 177 188 189 199 199 199 199 199 199	714 714 566 714 566 611 377 662 328 331 311 317 305 228 563 199 604 561 561 773	214 555 556 338 234 457 243 380 232 4457 243 380 130 130 188 127 108 1100 140 107 282 245 995 838
BT   NATION   DECEMBER   Pre-specific   Pre-speci	369 369 412 412 259 259 259 251 154 154 154 157 170 208 808 90 917 245 4517 600	566 542 661 377 662 338 331 311 317 365 366 228 561 561 561 561 561 561 561 561	457 243 380 332 380 332 124 260 130 188 127 108 146 140 207 107 282 245 995 838
APT   Ministry   Project	369 369 412 412 259 259 259 251 154 154 154 157 170 208 808 90 917 245 4517 600	661 377 662 328 328 334 331 311 3117 305 180 66 228 192 363 192 361 160 60 64 713	457 243 380 332 380 332 124 260 130 188 127 108 146 140 207 107 282 245 995 838
No.   Proc.	369 369 412 412 259 259 259 251 154 154 154 157 170 208 808 90 917 245 4517 600	662 328 334 331 311 317 305 180 96 225 192 363 150 604 361 1678 713	380 332 124 260 130 185 127 103 146 100 140 107 282 245 995 838
20.0 Mol	259 251 219 364 154 119 118 117 173 170 165 170 328 719 808 99 917 245 4517 600	334 331 311 317 305 180 96 226 192 383 150 604 361 1678 713	260 130 186 127 108 146 100 140 207 107 282 245 995 838
1865   1877   Proceedings	354 154 119 118 137 37 165 173 170 328 719 808 99 917 245 4317 600	311 317 305 180 96 226 192 363 150 604 361 1678 713	186 127 108 146 100 140 207 107 282 245 995 838
No.   Col.   C	119 118 118 137 37 165 173 170 328 719 888 899 917 245 4317 600	180 96 226 192 363 150 604 361 1678 713	108 146 100 140 207 107 282 245 995 838
No.   Col.   C	37 165 173 170 328 719 898 99 917 245 4317 600	363 150 604 361 1678 713	207 107 282 245 995 838
Mathematics	165 173 170 328 719 898 99 917 245 4317 600	363 150 604 361 1678 713	207 107 282 245 995 838
Column   C	719 898 99 917 245 4317 600	1678 713	995 838
Column   C	719 898 99 917 245 4317 600	1678 713	995 838
10.5   Pricing   Text	99 917 245 4317 600		
10.5   Pricing   Text	245 4317 600	402 5940	
60   Prickle   Not   Not   Prickle   Not	600 385		180
March   Marc		380 268	362 245
March   Marc	1013	1593 27	605 171
March   Marc	32 355	83 452	105 133
255   PRIOR   OFFN   THE	146 227	224 203	99 147
645   PRINET   65 HBST   5343   Symptom Exempton yearner	699 35	13 50	114 39
NEW   PRISE	1085 474	1020 642	593 361
175   1763   1764   1765   1	116 1291	432 1259 475 1568	134 1153
175   1763   1764   1765   1	1239		884
175   1761-17	387 456 288		414 310 45
185	280 1133		420 565
185	376 254	430 1103	250 196
201   Notice   Product	5760 262		3594 196
272   Wints   19-No.   Professional Confessional Confes	505 2280 412	250 3093 640	231 1403
201   Notice   Product	38	60	86 134
788	16 881	19	79
244         PROD-1         all F4E         \$509         Education in Ministration for Month on Early of PMN cop banding proteins         0.0	34 452	51 456	132
100   PR007.1   CRXV12   Y15   Cylin-dependent protess-rate lesses 10   0.0   0.0   0.0   0.0   0.0   0.0   0.5   284   148   149	765 632		640 554
837 NN110 TRACO Pan-specific Tumor necrois factor neceptor type 1 associated DEATH domain protein 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 1163 1159 733 PR098 Ruf1 S259 Ruf1 prote-oncogene-encoded protein-serine infrasea 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 35 36 36 365 NN159	438 1260 1133	450 973	260 809
	1133 42 2747	1593 60 1604	90 2542
861 PNS44 VIM Y117 Wmmfn 0,0 0,0 0,0 0,0 0,0 2814 1788 1788 1778 1789 1797 1798 1798 1798	2747 2482 7305	2412	2542 2062 8948
MEAN	872 183	8174 813 393	595 245
264   PRISC2   GER	167 738	192	169
61 NK25/-1 BICKU (BLXXIII) Philipspecine (3-metryly-zoxoduzanoare enrylarogenase (pozamete) Naziae, miocronional (), 0 (	4725 1309	6119 A	4677 912
525 NK105-5 MKKG Pan-specific MAPKERK protein-selme kinase 6 (MKK6) 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 6443 9330 722 P5001 PYK pty Generic psophotynosine 0, 0, 0, 0, 0, 0, 0, 0, 5371 8108	5452 5049		5197 3727
543   NK16-3   ImTOR   Pan-appoilte   Mammalian tataget of rapamycin (FRAP)   0,0   0,0   0,0   0,0   0,0   0,0   3438   5028   13   14   15   15   15   15   15   15   15	4958 5384		3742 4444
107   NK048-7   PRKDC (DNAPK)   Pan-specific   DNA-activated protein-serine kinase   0,0 0,0 0,0 0,0 0,0 10035   17886   1788	579 8385 114		105 16506 568
17	114 15596 5740	15235 1 6708	16172 3816
	241		53 2921
Total   Mid-Sci   Med   Pass position   Pass	3495 3272 2987 894	3496	2921 2859 3161
40         N000-5-0         NATIA         Prospectific         Account monochamber generation frames up not you find the property of the property o	774	915	745 570
3   PR14   6-6PT   F46   Chargette Institute   F46   Cha	428 2988	536 1810	444 2180
1	2988	1088	291 936
	2988 727 1077	738 1099	790
199   PK119   2K2   TB   Oxigory priors-earn's losses 2   0,0 0,0 0,0 0,0 0,0 0,0 0,0	727 1077 648 839		531 9620 4265
	727 1077 648 839 587	7674	5618
220 NOVA-1-3 DUSPO Parisapecine Duars specinically protein prospinistation 9 0,0 0,0 0,0 0,0 0,0 0,0 4479 5550 447 NKRS-4 HKZ Pansapecific large protein-prospinistation (2008) 10212	727 1077 648 839 587 11049 7199 6129		5044 6422 5947
28   MXX-0-2 MX2   Priling   Pensyapolin   Pen	727 1077 648 839 587 11049 7199 6129 5627 6507		1465 3121 1855
	727 1077 648 839 587 11049 7199 6129	1841	3121
180         PN110         Crystalin aB         S45         Crystalin alpha B (heat-shock 20 kDa like-protein)         0, 0	727 1077 648 839 587 11049 7199 6129 5627 6507 7343 1711	1841 6125 2687 466	3121 1855 301

Average - Smaller	S. Dev Smaller	%S.Dev. Smaller
7631 7733	1854 1242	24 16
5841 5319	1351 1546	24 29
2590 2260	742 521	29 23 21
1292 1219 792	209 277 239	23 30
674 816	225 312	33 38
902 775	157 293	17 38
445 629	293 91 215	38 20 34 35
445	212	48
423 428	136 87 105	25 20 24
473 364	155 120	24 33 33
386 285	152 94	33 39 33
277 289	85 32 67 73	31 11 33
247 223	73 69	30 31
126 134	29 25	23 19
193 167	105 78 77	54 47 36
215 170	77 63 150	36 37 47
315 357 811	68	19
641 201	223	62 35 57
359	425 126	115 35
5805 519	1384 123	24 24
284 946 56	356 59	19 38 106
58 297	30 136	53 46
147 230	53 53	36 23
186 39	259 6	139 16
815 475	205 128 279	25 27 66
1143	218	19
1027 461	330 206 251	28 32 45 41
617 332	219	41 66
322 842 261	69 480	21 57
395 5249	128 355 1213	49 90 23
482 241	259 146	54 61
2085 426	669 147 21	32 34 42
78 20	21 29 25	38
651	372	67
380 871 667	75 187	68 20 21
310	315 116	
871 1170	236 252	37 27 22 39
1935 2311	634 355	39 33 15
7227 778 207	1244 99	17
	107 37	52 25
687 4970 1219	127 793 315	18 16 26
6984 5930	1651 1602	24 27
4604 7101	891 3155	19 44
307 13333 332	181 3603 148	59 27 45
332 17994 5597	148 3270 1151	45 18 21
205	180	88 36
4310 3813 3000	1540 985 421 177	36 26 14 21
850 708	138	20
383 1877	127 669	33 36 39 32
757 933 538	292 295 154	39 32 29
742 581 10913	243 152	33 26
10913 7062	2129 1689	20
5443	844 677	12 12
9486 9647 1588	4899 3562 159	52 37 10
5924 2011	1745 378	29

					Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
					1597	1688	1703	1745	1040
Flag- Patient 1- Bigger	Flag- Patient 2- Bigger	Flag- Patient 3- Bigger	Flag- Patient 4- Bigger	Flag- Patient 5- Bigger	Globally Normalized - Patient 1- Bigger	Globally Normalized - Patient 2- Bigger	Globally Normalized - Patient 3- Bigger	Globally Normalized - Patient 4- Bigger	Globally Normalized Patient 5- Bigger
0, 0	0, 0	0, 0	0, 0	0, 0	10693 10281	9884 13001	11201 12514	20139 10086	9705 11812
0, 0	0, 0	0, 0	0, 0	0,0	11708 6257	9182 8650	7054 10248	10901 7436	7056 9055
0, 0	0, 0	0, 0	0, 0	0,0	4259 2021	3548 3729	3183 4131	4993 5196	5337 3241
0, 0	0, 0	0, 0	0, 0	0, 0	2490 1278	2918 1828 857	2109 2419	2523 2367	1397 1539
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	994 1109	857 1385	1194 1803 1597	2442 1642 1603	2043 1580 2028
0, 0	0, 0	0, 0	0, 0	0,0	1109 1175 1028	1385 1027 1269	1546	1524	1541
0, 0	0, 0	0, 0	0, 0	0, 0	930 1203	899 944	1510 1340	1614 1239	1322 1165 715
0, 0	0, 0	0, 0	0, 0	0,0	808 702	1333 1192	1116 964	834 671 744	625 742
0, 0	0,0	0, 0	0, 0	0,0	490 846	647 1003	835 737	1003	1106
0, 0	0, 0	0, 0	0, 0	0,0	686 371	1076 578	950 798	589 934	420 941
0, 0	0, 0	0,0	0, 0	0,0	674	634	726	626	589
0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	294 454 513	466 578 656	758 817 826	809 440 562	834 722 259
1, 1 0, 0	0, 0	0, 0	0, 0	0, 0	308 416	420 593	501 620	540 416	644 342
0, 0	0, 0	0, 0	0, 0	0, 0	419 463	573 401	575 511	423 303	341 576
0, 0	0, 0	0, 0	0, 0	0,0	369 496	620 567	299 400	339 102	359 409
0, 0	0,0	0, 0 0, 0 0, 0	0, 0	0,0	164 369 225	669 555 417	548 376 354	298 300 339	247 326 386
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0,0	225 239	417 272	354 379	339 340	366 307
0, 0	0,0	0,0	0, 0	0,0	328 441	310 1013	814 614	970 534	1020
0, 0	0,0	0, 0	0, 0	0,0	522 528	813 548	1610 1187	1730 1061 93	2156 1778
0, 0	0, 0	0, 0	0, 0	0, 0	462 1545 425	8 627	536 1011 993	1650 802	345 2032 818
0, 0	0,0	0, 0	0, 0	0.0	12686 499	9262 830	6662 1277	10574 721	4451 967
0, 0	0,0	0, 0	0, 0	0, 0	257 914	330 829	519 2406	417 2031	604 1441
1, 1 0, 0 0. 0	0,0	0, 0	1, 1 0, 0 0. 0	0,0	472 53	596 64	11 110	366 94	208 110
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0	53 678 258	64 636 557 375	110 554 536 492	94 335 228 327	110 428 178
0, 0	1, 1	1, 1	1, 1	0, 1	220 577	26	675	327 327	445 717
0, 0	0, 0	0, 0	0, 0	0, 0	30 879	35 2075	123 1389	98 967	91 1061
0, 0	0, 0	0, 0	0, 0	0,0	457 553	478 1022	1113 893	813 555	922 428
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	1063 198 1410	2157 463 1121	1604 1084 1363	1538 968 1639	2222 605 2896
0, 0	0, 0	0, 0	0, 0	0, 0	1410 294 606	1121 629	1363 1135	1639 771	2896 1009 1194
1, 1	1, 1	1,1	0, 0	0,0	720	471	836	192	419
0, 0	0, 0 0, 0 0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	266 829	937 89	861 515	343 1669 477	511 2360 901
0, 0	0,0	0, 0	0, 0	0,0	157 327 17129	469 5375	2138 8744	484 4643	1601 5404
1, 1	0,0	0, 0	0, 0	0,0	33 110	1217 182	1116 518	605 828	795 233
0, 0	0, 0	0, 0	0, 0	0, 0	1205 216	1801 310	3817 717	3187 618	8431 2997
0, 0	0,0	1, 1 0, 0 0. 0	1, 1	0,0	21 35	29 57	48 70	1359 1089	48 89
0, 0	0, 0	0, 0	1, 1	0,0	9 1106	10 2412	70 11 970	949	28 159
0, 0	0, 0	0, 0	0, 0	0,0	18 370	465 641	27 705	36 291	76 820
1, 1	0,0	0, 0	0, 0	0, 0 1,1	1820 583	1735 518	1330 942	835 1416	755 1491
0, 0	0, 0	0, 0	0, 0	0,0	254 498 1190	371 509 1410	497 1571 2181	492 1647 1470	681 2192 2347
0, 0	0,0	0, 0	0, 0	0,0	1190 60 1904	75 1447	94 1754	1470 82 3868	76 5198
0, 0	0, 0	0, 0	0, 0	0, 0	2653 5274	3007 7275	3051 11125	5463 10725	2691 18261
0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0. 0	0, 0 0, 0 0. 0	0,0	956 140	1139 386 158	917 371	1197 330	1435 269 299
0, 0 0, 0 0, 0	110 509 5793	158 570 6113	244 1224	256 1144 10405	299 1520 6913				
0, 0	0,0	0, 0	0, 0	0,0	5793 1228	1771	2357	10405 1926	1479
0, 0	0, 0	0, 0	0, 0	0,0	7165 6890	9480 8170	8399 8353	9657 10540	15340 8467
0, 0	0,0	0, 0	0, 0	0,0	4708 14631	5586 12466 1202	7594 6952	9795 10390 441	8467 5229 6087 511
0, 0	0,0	0,0	0, 0	0,0	19053	16167	14446 520	18169	26792
0, 0	0,0	0, 0	0, 0	0,0	27816 7558	25430 7103	24468 8443	20771 9843	28915 6560
0, 0			0, 0		289	680 6188	291 4980	14 7667	168 4507
0, 0	0, 0	0, 0	0, 0	0, 0	7312 3181	5164 3630	4252 4556	6318 5750	3696 3870
0, 0	0, 0	0, 0	0, 0	0,0	828	1115 1308	1439 1313	1152 569	1403 676
0, 0	0, 0	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	1078 320 1629	1308 383 1550	848 2791	568 3268	558 3859
0, 0	0, 0	0, 0	0, 0	0, 0	809 806	845 824	1261 1817	1272 1346	1085 1702
0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	439 575	539 637 643	993 768	865 1227 784	906 1955 1070
0, 0	0,0	0,0	0,0	0,0	592 11044	12678	948 16010	13874	22168
0, 0	0, 0	0, 0	0, 0	0,0	10642 9985 4674 15015	10061 7250	9668 8567	10719	7723 8056
0, 0	0,0	0, 0	0, 0	0,0		5900 15672	7535 10065	7461 15385	11947 9069
0, 0	0,0	0,0	0, 0	0,0	16110 1719	17082 2069 8312	11372 2254 7224	12964 2397 9323	8763 2452 6070
0, 0	0, 0	0, 0	0, 0	0,0	9592 1818 616	2105 467	7224 3105 958	9323 3363 1107	3360
0, 0	0,0	0, 0	0, 0	0,0	2739 8790	2916 7967	2510 9629	1671 9027	1709 5148
υ, υ	Š	5, 5	5,5	Š	3	1.000	FV4.F	SVA.	3170

verage - Larger	S. Dev Larger	%S.Dev Larger	%CFC - Average Larger from Average Smaller	Student 1 test p value
12324 11539	3945 1171	32 10	61 49	.048
9180 8329	1918 1371	21	63 57	.010
4264 3663	820 1044	19	65 62	.045
2287		28 22	62 77	.010
2287 1886 1506	514 449 624	24 41	77 55 90	.019
1504	239	16	123	.001
1381	205	15	53	.016
1255 1178	294 131	23 11	62 165	.038
961 831	229 216	24 26	53 93	.023
827 816	174 226 134	21	86 52	.044
789		28 17	86	.022
744 724 650 632 602	239 220 47	32 30 7	74 53	.034
650 632	47 215		78 64	.012
602	215 148	34 25	64 111	.006
563 483	186 113	33 24	103 67	.035
477 466	109 93	23 20 21	135 89	.007
451 397	93 93 114 159		89 102 216 194	.046
395 385	159 191	29 40 50		.019
385 340	89 63	23	99 131 58	.006
340 307 610	63 50 261	19	58 81 93	.046
610 724		34	93 103	.055
1366 1020	606 463	44 45	68	.058
421	194 701	46 56	110	
1249 733	193	56 26	239 104	.063 .065
8727 859	2895 259	33 30	50 65	.074
425 1524	125 616	29 40	50 61	.076
331	204	62	494	.084
86 526	24 128	27 24	50 77	.091
351 372	161 95	24 46 26	138 62	.099
464 75	258	56	150	.109
75 1274	36 436	49 34	91 56	.113
757 690 1717	255 227	34 33	59 63	.114
1717	429 326 627	25 49 37	50 54 64	.127
1686	627 296	37 39	64 66	.139
1122	496 228	44	82 59	.169
480 1331	154 600	32 45	49 58	.195
1331 428	900 290 729	45 68 73	58 64 154	.248 .248 .252
1004 8259	729 4657	73 56	154 57	.252
753 374	422	56 71	56 56	.287 .296
3688	422 266 2549 1030	69	77 128	.323
301	529	176	501	.392
268 144	411 259	153 180	243 406	.413 .431
1119	727 172	65 138	72 107	.437
565	202	36	49	.142
1295 990	441 406	34 41	49 49	.085
459 1283 1719	142 672 457	31 52 27	48 47 47	.129
1719	457 11	27 14	47 47	.162
2834 3373 10532	1457 1057	51 31	46	.200
	4436 186	42 16	46 46 45	.121
299		30	45	.226
299 213 993 7143	89 69 391 1674	39	45 45 44	.026
	1674 386	23	44	.022
10008 8484 6582	2811 1173	28 14 29	43 43	.176
6582	1881	29	43	.029
436	3232 436	100	42	.661
18925 470	4246 121	22 26	42 42	.055
25480 7901	2845 1150	11 15	42 41	.017
7901 288	220	76	41	.035
6047 5346	1172 1326	19 25	40 40	.108
4197 1188	895 222	21 19	40 40	.020
989 535	313 184	32 34	40	.215
2619 1054	907 197 425	35	40 40 39	.105 .164 .092
1299	197 425	19 33	39	.164
748 1032	218 515	29 50	39 39	.034
1032 807	515 180 3862	50 22 25	39 39	.271 .101 .138
9763 9477	1091 2213	11 23	38 38	.010
7503	2213 2463 2862	23 33 22	38 38 37	.058 .174 .156
13041 13258 2178	3053	23	37 37 37	.156
2178 8104	265 1316 667	12 16	37 37	.007
2750 587	657 275	24	37 37 37	.076
2309 8110	521 1575	23	35 36	.085
0110	15/5	19	35	.073

Block	Row	Column	Refseq	Uniprot Link
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7	8	2	NP_006247 NP_003290	P14625
3	10	6	NP_004865 NP_002730	095429
6	7	11		P84243
6	8	9	NP_003521 NP_001385 NP_000312 NP_002818	Q13115 P06400
2	99	10 10	NP_002818	P18031
4	8	7	NP_002219 NP_000199	P05412 P06213
5	10	11	NP_000199 NP_003168 NP_002722	P43403
2	8	11	NP_000242	P43246
6	10	11	NP_005424	P07947
5	7	8	NP_002469.2 NP_001531	P04792
7	8 7	10	NP_000236.2 NP_002006.2	P08581 Q12778
10	10	5	NP_006810	P31948
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10	7	3 8	NP_001959 NP_063937	P06730
6	8	2	NP_003521	P84243
7 9	9	11	NP_006238 NP_003812	P53041 O43353
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2	8	6		P10721
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7	10 6			P12931
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6	10	1	NP_001782	P63000
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14	10	7	NP_005901 NP_004746	P10636
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7 10	7	5 7	NP_005219 NP_005901	P00533
15	8	3	NP_005535	P35568
9	6 7	8		O15075 P23528
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4	10	9		P08962
10	10	8	NP_005901	P10636
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9 11 7	10 7	2	NP_003371.2 NP_004410.3 NP_005219	Q16690
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7	8 6	1	NP_004963 NP_001617	P31751
/				
6	7	11	NP 065681	P07949
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6	7 9 8 10	1 11 1 2	NP_001887 NP_065681 NP_002147 NP_002438 NP_001876	P07949 P10809 Q04912 P02511

										Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
					Flags	Flags	Flan	Flan	Flags	1545 Globally	1490 Globally	1864 Globally	1726 Globally	2278 Globally
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag- Patient 1- Smaller	Flag- Patient 2- Smaller	Flag- Patient 3- Smaller	Flag- Patient 4- Smaller	Flag- Patient 5- Smaller	Globally Normalized - Patient 1- Smaller	Globally Normalized - Patient 2- Smaller	Globally Normalized - Patient 3- Smaller	Globally Normalized - Patient 4- Smaller	Globally Normalized - Patient 5- Smaller
409	PN118	IRS1	5639	Insulin receptor substrate 1	0, 0	0, 0	0,0	0, 0	0,0	161	182	Smaller 412	440	Smaller 464
521 340 716	NK103-5 k179-PN180-PN1 PP006	MKK4 HDAC4/5/9 PTEN	Pan-specific S246/259/220 S380/T382/T383	MAPK/ERK protein-serine kinase 4 (MKK4) Histone deacetylase 4	0, 0 0, 0 0, 0	0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	12743 1050 548	12674 771 298	9961 1604 596	14123 1360 633	9046 1348 557
248 120	NN168 NP003-2	Elk1 Cdc25C	Pan-specific Pan-specific	rinospinausym osinosay, 3-dispinospinaus 3-pinospinause ama proxem priospinause ETS domain-containing protein Els-1 Cell division cycle 25C phosphatase	0, 0	0,0	0,0	0,0	0,0	384 10026 1774	167 13950	295 12000	205 13194	186 11781
743 606 796	PN071 PK061 PN077	Rb PAK1/2/3 SOX9	T826 S144/S141/S154 S181	Retinoblastoma-associated protein 1 p21-activated kinase 1 (alpha) (scrine/threonine-protein kinase PAK 1)	0, 0 0, 0 0, 0	0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	1774 628 1463	2133 416	2288 513 1256	2187 772 1408	1863 409 1314
316 634	PK641 NN178-2 NN008	FRK PDK4	Y387 Pan-specific	SHY (sex determining region 17)-box 9 (campomeric dysplasia, autosomal sex-rev Tyrosine-protein kinase FRK [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial	0, 0	0,0	0, 0 0, 0 0, 0	0,0	0,0	8710 7710	2111 7737 12477	1256 8457 8140	8076 8680	1314 5585 7761
65 175 804	NN008 PN024 NN102-NN124	Bcl-xS/L CREB1 STAT1	Dan conside	BcI2-like protein 1 CAMP response element binding protein 1	0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0,0	935 3145 1469	1537 3351 2943	1075 3470 718	1414 4023 1166	930 3090 1252
830 20 632	PN090 PK072-3 NN181-1	Tau AM1 (PKBa) PDK3	S133 Pan-specific S713 S473	Suz-see protein 1  Signal transducer and activator of transcription 1 alpha  Microtucke-associated protein tau  RAC-abha serimethreorine acceler insee	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	1080 465	703 291	718 1300 502	1166 1221 285	1252 1131 318
632 326 224	NN181-1 NK067	PDK3 GRK2 DUSP8	Pan-specific Pan-specific Pan-specific	Pyruvate dehydrogenase kinase isoform 3 G protein-coupled receptor-serine kinase 2 Dual specificity protein phosphatase 8	0, 0 0, 0 0, 0	0, 0	0,0			56 1008 4706	140 2277 6382	81 920 4495	58 1106 8353	123 1826 3708
501 429	NK067 NP042-3 NK105-1 NK217-2 PN053-1	MEK6 INK1	Pan-specific Pan-specific Pan-specific	Dual specificity protein phosphatase 8 MAPK/ERK protein-serine kinase 6 (MKK6) Lun Marminus mntein-serine kinase (stress-activated notein kinase (SAPKI) 1	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	4706 300 7870 4909	6382 177 23302	547 5501	8353 467 5239 7508	325 4687			
559 166		NFKB p65 (Rel A) Cofilin 1	S276 S3	NF-kappa-B p65 nuclear transcription factor Cofilin 1		0, 0	0,0			313	4948 58	7683 64	43	6095 82
793 719 121	NN097 NP025 NP003-3	SOCS4 PTP1C Cdc25C	Pan-specific Pan-specific Pan-specific	Cotin 1 Suppressor of cytokine signalling 4 (SOCS7) Protein-tyrozine phosphatase 1C (SHP1, SHPTP1) Cell division cycle 25C phosphatase	0, 0 0, 0 0, 0	1, 1 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	1737 2537 6647	2279 927 10696	1908 3254 5595	2787 2677 8775	2323 2182 4820
635	NN178-3	PDK4	Pan-specific Pan-specific		0, 0	0,0	0,0	0,0	0,0	10527	11035	10756	10728	7256
56 631 726 833	NK009-2 NN180-2 PG005	AurKC PDK2 PYKSD8 Tau	Pan-specific pTyr T231	Aurora Kinase C (serineithreonine-protein kinase 13) Pyruvate dehydrogenase kinase isoform 2 Generic phosphotyrosine Microtubule-associated orotein tau	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0	5276 8872 11476	6298 8880 14672 386	5994 8440 21144 670	7888 9983 23770 1075	5568 6201 13058 364
710 157	PG005 PN122 PK786 PK579	Tau PRP4K Chk1	Y849	Microtubule-associated protein tau  Protein-serine kinase PRP4 homolog  Cherknoid motein-serine kinase 1	0, 0	0, 0 0, 1 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	338 2624 2430	386 2791 4889	5602	1075 5037 2215	364 3792 3796
665 52 746	PK579 PK084 NK193-2	PKCg AurKB	S345 T674 Pan-specific	Protein-serine kinase C garma Aurora Kinase B (serinerthreonine protein kinase 12)			0.0	0.0	0.0	2430 1687 2932 8455	2009 4626 9434	2797 2155 2598 11734	2095	2169 2649 8232
633	NK193-2 NK244-1 NN181-2	PDK3	Pan-specific Pan-specific Pan-specific	Aurora Kinase B (serinerthreonine protein kinase 12) Proto-oncogene tyrosine-protein kinase receptor Ret Pyruvate dehydrogenase kinase isoform 3	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0,0	0, 0	0, 0	22065	29874	18236	3523 13658 19717	16403
29 624 437	NK131-3 NK243-3 PN048-2	Akt3 (PKBg) PDGFRb Jun	Pan-specific Pan-specific S73	RAC-gamma serine/threonine-protein kinase Platelet-derived growth factor receptor kinase beta Jun proto-oncogene-encoded AP1 transcription factor	0, 0	0,0	0,0	0, 0	0, 0	7993 4595 1297	10160 5847 2309	7909 6726 1948	10417 6637 1591	8589 5557 1772
622	PK759 NN179-1	Jun PDGFRa PDK1	Y768 Pan-specific	Jun proto-oncogene-encoded AP1 transcription factor Platelet-derived growth factor receptor kinase alpha Pyruvate dehydrogenase kinase isoform 1	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	1297 1857 13314	2309 2397 13949	2418 13502	2789 16432	2789 10477
794 37 789	NN098 PN189 PN197	SOD (Cu/Zn) APP SNCA (a-Synuclein)	Pan-specific T743 S129	Superoxide dismutase 1 Amyloid beta A4 protein Alpha-synuclein	0, 0	0,0	0,0	0, 0		707 1072 158	492 819 125	389 1227 250	837 1620 268	886 1234 205
789 823 335	PN048-2 PK759 NN179-1 NN098 PN189 PN197 PN111 NK069-NK070-2	Synapsin 1 GSK3a/b	S603 Pan-specific T514	Alpha-synuciein Synapsin 1 isoform la Glycogen synthase-serine kinase 3 alpha/beta Protein-serine kinase C gamma A-Raif proto-oncogene serine/threorine-protein kinase	0, 0 0, 0 0, 0 0, 0 0, 0	1, 1 0, 0 1, 1 0, 0	1, 1 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	102 9528	60 10751 5664 2596	76 9864	208	171 7437
662 38 524 45	NK205-2	PKCg A-Raf MKK6	T514 Pan-specific Pan-specific	Protein-serine kinase C gamma A-Raf proto-oncogene serine/threonine-protein kinase MAPK/ERK protein-serine kinase 6 (MKK6)	0, 0	0,0	0,0	0, 0	0,0	2084 1149		3029 1503	3459 1929	2221 1809
45	NK105-4 NK007-2 NK205-4	ASK1 A-Raf		Apoptosis signal regulating rections serine kinase 1  A-Raf proto-oncogene serine/threonine-protein kinase  DnaJ homolog, subfamily B member 1	0, 0	0, 0	0,0 0,0 0,0 0,0 0,0	0, 0	0, 0	1362 1251 14430	3310 1534 14781	1728 1191 14119	2459 1914 18412	3046 1772 9761
39 363 221 741 653	NK205-4 NN057-2 NP041-1 PN065 PK079-1	Hsp40 DUSP7	Pan-specific Pan-specific Pan-specific Pan-specific	DnaJ homolog, subfamily B member 1 Dual specificity protein phosphatase 7	0, 0 0, 0 0, 0 0, 0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	14430 12986 6231	14781 6102 6413 2167	14119 17125 5961 1817	18412 14123 9281 1655 1318	9761 13836 7700
653 251	PK079-1 NN173	PKCd Epcam	S645 Pan-specific	Hetinolastoma-associated procein 1 Protein-serine kinase C delta Epithelial cell adhesion molecule	0,0	0,0	0,0	0,0	0,0	1355 1086 437	615 332	1817 986 519	1318 621	1015 394
799 412	NK172-2 NK084-5	Src JAK1	Pan-specific Pan-specific	Src proto-oncogene-encoded protein-tyrosine kinase Janus protein-tyrosine kinase 1	0, 0	0, 0 0, 0 0, 0 0, 0	0,0	0, 0	0,0	25166 10845	35710 17966	23095 10764	23461 12473	20449 11098
714 704 519	NP023-5 NK048-4 PK714	PTEN PRKDC (DNAPK) MKK3	Pan-specific Pan-specific Y230	Phosphalidylinositol-3.4,5-trisphosphate 3-phosphatase and protein phosphatase DNA-activated protein-serine kinase MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta)	0, 0 0, 0 0, 0	0,0	0,0	0,0	0, 0	11643 11856 5205	13431 19887 5793	11379 9436 8151	16118 9754 5592	10288 9078 7525
50	NK008-4	AurKA DUSP4	Pan-specific Pan-specific	Aurora Kinase A (serine/threonine protein kinase 6) Dual specificity protein phosphatase 4	0, 0	0, 0	0,0	0, 0	0, 0 0, 0 0, 0 0, 0	23258 16738	32437 25953	16878 13175	17726 15461	8906 16887
476 102 809	PK046-2 PN167 NN104	MEK1 Cateriin b STAT3	S292 Y333 Pan-specific	MAPK/ERK protein-serine kinase 1 (MKK1) Caterin (cadherin-associated protein) beta 1 Signal transducer and activator of transcription 3	0, 0	0, 0	0,0	0, 0	0, 0 0, 0 0, 1	1718 1527 1628	1511 986 2014	1631 1351 487	1972 1134 481	1938 1096 1412
598	PK145	p70 S6K	T229 S347	signar nanscuter and activation of unanscription 3 Ribosomal protein 96 kinase beta-1 Cyclin-dependent protein-serine kinase 9 Cyclin-dependent protein-serine kinase 7	0,0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	0,0	808	704 2066	1015	1499	945
147 30 856	NK030-2 NK003	CDK7 ALK VGFR2	Pan-specific Pan-specific	Ariapiastic tymphoma kinase	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0,0 0,0 0,0 0,0 0,0	0, 0	0,0	2865 3175	1562 3969 3564	2322 3909 1946	3119 3527	3208 4226
621	PN146 PK758 PN199 PN078-PN135	FRS2 PDGFRa	Pan-specific Y349 Y762	Vascular endothelial growth factor receptor-tyrosine kinase 2 (Fik1) Fibroblast growth factor receptor substrate 2 Platelet-derived growth factor receptor kinase alpha	0, 0	0,0	0,0	0, 0	0, 0	3115 666 4684	675 5040	548 6104	574 6588	3125 348 4752
547 805	PN199 PN078-PN135	Myc STAT1	T58 S727	Myc proto-oncogene protein Signal transducer and activator of transcription 1 alpha	0, 0 1, 1 0, 0	0, 0 1, 1 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	1627 637	1269 665	2500 602	2786 720	2035 387
614 232 284	PN059 PK121 PK016-3	Paxilin 1 EGFR ERK5	Y31 T693 T218+Y220	Pacifilin 1  Epidermal growth factor receptor-tyrosine kinase  Eytraneli far remulated nortein-sedine kinase 5 (Rin MAP kinase 1 (RMK1))	0, 0			1,1		23 613 998	14 394 495	973 1154	801 1158 1228	377 759 793
284 736 552	PK016-3 PN066 NK117-5	Rb Nek2	T218+Y220 S612 Pan-specific	Extracellular regulated protein-serine kinase 5 (Big MAP kinase 1 (BMK1)) Retinoblastoma-associated protein 1 NIMA (never-in-mitosis)-related protein-serine kinase 2	0, 0 0, 0 0, 0 0, 0	0,0	0,0	0, 0	0, 0	998 1434 1332	2759 1523	1521 1666	1621 1847	1383 1776
520 239 768	NK103-4 NN038-1 PK147	MKK4 eIF2a sav	Pan-specific Pan-specific T412	MAPK/ERK protein-serine kinase 4 (MKK4) Eukaryotic translation initiation factor 2 alpha Eliboromy protein SR (kinase bets 1	0, 0	0, 0	0,0 1,1 0,0	0, 0	0, 0	6512 194 75	10475 61 41	8223 232	8570 706 52	7665 411 118
202 744	NP006 NN170 NN017-2	DUSP1 (MKP1) RelB	Pan-specific Pan-specific	Eukaryotic translation initiation factor 2 alpha Ribosomal protein 56 kinase beta-1 MAP kinase phosphatase 1 (CL100, VH1) Transcription factor ReiB	0, 0	0,0	0,0	0, 0	0,0	1351 690	1836 296	1065 921	1396 1688	1248 859
98 514 414	NN017-2 NK101-4 NK085	Caspase 7 MKK3 JAK2	Pan-specific Pan-specific Pan-specific	Caspase 7 (ICE-like apoptotic protease 3 (ICE-LAP3), Mch3) MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta) Janus protein-tyrosine kinase 2	0, 0 0, 0 0, 0	0, 0	0,0	0, 0		1313 6181 929	803 7327 594	1695 7069 1075	1442 8938 1431	1330 5746 1030
4	CN005 NK104-3 PK007-3	4G10 MEK5	pTyr Pan-specific	Jamus protein-grossine (Clone 4610) MAPK/ERK protein-serine kinase 5 (MKK5) Cyclin-dependent protein-serine kinase 1/2	1, 1 0, 0 0, 0	1, 1	1, 1 0, 0 0, 0	0, 0	0, 0 1,1 0, 0 0, 0	2683 4053	1845 4433	26 3822	6034 2717	118 2687
131 249 843	PK007-3 PN149 CN002	CDK1/2 Elk1 Tubulin	Y15 S383	ETS domain-containing protein Elk-1	0, 0 0, 0 0, 0	1, 1 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	350 425 1115	176 401 1087	551 482 1226	542 528 1251	252 350 1088
468 819	NN067 NK174	Md1	Pan-specific Pan-specific Pan-specific	Tubulin Myeloid cell leukemia differentiation protein 1 Spleen protein-tyrosine kinase	0, 0	0,0	0,0	0, 0	0,0	2891 8414	3919 7058	2074 7810	1477 8894	4290 5043
855 291 506	NND67 NK174 NK226-2 PK020 NK229-2	Syk VGFR1 FAK MELK	Pan-specific 8722	Vascular endothelial growth factor receptor 1 Focal adhesion protein-tyrosine kinase	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	9841 330 5136	10528 1008 7350	10982 957	11573 909 4876	9323 482 3724
506 605 731	PK130 NK155-5	MELK PAK1 Raf1	Pan-specific T212 Pan-specific	Maternal embryonic leucine zipper kinase p21-activated kinase 1 (alpha) (serine/threonine-protein kinase PAK 1) Raf1 proto-processe-encoded protein-serine kinase	0, 0 0, 0 0, n	0, 0	0,0 0,0 0,n	0, 0 0, 0		4547	1256	4415 1862 7302	4876 2363 7898 3280	3724 1258 5438
	PK065 PK063 NK205-5	PDGFRb PDGFRa A-Raf	T212 Pan-specific Y716 Y754 Pan-specific	Raff proto-oncogene-encoded protein-serine kinase Platelet-derived growth factor receptor kinase beta Platelet-derived growth factor receptor kinase beta Platelet-derived growth factor receptor kinase alpha ARaf proto-oncogene serine/threorine-protein kinase	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	2516 4348 4830	2124 2986 6504	3114 3207 5199	3280 2938 8405	1908 1855 4934
625 620 40 149 153	NKU32 NKO24 2	A-Raf CDK9 Chk1	Pan-specific Pan-specific Pan-specific	A-Raf proto-oncogene serine/threonine-protein kinase Cyclin-dependent protein-serine kinase 9 Checkpoint protein-serine kinase 1	0,0	0,0	0,0	0,0	0.0	4830 1680 1362	6504 2389 1179	5199 1363 1396	8405 1623 1740	1419
424 33 532	PK669 PK523	JAK3 ANKRD3 mMOB1	Y980+Y981 S438 Pan-specific	Checkpornt protein-senne kinase 1 Janus protein-tyrosine kinase 3 Ankyrin repeat domain protein-senne kinase 3 (RIPK4, DIK)	0, 0	0,0	0,0	0,0	0,0	1362 2754 1636 3372	3460 1620 5026	3055 2832 4264	3219 2229 4556	3344 3389
532 526 347	PK669 PK523 NN132 NK106-4 PN039	MKK7	Pan-specific Pan-specific S28	MAPK/ERK protein-serine kinase 7 (MKK7)	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	3823	5269	4264 3335 5503	4556 4892 5337	3344 3389 3490 4014
349		Histone H3 Histone H3	T3	Historia H2 2			0,0	0,0	0,0	4389 3327	4610 4237 8748	4795	4924	4354
515 640 453 223	NK101-5 NK127-1 PK040 NP041-3	MKK3 PKA Lok DUSP7	Pan-specific Pan-specific Y192	MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta) cAMP-dependent protein kinase catalytic suburit alpha Lymphocyte-specific protein-tyrosine kinase	0, 0	0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 1,1 0, 0 0, 0	9209 600 2324 9472	8748 509 2302	9210 446 2301 8482	9280 726 1941 9629	9886 272 1370 7084
859	MYDGA 2	VGFR3	Pan-specific Pan-specific	Dual specificity protein phosphatase 7 Vascular endothelial growth factor receptor-protein-tyrosine kinase 3 (VEGFR3)	0, 0	0,0	0,0	0.0	0.0	13901	2302 11410 15274	14527	16166	12304
345 219 309 816	PN037 NP040-2 PK637 NN107 PN194	Histone H2B DUSP6 FGFR3 STAT6	S14 Pan-specific Y647+Y648	Histone H2B Dual specificity protein phosphatase 6 Fibroblast growth factor receptor 3	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0	0,0	3371 873 7637 1132	5694 1868 11307	4828 1065 10310	5179 1570 9997	4719 2578 8649
311	NN107 PN194	FKHR	Pan-specific S256	Signal transducer and activator of transcription 6	0, 0	0, 0	0,0	0,0	0,0	506	1354 254	803 1019	948 1398	1039 564
473 230 416	NK099-7 NK052-5 NK085-3 NK054-5	MEK1 EGFR JAK2	Pan-specific Pan-specific Pan-specific	MAPPACERK proches or  MAPPACERK procheseline kinase 1 (MKK1)  Epidermal growth factor receptor-tyrosine kinase  Januar protein-tyrosine kinase 2  ErbB2 (Neu) receptor-tyrosine kinase	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0,0	14435 13172 14273	22326 21789 22151	10817 16067 10313	13190 23324 8807 5127	10848 17059 14820
256	NK054-5	JAK2 ErbB2	Pan-specific Pan-specific	ErbB2 (Neu) receptor-tyrosine kinase	0, 0	0,0	0,0	0,0	0,0	14273 3997	22151 4501	10313 4089	5127	4048

Average - Smaller	S. Dev Smaller	%S.Dev. Smaller
332 11709	132 1896	40
1226	288 118	23 22
247 12190	81	33
12190 2049	1341 197 138	11
548 1510	138	25 20
7713	1114 1795 251	14
8953 1178	1/95 251	20 21 10 50
3416 1510	333 757	10 50
1087 372	206 92	19 25
92	34	38 37 30
5529	532 1659	30
9320	7075	76
6229 112	1196 101	19 90 17
2207	101 365 775	
2315 7307 10060	775 2154 1412	33 29
6205 8475	912 1247	14 15
16824	1247 4782	15 28
567 3969	281 1186	50 30
3225 2023	993 177	31 9
2023 3266 10303	177 755 2086	9 23 20
21259	4689	22
9014	1070 780	12
1784 2450	340 342	19
13535	342 1896	14
662 1194	193 261	29 22
1194 201 123	261 54 57	27 46
9614	1173	12
3291 1797	1291 482 745 282	39 27 31 18
2381 1532	745 282	31 18
14301	2749	19
12834 7117 1712	1236	28 17
1004	2/2	16 23
460 25576 12629	101 5287	22
12629 12572	5287 2739	21 22 16
12002	2040 4059 1163	34
19841	7787	18 39
1754	4363 177	10
1219 1205	177 194 619 275 247	16 51 28 9
994	275 247	28
2615 3761	610 369	23 10
3761 2946 582	369 537	10
562 5434	118 770	21
2043	554 114	27
350	303	19 86
779 934	267 265	34 28
1744 1629	514 184	29 11
8289	1297 223 28	16
321 67	223	69 42
1379 891	255 454	51
1317 7052	291 1104	22 16
7052 1012 2141 3542	1104 269 2106	16 27
2141 3542	269 2196 713	103 20
374 437	151 62	40
1153		6
2930 7444	1065 1349	36 18
10449 737	799 277	8 38
5100 1634 6285	1223 426 1214	38 24 26 19
6285 2588	1214 536	19
3067 5974	794 1355	26 23
5974 1695 1572	1355 367 356	23 22 23
1572 3166	356 246	23 8
2341	689	29 15
4142 4266 5179	710	17
5179 4328	608 563	12 13
9266 511	363 152	4
2048	368	18
9216	1424	15
14434	1307	
14434 4758 1591	773 607	16 38
4758 1591 9580	773 607 1291	16 38 13
14434 4758 1591 9580 1055 748	773 607 1291 185 408	16 38 13 18 55
4758 1591 9580	773 607 1291 185	16 38 13 18 55 30 21

					Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
Slage	Elan	Elan	Elan	Elan.	1597 Globally	1688 Globally	1753	1745	1646 Globally
Flag- Patient 1- Bigger	Flag- Patient 2- Bigger 0, 0	Flag- Patient 3- Bigger 0, 0	Flag- Patient 4- Bigger	Flag- Patient 5- Bigger	Globally Normalized - Patient 1- Bigger	Globally Normalized - Patient 2- Bigger	Globally Normalized - Patient 3- Bigger	Globally Normalized - Patient 4- Bigger	Normalized - Patient 5- Bigger
0, 0	0, 0	0, 0	0, 0	0,0	11642 913	15118	15705 1311	16554 1876	19546
0, 0	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0,0	913 378 167	1039 552 189	706 436	616 289	3091 1275 575
0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0, 0		15984	14082 3258	20900	14843
0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	2940 493 1505	3120 537 2604	3258 888 2214	2386 719 1771	1916 994 1857
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	8470 14756 1351	9923 11120	10643 9822	14284 13645 1753	7469 9563 1072
0, 0	0,0	0, 0	0, 0	0,0	1351 3958	1727 3815 2770	1842 4798 1105	1753 5067	1072 4801
0.0	0,0	0, 0	0.0	0,0	3866 1181 347	2770 1428 648	1105 1731 571	1285 1335	883 1456 302
0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0,0	128	126	23	570 216	107
0, 0	0,0	0, 0	0, 0	0,0	1599 4416 358	2082 6750	1949 8450 697	1234 10184 427	2463 6321 559
0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	356 20272 7888	331 14096 7272	697 10836 9626	7875 7458	559 7684 8339
0, 0	1.1	0, 0	0, 0	0, 0	325	230	24	34	112 3077
0, 0	0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	1817 1929 7553	2554 2862 9180	3561 1926 10086	3308 3539 14709	4725 5732
0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	15086 6872 12890	11997 7061 11494	11708 7780 10471	14574 11212 10637	11700 6998 8975
0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	12890 18807 454	11494 19755	10471 25807 877	10637 22228 887	8975 21459 933
0, 0	0, 1	0, 0	0, 0	0,0	3227	19755 479 5059	7259	6125	3621
0, 0	0, 0	0, 0	0, 0	0.0	5282 2853	3581 3087	3441 3022 3675	4935 1887	3296 2027
0, 0	0,0	0, 0 0, 0 0, 0	0, 0	0, 0	4318 12792	3972 12140	14194	5372 13118	3426 12929 22346
0, 0	0,0	0,0	0, 0	0,0	31523 11118 5799	31669 13060 6978	22813 13443 7584	25504 10858 10455	22346 8257 6059
0, 0	0,0	0, 0	0, 0	0,0	2301 2165	2598 2276	7584 2505 2876	2283 5352	1508 2668
0, 0	0, 0	0, 0	0, 0	0,0	18255	15634 777	15552	18662	16519 1029
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	470 1003 164	777 1321 195	906 1563 250	955 1950 287	1029 1626 353
0, 0	1, 1			0,0	164 139 11154	51	250 302 13205	287 151 12989	353 120 9455
0, 0	0, 0 1, 1 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	11154 3797 2076	12844 4439 2905	13205 4886 2198	12989 4261 2025	9455 3026 1897
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	1898 1268	3638 2705	4043 2127	3159 2034	1967 1323
0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	13314 12251 5317	17494 9725 7183	18818 17606 10173	18462 21829	20152 17614 9082
0, 0	0, 0	0, 0	0, 0	0,0	2250	7183 2770	10173 2340	21829 12024 1663	1498
0, 0	0, 0	0, 0	0, 0	0,0	590 461	938 615	2383 701	1290 567	966 485
0, 0	0, 0	0, 0	0, 0	0, 0	35416 15181	35211 19144	23730 15200	30424 14155	31897 13471 10035
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	11786 18633 5754	14466 14709 7206	14677 13636 10594	19198 13208 8979	16635 13058 6830
0, 0	0.0	0.0	0, 0	0.0	24355	23510 21447	19681 18375	22755	
0, 0 0, 0 0, 0 0, 0	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0	21649 2141 1061	23510 21447 2209 1325	2253 1716	18609 2113 1652	30483 27266 1951 1651
0, 0	0, 0	0, 0	0, 0	0, 1	2493 749	2765 1267 2858	547	774 1279 5333	732
0.0	0, 0	0, 0		0, 0 0, 0 0, 0	3330 2405 3560	2858 3291	1419 2964 3592	5333 2781 3927	1321 2653 3777 6543
0, 0	0,0	0, 0	0, 0	0, 1	4245	3291 4343 3383	3592 4420 2859	4466	2889
0, 0	0,0	0, 0	0, 0	0, 0	688 5598 1718	987 5986	866 8022	430 7437 2956	431 5783 3160
0, 0	0, 0	0, 0	0, 0	0,0	399	625	2558 1172	722	701
1, 1 0, 0 0. 0	0,0	0,0	1, 1 0, 0 0. 0	0,0	571 389 712	14 459 1338	14 1047 1453	15 983 970	1488 1788 1113
0, 0	0, 0	0, 0	0, 0	0,0	712 2104 1742	1338 2559 1865	1453 2266 1779	970 2029 2397	1113 1474 1956
0, 0	0,0	0,0	0, 0	0,0	7865 74	9655 164	11751	11601 563	8564 485
0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	79 1627	106 2060	76 1568	57 1361	79 1581
0, 0	0.0			0.0	511 909	636 1151	1195 1869	1391 2237	1561 1655
0, 0	0, 0	0, 0	0, 0	0,0	6068 615	7885 1006	8682 1098	10148 1372	1655 9098 1893
1, 1 0, 0	1, 1 0, 0 0, 0	1, 1 0, 0 0, 0	1, 1 0, 0 0, 0	1, 0 0, 0 0, 0	3829 5878	3626 4273	2720 5212	15 2933	2466 2629
0, 0	0,0	0, 0	0, 0	0,0	219 378	330 432 1936	678 551	511 499	472 721 719
0, 0	0,0	0, 0	0.0	0, 0	1659 3209	3863	1606 4148	3614	2399
0, 0	0, 0	0, 0	0, 0	0, 0	8529 12690	8003 11132	10155 12562	8076 12327	8993 12677
0, 0	0, 0	0, 0	0, 0	0, 0	652 6612	999 6643	1162 6523	812 5994	699 4120
0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	1028 5498 2169	1717 5723 2250	2569 7383 4274	1990 10185	2274 8029 2910
0, 0	0.0	0, 0	0, 0	0,0	2770 5643	5308 5515	4883 8154	3705 8482	1239 7071
0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0	2165 1847	2438 2005	2114 2112	1718 1584	1419 1593
0, 0	0, 0	0, 0	0, 0	0,0	2886 2468	3129 2900	4526 2767	4611 3524 5888	3219 1910
0, 0	0,0	0, 0 0, 0 0. 0	0, 0 0, 0 0. 0	0,0	4361 3704 5376	2900 4722 5260 5934	2767 4771 6131 6376	5888 4937 6144	4205 4609 5967
0, 0	0, 0	0, 0	0, 0	0, 0	5376 3908	5934 4167	6376 5599	6144 5342	5967 5882
0, 0	0, 0	0, 0	0, 0	0, 0	10026 514	11484 813	9692 481	10065 400	12041 728
0, 0	0, 0	0, 0	0, 0	0, 0	2871 9673	3117 12758	2582 10080	1824 11765	1357 8379
0, 0	0,0	0, 0	0, 0 0, 0 0. 0	0,0	18586 4978 1296	16329 4486 2635	15071 5232 1887	15278 6057 1761	17102 6379 1486
0, 0	0, 0	0, 0	0, 0	0, 0	1296 13911 2020	2635 12445 1327	1887 12321 611	1/61 8365	1488 7545
0, 0	0, 0	0.0	0.0	0.0	555	969	833	977 15300	928 14239
0, 0	0,0	0, 0	0, 0	0,0	17804 16729	17502 20384	16542 22418	15390 24834	14336 19649

		Globally Normalized Median	Median	Globally Normalized Median	Globally Normalized Median	Median											
Average - S. Dev %S.Dev. Patie	ig- Flag- Flag- Flag- ent Patient Patient Patient	1597 Flag- Globally	1688 Globally	1753 Globally	1745 Globally	1646 Globally			S Dev .	%S Dev .	%CFC - Average	Student T					
Smaller Smaller Smaller Bigg	ger Bigger Bigger Bigger	Flag- Patient Normalized 5- Bigger Bigger	- Globally - Normalized - Patient 2- Bigger	Globally Normalized - Patient 3- Bigger	Globally Normalized - Patient 4- Bigger	Globally Normalized - Patient 5- Bigger	Aver	ger	S. Dev Larger	%.S.Dev Larger	Average Larger from Average Smaller	test p value	Block	Rov	Colum	n Refseq	Uniprot Link
332 132 40 0,0 11709 1896 16 0,0 1226 288 23 0,0 526 118 22 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 205 0, 0 11642 0, 0 913 0, 0 378	354 15118 1039	671 15705 1311	465 16554 1876	538 19546	15 16 7	17 713 46	159 2543 795	36 16 48	35 34 34	.059 .110 .310 .303	11 7 6 11	9 7 10	3 2 9	NP_005535 NP_003001 NP_006028.2 NP_000305	P35568 P45985 2 P56524
247 81 33 0,0 247 81 1 33 0,0	0 0,0 0,0 0,0	0.0 167	552 189 15984	706 436 14082	616 289 20900	3091 1275 575 14843	7 3 16	31	154 2420	43 47 15	34 34 33	.303 .438	6	7	4 7	NP_001107595	P60484 i.1 P19419 P30307
2049 197 10 0,0 548 138 25 0,0 1510 209 20	0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0	0, 0 2940 0, 0 493	3120 537	2252	2386 719 1771	1916 994	7.	24 26	501 194 382	18 27	33 33	.042	2 11	10 9 10 7	4 6	NP_000312 NP_002567 NP_000337	P06400 Q13153
7713 1114 14 0,0 8953 1795 20 0,0 1178 251 21 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 8470 0, 0 14756 0, 0 1351	9923 11120 1727	3,596 888 2214 10643 9822 1842	14284 13645 1753	7469 9563 1072	10	158	2341 2075 292	23 18 19	32 32 31	.079 .124	7	7 9	9 7 5	NP_002022.1 NP_002603.1 NP_612815	P42685 Q16654
3416 333 10 0, 0 1510 757 50 0, 0	0 0,0 0,0 0,0 0 0,0 0,0 0,0	0, 0 3958 0, 0 3866	3815 2770	4798 1105	5067 1285	4801 883	44	88 82	503 1152	11 58	31 31	.007	5 11	6 6 10	9 8	NP_004370 NP_009330	P16220 P42224
1087 206 19 0, 0 372 92 25 0, 0 92 34 38 0, 0	0 0,0 0,0 0,0	0, 0 1181 0, 0 347 0, 0 128	1428 648 126	1731 571 23	1335 570 216	1456 302 107	14 4 1:	20	180 137 62	13 28 51	31 31 31	.042 .268 .507	8 14	9	6	NP_005901 NP_005154 NP_001135858	
1428 532 37 0.0 5529 1659 30 0.0 363 130 36 0.0 9320 7075 76	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 1599 0, 0 4416 0, 0 356 0 0 20272	2082 6750 331	1949 8450 697 10836	1234 10184 427 7875	2463 6321 559 7684	18 72 4	65 24 74	419 1959 137 4684	22 27 29 39	31 31 31	.109 .091 .078	3 7 8	8 7 9 8	4 3	NP_001610 NP_004411.2 NP_002749	P25098 ! Q13202 P52564
6229 1196 19 0,0 112 101 90 0.0	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 7888	331 14096 7272 230	10836 9626 24	7875 7458 34	7684 8339 112	12 81	153 16	840 116	10 80	30 30 30	.078 .462 .021	1 14	7	11	NP_002749 NP_002741 NP_003989 NP_005498	P45983 Q04206 P23528
2315 775 33 0,0 7307 2154 29 0.0	0 1,1 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,	0, 0 1929 0, 0 7553	2554 2862 9180	3561 1926 10086	3308 3539 14709	3077 4725 5732	28 29 94		620 1057 3019	22 35 32	30 29 29	.074 .406 .187	11 6 11	10 9 6	5 10 7	NP_543143 NP_002822 NP_001781	Q8WXH5 P29350 P30307
10080 1412 14 0.0 6205 912 15 0.0 8475 1247 15 0.0	0 0,0 0,0 0,0	0.0 15086	11997 7061 11494	11708 7780 10471	14574 11212 10637	11700 6998 8975	13 75 10		1496 1645 1286	11 21 12	29 29 29	.023 .014	10 2	6	7 3 6	NP_002603.1 NP_003151 NP_002602	Q16654 Q9UQB9 Q15119
16824 4782 28 0,0 567 281 50 0,0 3969 1186 30 0,0	0 0,0 0,0 0,0 0 0.1 0.0 0.0	0,0 6872 0,0 12890 0,0 18807 0,0 454 0,0 3227	19755 479 5059	25807 877 7259	22228 887 6125	21459 933 3621	210 7.	244	2421 213 1510	11 29	28 28 27	.050 .262	2 10	10	9	NP_005901	P10636
3225 993 31 0,0 2023 177 9 0,0	0 0,0 0,0 0,0	0.0 5282	3581 3087	3441 3022 3676	4935 1887	3296 2027	41	07 75	830 512 679	20 20 16	27 27 27	.352	10	6 9	10	NP_001265 NP_002730	014757 P05129
10303 2086 20 0, 0 21259 4689 22 0, 0	0 0,0 0,0 0,0	0, 0 4318 0, 0 12792 0, 0 31523	3972 12140 31669	3675 14194 22813	5372 13118 25504	3426 12929 22346	13 26	771	666 4084	5 15	27 27 26	.105 .042 .011	2	6 9 9	2 11 7	NP_004208 NP_065681 NP_001135858	3.1 Q15120
9014 1070 12 0,0 5873 780 13 0,0 1784 340 19 0,0	0 0,0 0,0 0,0	0, 0 11118 0, 0 5799 0, 0 2301	13060 6978 2598 2276	13443 7584 2505 2876	10858 10455 2283 5352	8257 6059 1508	11 73 22 30	75	1853 1667 385 1171	16 23 17	26 26 26	.089 .064 .100	3 2 6	6 9 8 9	5	NP_005456 NP_032835 NP_002219	P09619 P05412
2450 342 14 0,0 13535 1896 14 0,0 662 193 29 0,0 1194 261 22 0,0	0 0,0 0,0 0,0 0,0 0 0 0,0 0,0 0,0 0,0 0 0 0,0 0,	0, 0 2165 0, 0 18255 0, 0 470 0, 0 1003	2276 15634 777 1321	2876 15552 906 1563	5352 18662 955 1950	2668 16519 1029 1626	16 8 14	224	1171 1304 197 317	38 8 24 21	25 25 25 25	.284 .018 .249	10 15	9 10	5	NP_006197.1 NP_001265478 NP_000445 NP_000475.1	P16234 3.1 Q15118 Q6ND84
201 54 27 0,0 123 57 46 0.0	0 0,0 0,0 0,0	0,0 164	195	250 302	287 151	353 120	2	50	67 82	27 54	24 24	.037 .155 .599	11	10	7	NP_000336.1	P05067 P37840 P17600
9614 1173 12 0,0 3291 1291 39 0,0 1797 482 27 0.0	0 1,1 0,0 1,1 0 0,0 0,0 0,0 0 1,1 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,	0, 0 11154 0, 0 3797 0, 0 2076	12844 4439 2905	13205 4886 2198	12989 4261 2025	9455 3026 1897	11: 40 22	82 20	1436 633 356	12 16 16	24 24 24	.001 .224 .065	1 3	7 9 6	8	NP_063937 NP_002730 NP_001645.1	P49840 P05129 P10398
2381 745 31 0,0 1532 282 18 0,0 14301 2749 19	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 1898 0, 0 1268 0, 0 13314	3638 2705 17494	4043 2127 18818	3159 2034 18462	1967 1323 20152	29 18 17	41 92	870 538 2329	30 28 13	24 23 23	.359 .299 .175	3	9	3 6	NP_002749.2 NP_005914 NP_001645.1	P52564 Q99683 P10398
12834 3645 28 0,0 7117 1236 17 0.0	0 0,0 0,0 0,0	0, 0 12251 0, 0 5317	9725 7183	17606 10173	21829 12024	17614 9082	15 87	905 56	4299 2328	27 27	23 23	.114	7 1 11 2 5	7	3	NP_006136	
	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 2250 0, 0 590 0, 0 461	2770 938 615	2340 2383 701	1290 567	966 485	21 12 5	96	616 87	50 15	23 23	.099 .512 .149	5	9	6	NP_000312 NP_006245 NP_002345.2	Q05655
25576 5287 21 0,0 12629 2739 22 0,0 12572 2040 16 0,0 12002 4059 34 0,0	0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0	0, 0 35416 0, 0 15181 0, 0 11786 0, 0 18633	35211 19144 14466 14709	23730 15200 14677 13636	30424 14155 19198 13208	31897 13471 16635 13058	31 15 15	130 153	4258 1968 2466 2074	14 13 16	23 22 22 22	.078 .014 .061 .264	11	10 8 10 10	4	NP_005408 NP_002218 NP_000305.3	P23458 P60484
6453 1163 18 0,0 19841 7787 39 0,0		0, 0 5754	7206 23510	10594 19681	8979 22755	6830 30483	78	73	1712 3535	14 22 15	22 22	.431				NP_002747.2	
17643 4363 25 0,0 1754 177 10 0,0 1219 194 16 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0	0, 0 21649 0, 0 2141 0, 0 1061	21447 2209 1325	18375 2253 1716	18609 2113 1652	27266 1951 1651	21- 21- 14		3206 104 251	15 5 17	22 22 22	.187 .046 .233	7 5 4 15	7 8 6	2 8 9	NP_001385.1 NP_002746 NP_001896 NP_003141	Q13115 Q02750 P35222
1205 619 51 0,0 994 275 28 0,0 2826 247 9 0,0		0, 1 2493 0, 0 749 0, 0 3330	2765 1267 2858	547 1419 2964	774 1279 5333	732 1321 2653	14 12 34	07 28	960 235 978	66 19 29	21 21 21	.404 .228 .316	10	9	8	NP_001252.1	
2615 610 23 0,0 3761 369 10 0,0 2946 537 18 0,0	0 0,0 0,0 0,0	0, 0 2405 0, 0 3560 0, 1 4245	3291 4343 3383	3592 4420 2859	2781 3927 4466	3777 6543 2889	31 45 35	69 58	509 1039 673	16 23 19	21 21 21	.268 .104 .151	2	6	8 2 9	NP_001790 AAB71619 NP_002244	P50613 Q9UM73 P35968
562 118 21 0,0 5434 770 14 0,0 2043 554 27 0,0	0 0,0 0,0 0,0	0, 0 688 0, 0 5598	987 5986 1917	866 8022 2558	430 7437 2956	431 5783 3160	65 24	81 65	225 976 564	33 15 23	21 21 21	.251 .005	5 11 2		9	NP_001036020 NP_006197.1	P16234
602 114 19 1,1	1 1,1 0,0 0,0	0, 0 399 0, 0 571 0, 0 389 0, 0 712	625 14	1172 14	722 15	701	7.	24	252 578	35 137	20 20	.441	7	9 10 9 7 7	8	NP_009330 NP_002850 NP_005219 NP_620602	P42224 P49023
779 267 34 0.0 934 265 28 0.0 1744 514 29 0.0 1629 184 11 0.0	1 0.0 1,1 1,1 0 0.0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,0	0, 0 712 0, 0 2104 0, 0 1742	459 1338 2559 1865	1047 1453 2266 1779	983 970 2029 2397	1788 1113 1474 1956	9 11 20		504 264 356 236	24 17 12	20 20 20 20	.535 .431 .126	1 6 5	7 10 8	7 3 9	NP_620602 NP_000312 NP_002488	P00533 Q13164 P06400
8299 1297 16 0,0 321 223 69 0,0 67 28 42 0,0	0 0,0 0,0 0,0 0 0,0 1,1 0,0	0,0 7865 0,0 74 0,0 79	9655 164	11751 625	11601 563	8564 485	98	87	1569 221 16	16 58	19 19	.110	3 2 8	9 7	2 2 5	NP_003001 NP_004085 NP_003152 NP_004408	P45985 P05198 P23443
1379 255 19 0,0 891 454 51 0,0	0 0,0 0,0 0,0	0,0 1627	2060 636	1568 1195	1361 1391	1581 1561	16		229 415	14 39	19 19 19	.110 .559 .498 .041	9	9	10		P28562 Q01201
1317 291 22 0,0 7052 1104 16 0,0 1012 269 27 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0	0, 0 909 0, 0 6068 0, 0 615	1151 7885 1006	1869 8682 1098	2237 10148 1372	1655 9098 1893	15 83 11	76 97	481 1366 424	31 16 35	19 19 18	.269 .087 .419	7 3	9 8	1 5	NP_01218 NP_002747 NP_004963	P55210 P46734 O60674
2141 2196 103 1,1 3542 713 20 0,0 374 151 40 0,0	0 0,0 0,0 0,0	1, 0 3829 0, 0 5878 0, 0 219	3626 4273 330	2720 5212 678	15 2933 511	2466 2629 472	25 41 4	12	1361 1258 157	54 30 36	18 18 18	.822 .187 .352	16 8 3	9	1 2	NP_660143 NP_001777	Q13163 P06493
437 62 14 0,0	0 0,0 0,0 0,0	0, 0 378 0, 0 1659 0, 0 3209 0, 0 8529	432 1825 3863	551 1606	499 989 3614	721 719 2399	5 13 34 87	16 59	118 427 608 787	23 31 18	18 18 18	.359	10 1 1	7	4 6	NP_001107596 NP_001061.2 NP_068779 NP_003168	5.1 P19419 2 P23258 007820
2930 1065 36 0,0 7444 1349 18 0,0 10449 799 8 0,0 737 277 38 0,0		0,0 12690	8003 11132 999	4148 10155 12562 1162	8076 12327 812	8993 12677 699	87 12	278	787 588 191	9 5 22	18 17 17	.528 .195 .030	1 4	10	9	NP_001153392	P43405 2.1 P17948 005397
737 277 38 0,0 5100 1223 24 0,0 1634 426 26 0,0 6285 1214 19 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 6612 0, 0 6612 0, 0 1028 0, 0 5498	6643 1717 5723	6523 2569 7383	5994 1990 10185	4120 2274 8029	59 19 73	78	958 527 1707	22 16 28 23	17 17 17	.176 .143 .383 .149	11 3 6	8		NP_005598 NP_001243614 NP_002567 NP_002871	014680 013153 P04040
9288 1214 19 0, 0 2588 536 21 0, 0 3067 794 26 0, 0 5974 1355 23 0, 0	0 0,0 0,0 0,0	0, 0 5498 0, 0 2169 0, 0 2770 0, 0 5643	5723 2250 5308 5515	4274 4883 8154	3540 3705 8482	2910 1239 7071	36 35	28	796 1472 1231	23 26 41 18	17 17 17	.149 .193 .514	10	9 6	4	NP_002600.1 NP_006197.1 NP_001645.1	P09619
1695 367 22 0,0 1572 356 23 0.0	0 0,0 0,0 0,0	0, 0 2165 0. 0 1847	2438 2005	2114 2112	8482 1718 1584	1419 1593	15	71 28	1231 359 213	18 18 12	17 16 16	.133	11 2 2 7	6 6 8	9	NP_001645.1 NP_001252.1 NP_001265	P50750 014757
3166 246 8 0,0 2341 689 29 0,0 4142 630 15 0,0	0 0,0 0,0 0,0	0,0 2886 0,0 2468 0,0 4361	3129 2900 4722	4526 2767 4771	4611 3524 5888	3219 1910 4205	36 27 47	14 89	739 529 589	20 19 12	16 16 16	.257 .517 .078	3 6	8	10	NP_000206 NP_065690.2 NP_056202	P52333 P57078 Q9Y3A3
4266 710 17 0,0 5179 608 12 0,0 4328 563 13 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 3704 0, 0 5376 0, 0 3908	5260 5934 4167	6131 6376 5599	4937 6144 5342	4609 5967 5882	49 59 49	28 59 80	795 331 792	16 6 16	16 15 15	.293 .029 .067	11 2 10		3 11	NP_005034 NP_003521 NP_003521	014733 P84243 P84243
9266 363 4 0,0 511 152 30 0,0	0 0,0 0,0 0,0	0, 0 10026	11484 813 3117	9692 481 2582	10065 400 1824	12041 728 1357	10	962 87	925 157 660	9 27 28	15 15 15	.034 .611 .155	10 11 14 2	7 9 9	1 8 8	NP_002747 NP_002721	P46734 P17612 P06239
9216 1424 15 0,0 14434 1307 9	0 00 00 00	0, 0 9673	3117 12758 16329 4486	2582 10080 15071 5232	1824 11765 15278 6057	8379	10 16 54	172	660 1553 1286 697	15 8 13	14 14 14	.014	3 1	8 7 10 7	8 4 10	NP_005347 NP_001938.2 NP_002011.2 NP_778225 NP_001937.2	2 Q16829 2 P35916 P33778
9580 1291 13 0,0 1055 185 18	0 0,0 0,0 0,0	0, 0 4978 0, 0 1296 0, 0 13911 0, 0 2020	4486 2635 12445 1327	5232 1887 12321 611	1761 8365 1201	6379 1486 7545 854	54 18 10	918	460 2496 481	25 23 40	14 14 14	.272 .558 .396 .506	12	8	2	NP_001937.2 NP_000133.1 NP_003144	016828 P22607 P42226
748 408 55 0,0 14323 4236 30 0,0 18282 3748 21 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 2020 0, 0 555 0, 0 17804 0, 0 16729	969 17502 20384	833 16542 22418	977 15390 24834	928 14336 19649	12 8 16	52	157 1300 2719	40 18 8	14 14 14	.631 .330 .118	3 1 11	7 8 7	- 8	NP_002006.2 NP_002746 NP_005219	012778 002750
18282 3748 21 0,0 14073 4642 33 0,0 4352 427 10 0,0	0 0,0 0,0 0,0 0 0,0 0,0 0,0 0 0,0 0,0 0,	0, 0 16729 0, 0 24669 0, 0 4911	21099 4660	13580 4884	24834 8815 6180	11859 4086	20 18 49		2719 5929 685	37 14	14 14 14	.118 .456 .046	11 15 10	8 7	5 6	NP_005219 NP_004963 NP_004439	060674 P04626

	%S.Dev Larger	%CFC - Average Larger from Average Smaller 35	Student T test p value		Block	
	36 16	35	.059	1	11	ŀ
-		34 34 34	.110	lŀ	6	ŀ
	48 43	34	.310 .303 .438	l		ļ
-	47 15	34 33	.021	lŀ	7	ŀ
	18	33	.042	l	2	ŀ
-	27 19	33 32	.254 .032	lŀ	7	ŀ
	23 18	32 32	.079	l	7	ŀ
-	18	31	.028	lŀ	6	ŀ
	11	31	.007	l	5	ŀ
-	13	31	.042	lŀ	2	ŀ
	28 51	31	.268 .507	l	8	ļ
			.109	lŀ		ŀ
	22 27	31 31	.109 .091 .078	l	7	ŀ
	29 39	31 30	.078	lŀ	8	ŀ
	10	30	.021		1	ŀ
	80 22	30 30	.415	li	14	ŀ
	35 32	29 29	.406 .187	l	6 11	
	11	29	.023	l	10	ŀ
	21 12	29 29	.014	lŀ	10	ŀ
	11	28	.050	l	2	ŀ
-	30	28	.262	lŀ	10	ŀ
	20 20	27 27 27	.262 .061 .352		10	F
-	20 16 5	27 27 27	.141	ıŀ	2	ŀ
	5 15		.042	ı		f
	16	26 26	.089	ıŀ	3	t
1	23 17	26 26 26	.089 .064 .100	ı	2	ŀ
	38	25	.284	l	6	t
	8 24 21	25 25 25	.018	ı	10 15	ŀ
	21	25	.037	l	3	ŀ
	54 12	24 24 24	.599	lŀ	2	ŀ
			.001		2	ŀ
	16 16	24 24	.224	lŀ	3	ŀ
	30 28	24 23	.359		3	ŀ
	13	23	.175	l	7	ŀ
-	27 27	23	.114	lŀ	11	ŀ
	22	23	.099	l	2	ŀ
	50 15	23	.512	lŀ	-	ŀ
	14	23 22	.149 .078	l	3	ŀ
-	13	22	.014	lŀ	7	ŀ
	14 22	22	264		11	ļ
-	15 15	22 22 22	.117 .431 .187	lł	10	ŀ
-	15	22	.187	lŀ	7	ŀ
	5 17	22 22 21	.233	l	4	ŀ
	66 19			lŀ	15	ŀ
	29	21 21 21 21	.228 .316 .268 .104	l	10	ŀ
-	16 23	21	.268	lŀ	7	ŀ
	19	21	.151		5	ŀ
	33 15	21	.251	lŀ	11	ŀ
	23 35	21	.112		2	ŀ
	137		.850	l	3	ŀ
4	54 24	20 20 20	.850 .535 .431		11	ŀ
	17		.126	l	6	t
-	12 16	20 20 19	.015 .110 .559		5	ŀ
	58	19	.559	l	2	ŀ
-	20 14 39	19 19	.498		2	ŀ
	39 31	19 19	.408 .269	ı	9	F
	31 16 35	19 19 18	.269 .087 .419	ı	7	t
1	35 54	18	.419 822		3 16	f
	30	18	.187	ı	8	t
1	36 23	18	.352	ı	3	f
	23 31	18 18	.359 .404	l	10	t
	18	18 18 17	.528 .195	ı	10	ŀ
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	22 16	17 17	.176		11	ŀ
	28 23	17	.383		3	f
	26		.193	l	10	t
-	41 18	17 17 17	.193 .514 .230	1 }	11	ŀ
	18	16	.133		2	ŀ
	12 20	16	.400	1 1	7	ŀ
1	19	16	.517	ı	3	f
J	16	16	.293	ıŀ	11	t
1	6 16	16 15	.029	ı	2 10	f
	9	15	.034	ıt	11	t
1	27 28	15 15	.611 .155		14	ŀ
	28 15	14	.155 .014 .151		3	t
	8 13		.151	ı	10	ŀ
	13 25	14	.272 .558		3	ľ
-	23 40	14	.396 .506	ıŀ	12 6	ŀ
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	8 13	14 14	.330	ıŀ	11	ŀ
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										Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
					Flag- Patient	Flag- Patient	Flag- Patient	Flag- Patient	Flag- Patient	1545 Globally	1490 Globally	1864 Globally	1726 Globally	2278 Globally
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Patient 1- Smaller	Patient 2- Smaller	Patient 3- Smaller	Patient 4- Smaller	Patient 5- Smaller	Globally Normalized - Patient 1- Smaller	Globally Normalized - Patient 2- Smaller	Globally Normalized - Patient 3- Smaller	Globally Normalized - Patient 4- Smaller	Globally Normalized - Patient 5- Smaller
661 54	NK137 NK193-4	PKCg AurKB	Pan-specific Pan-specific	Protein-serine kinase C gamma Aurora Kinase B (serine/threonine protein kinase 12)	0, 0	0,0	0, 0	0, 0	0.0	1051 1292	763	1081	1088	1275 2467
342 35	NN050 NN004	hHR23B APG1	Pan-specific Pan-specific	UV excison repair protein RAD23 homolog B Hsp 70-related heat shock protein 1 (osmotic stress protein 94 (OSP94))	0, 0	0,0	0,0	0, 0	0, 0 1,1 0, 0	342 859	1273 210 1035	292 839	2963 118 943 621 3370	182 1441
451 31 829	NK092-3 PK520 PN107	Lck ALK Tau	Pan-specific Y1507 S422	Lymphocyte-specific protein-tyrosine kinase Anaplastic lymphoma kinase Microtubule-associated protein tau	0, 0 0, 0	0, 0	0,0	0, 0 0, 0	0, 0	827 4776 20	809 3493 541	636 7035 24	621 3370 484	595 7177 72
163 821	NK041	CK2a Syk	Pan-specific Y323	Microbibule-assiociated protein tali Casein protein-serine kinase 2 alpha/ alpha prime Spleen protein-tyrosine kinase	0, 0	0,0	0,0	0, 0	0,0	3276	4091 3419	5243 5607	5100 4858	4864 4970
419 225 422	PK034-2 NP043-2 NK086-3	JAK2 DUSP9 JAK3	Y1007+Y1008 Pan-specific Pan-specific	Janus protein-lyrosine kinase 2 Dual specificity protein phosphatase 9 Janus protein-lyrosine kinase 3	0, 0 0, 0 0, 0	0, 0	0,0	0, 0	0, 0	2740 8433 16228	2081 9392 34589	3160 10138 13652	2820 9268 17817	2939 8790 14151
228	NK052-1	EGFR Kit	Pan-specific Pan-specific	Janus protein-tyrosine kinase 3 Epidermal growth factor receptor-tyrosine kinase Mastrisem cell growth factor receptor Kit Insulin receptor substrate 1 RRC-apha serioriteronine-protein kinase	0, 0	0,0	0,0	0,0	0,0	5026 49061	5394 58080	4517 42703	5329 44237	4427
410 18 69	PN046-2 NK129-5 PK542	IRS1 Akt1 (PKBa)	Pan-specific Pan-specific Y1179 Pan-specific Y188	Insulin receptor substrate 1 RAC-alpha serine/threorine-protein kinase	0, 0	0, 0	0,0 0,0 0,0 0,0	0, 0	0,0	5026 49061 1103 10880 12887	5394 58080 1669 7953 11854	4517 42703 1395 7062 17387	5329 44237 1267 5505 16907	2430 5427
782 591	PN183 PN158	BLK Smad1 p53	S465 S33	B lymphoid tyrosine kinase Mothers against decapentaplegic homologs 1 Tumor suppressor protein p63 (antigenNY-CO-13)	0, 0	0,0		0, 0	0,0	623	627 398	457 655	524 786	11617 333 703
215 523 306	NP007-3 NK105-3 NK063-4	DUSP4 MKK6 FGFR2	Pan-specific Pan-specific	Dual specificity protein phosphatase 4 MAPK/ERK protein-serine kinase 6 (MKK6)	0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	21504 13103 4962	30421 16250 7380	18256 9010 4749	26004 9790 5108	21986 14859 3732
1 853	NN166	4E-BP1 VEGFR2	Pan-specific Pan-specific Y1059	Fibroblast growth factor receptor-tyrosine kinase 2 (BEK)  Eukaryotic translation initiation factor 4E binding protein 1 (PHAS1)  Vascular endothelial growth factor receptor-tyrosine kinase 2 (Fik1)	0, 0					1019	430	929	922	
313 260	PK161 NK240-1 NK231-3	FIt3 ErbB3	Pan-specific Y1059 Pan-specific Pan-specific Y771	Essany governisco (Espany) (Es	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0, 0	1665 6498 13404	823 6984 15034	1854 6856 11864	1896 9975 15998	2052 6847 14684
682 60 713	PN165 NN005 NP023-3	PLCg1 Bax PTEN	Pan-specific	Apoptosis regulator Bozz-associated A protein.  Discribist discretiol 2.4. E tricribischiste 3 abscribistaria and contain abscribistaria.	0, 0	0, 0	0,0	0, 0		656 2947 5452	699 2376 6028	820 1131 8776	1069 1342 8658	1093 1706 7723
34 364	NN005 NP023-3 PN504 NN057-3 PK072-5	ANXA2 Hsp40	Pan-specific Y238 Pan-specific S473	Noncoin Ac     DhaJ homolog, subfamily B member 1	0, 0	0,0	0,0	0, 0	0, 0 0, 0 0, 0 0, 0	2247 4654	2695 4154	3360 4284	2462 4426	3273 3938
21 740 641	PN069 PK067	Akt1 (PKBa) Rb PKA Calb	S473 S807+S811 T197	RAC-alpha serine/threorine-protein kinase Retinoblastoma-associated protein 1 cAMP-dependent protein kinase catalytic subunit alpha	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0,0	671 90 1531	710 99 2074	717 97 1456	613 136 1347	562 174 1077
553	PK732 NN149-1 NN163	Nek2 Crystallin aB GADD 153 (CHOP)	S171 Pan-specific Pan-specific	CHOP— Superinters protein shaker Custagive Care MIMA (prover - shreet shaker Custagive Care Crystallin alpha 8 (beat-shock 20 M28 (see protein Crystallin alpha 8 (beat-shock 20 M28 (see protein) CMA careage—Section (see protein MAPP-CERK kindse kindse 2 Crystallin alpha 8 (beat-shock 20 M28 (see protein) Crystallin alpha 8 (beat-shock 20 M28 (see protein) Crystallin alpha 8 (beat-shock 20 M28 (see protein)	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0	0,0	18805 5474 1363	22832 5213 1950	13157 6118 1654	11708	8848 4731
320 504 179	NN163 NK108-2 PN025	GADD 153 (CHOP) MEKK2 Crystallin aB	Pan-specific Pan-specific S19	DNA damage-inducible transcript 3 protein MAPK/ERK kinase kinase 2	0, 0 0, 0 0, 0	0,0	0, 0	0, 0 0, 0 0, 0	0, 0	1363 1406 1913	1950 1106 964	1654 1134 1099	1511 1390 1378	1847 1236 1125
425 862	PK035-1 PN094	JNK 1/2/3 Vimentin	T183/Y185 S33	Crysiaem apna 6 (near-shock 20 kDa Ike-procein) Jun N-terminus protein-serine kinase (stress-activated protein kinase (SAPK)) 1/2 Vimentin	0, 0	0,0	0,0	0,0	0,0	2949 3159	4006 1006	3316 2192	3619 4642	3937 2494
767	PK035-1 PN094 PN073 NN176 NN060-3 PK047-2	S6 VEGF-C	S235 Pan-specific	40S ribosomal protein SB Vascular endothelial growth factor C Heat shock 70 kDa protein 1	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 1, 1 0, 0 0, 0 0, 0	0, 0 1, 1 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 1,1 0, 0 0, 0 0, 0	1030 1869 6679	655 1197 4456	1181 1839 6353	1318 2577 6135	1226 3770 3901
852 370 477 701		Hsp70 MEK1 PRAS40	Pan-specific S298 T246	Head shook Of NATa protein 1 MAPK/ERRY protein-6 Markes 1 (MKK1) Proline-rich Akt substrate 40 kDa (Akt151) Palletel-drived growth factor receptor kinase alpha Epidermal growth factor receptor kinase alpha Epidermal growth factor receptor kinase alpha Head shook 60 kDa grotein alphabeta Distrated for the control of the	0, 0	0,0		0, 0	0,0	2277	1156	2428 413	1881	2470
617 231 372	NK242-1 NK052-6 NN061-16	PDGFRa EGFR Hsp90	Pan-specific Pan-specific	Platelet-derived growth factor receptor kinase alpha Epidermal growth factor receptor-tyrosine kinase	0, 0 0, 0 0, 0 0, 0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0	484 11017 13451 6149	321 11847 14502 5767	10149 10178 5694	222 10835 9919 6512	201 6894 12339 5200
218	NPU4U-1	Hsp90 DUSP6 PTEN	S380/T382/T383	Phosphatidulinositol, 3.4. Surisphosphate 3. phosphatase and protein phosphatase	0,0	0,0	0,0	0,0	0,0	6101	7605 611	4706	5601 1767	7545 1090
518 832	PK713 PN121 NN048-2 NN007	MKK3	S218 T205 Pan-specific	MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta) Microtubule-associated protein tau Glucose regulated protein 78	0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0,0	10238 985 5913 6097	10840 856 7659	7030 1427 6166 9660	4617 2582 6636	6766 1249 7032
518 832 331 64 84	NN048-2 NN007 PN015	Tau Grp78 Bol-XL Caldesmon	Pan-specific Pan-specific 8789	Glucose regulated protein 78 Bcl2-like protein 1 Caldesmon	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	5913 6097 1175	7659 4918 795	6166 9660 1357	6636 7411 1591	7032 6896 781
541 810 720	PK727 PN082-1 NP026	MST3 STAT3 PTP1D/SHP2		Mammalian STE20-like protein-serine kinase 3 Signal transducer and activator of transcription 3 Protein-tyrosine phosphatase 1D (SHP2, SHPTP2, Syp, PTP2C)	0, 0	0,0	0,0	0, 0 0, 0 0, 0	0,0	4037 1469 2134	3547 1075 663	3956 964 1490	3199 1246 3070	3665 814 4141
720 41 303	NP026 PK500 PK634	PTP1D/SHP2 A-Raf FGFR1	Y704 Pan-specific Y302 Y653+Y654	Protein-tyrosine phosphatase 1D (SHP2, SHPTP2, Syp, PTP2C)  A-Raf proto-oncogene serine/threorine-protein kinase Fibroblast growth factor receptor-tyrosine kinase 1	0, 0 0, 0 0, 0	0, 0	2134 5570 14002	663 7299 11277	1490 5631 13800	3070 6301 12695	4141 7562 8802			
300 293 516	NN043 PK021 NK101-6	Fast FAK MKK3	Pan-specific S732	Tumor necrosis factor ligand, member 6 Focal adhesion protein-tyrosine kinase MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta)	0.0	0,0	0.0	0.0	0.0	446 453 13989	332 499	255 434	355 524 7815	269 240
516 802 361	NK101-6 PK107 PN041 PN156	MKK3 Src	Pan-specific 8732 Pan-specific Y418 878	MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta) Src proto-oncogene-encoded protein-tyrosine kinase	0, 0	0,0	0, 0	0, 0	0, 0	13989 896	32650 967	9846 994	7815 1248	13000 1184
	PN156 PK116	NFKB p65 mTOR		Heat snock 27 kLa protein beta 1 (Hsps1) NF-kappa-B p65 nuclear transcription factor Mammalian taroet of raparnycin (FRAP)	0, 0	0,0	0,0	0,0	0,0	646 130	218 220	935 168	4536 696 172	570 189
545 194 208 117	PK116 NN034 NP046-2	mTOR DAXX DUSP12	S2448 Pan-specific Pan-specific Pan-specific	No-sappa-s pon nulosar transcription factors Mammatain large of ngamyricin (FRAP) Death-sastociated protein of (BRAD2) Duath-sastociated protein of (BRAD2) Duath-sastociated protein of (BRAD2) Duati specificity protein prosphilatase 12 Cell division cycle 258 prosphilatase 12 Cell division cycle 258 prosphilatase 13 Death Soldman (SRAD2) Death Death Soldman (SRAD2) Death Death Death Death Deat	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	130 4223 1488 7324	220 3811 2247 8767	168 4777 1576 8260 2389	172 3078 1450 8101 1779	189 2516 1822 5854
492 421	NP046-2 NP002-2 PK051-2 NK086-2	DUSP12 Cd:258 MEK3/6	189/193/5207/21	Cet division cycle 256 prospinatase MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta) Janus protein-bronshe kinase 3	0, 0	0,0		0, 0		2526	2666 8118	2389 8142	8101 1779 9791	1859
469 141 683	NK086-2 PN169 NK028-2 PN144	JAK3 MDM2 CDK5 PLCg1	Pan-specific S166 Pan-specific	Janus protein-tyrosine kinase 3 Double minute 2 Cyclin-dependent protein-serine kinase 5	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	7763 1233 8114 295	915 7301 174	1613 6204 294	9791 2008 6945	12125 1333 4280 199
683 509 375	PN144 NK110-3 NN165-1	PLCg1 Met hsp90b	Pan-specific	1-phosphatidylinositol-4,5-bisphosphate phosphodesterase gamma-1 Hepatocyte growth factor (HGF) receptor-tyrosine kinase Heat shock 90 kDa protein beta	0, 0	0, 0		0, 0 0, 0 0, 0 0, 0	0,0	295 6128 9961	174 6015 6291	294 6195 9949	325 5703 10051	199 3543 6400
280 441 46	PK624 NN153 PK143	ERK4 KDEL Receptor (KR10 ASK1	Pan-specific S186 Pan-specific S966	Neast shock 90 kiDa protein beta Extracelishar regulated protein-serine kinase 4 Extracelishar regulated protein-serine kinase 4 ER lumen protein refailining receptor 1 Apoptosiis signal regulating protein-serine kinase 1	0, 0 0, 0 0, 0 0, 0	0, 0	0,0	0, 0	0,0	7261 5298 341	4705 3606 282	4631 6713 526	4349 8025 845	4818 6088 552
846	NK181-3	TYK2	S966 Pan-specific Pan-specific	Apoptosis signal regulating protein-serine kinase 1 Protein-tyrosine kinase 2 (Jak-related) Heat shock 70 kDa protein 8	0, 0	0,0	0,0	0,0		5812	3872	4349	4556	3702
355 44 9 304	NN054-2 NK007 PK001 NK063-2	Hsc70 ASK1 Abi FGFR2	Pan-specific Y393 Pan-specific	Apoptosis signal regulating protein-serine kinase 1 Abelson prote-oncogene-encoded protein-tyrosine kinase Fibroblast growth factor receptor-tyrosine kinase 2 (BEK)	0, 0 0, 0 0, 0	0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	6324 1012 339 11984	6802 1045 553 17366	7307 1156 661 9423	7811 1163 637 7219	5939 2169 415 10482
304 869 499	NK254-3	FGFR2 WNK3 MEK5	Pan-specific Pan-specific	Fibrioblast growth factor receptor-tyrosine kinase 2 (BEK) Serine/threcnine-protein kinase WNK3 MADM/EBK protein entire kinase E (MKKE)	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0, 0	11984 2845	3658	9423 1948	1790	10482 2937 5232
391 181 6	NK104-4 NN065 NK234-3	INBb CSF1R AAK1	Pan-specific Pan-specific Pan-specific 9637	Nov-Niches protein seniors statuse 9 (NRNs) Inhibitor of NF-kappa-B beta (thyroid receptor interacting protein 9) Macrophage colony-stimulating factor 1 receptor AP2-associated protein kinase 1	0.0	0.0	0.0	0, 0	0.0	1038 11491	7863 1960 7291 6007	623 7066 7816	5360 437 8316 4841	1306 5511 5849
6 868 527 556	NK234-3 PK503 NK254-1	WNK3	Pan-specific	Serine/threonine-protein kinase WNK3	0, 0	0, 0	0, 0	0,0	0,0	11491 7707 6994	9721	6114	5364	5724
556 457	NK106-5 NN071 PK042-PK144	MKK7 NFkappaB p65 LIMK1/2	Pan-specific Pan-specific Y507/T508	MAPK/ERK protein-serine kinase 7 (MKK7) NF-kappa-B p65 nuclear transcription factor LIM domain kinase 1/2	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	7040 2076 1605	8527 2428 1310	5164 861 789	4279 1313 1104 7290	6168 1077 616 11048
507 482	PK042-PK144 NK229-3 NK100-1	MELK MEK2	Pan-specific Pan-specific	LIM domain kinase 1/2 Maternal embryonic leucine zipper kinase MAPK/ERK protein-serine kinase 2 (MKKZ)	0, 0 0, 0 0, 0 0, 0 0, 0	0.0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	12319 745	15960 510	8883 1228	702	11048 1104 5411 2503
618 456 396	NK242-2 NK093 NN161	LIMK1 IKKgNEMO	Pan-specific Pan-specific Pan-specific	Platelet-derived growth factor receptor kinase alpha LIM domain kinase 1 I-kappa-B kinase gamma/NF-kappa-B essential modulator	0, 0	0,0	0,0	0, 0	0,0	7189 1738 585	7739 896 762	6113 3554 285	6660 3223 109	217
700	PN532	IKKgNEMO PPP1R11 YSK1 MST1	Pan-specific Y64 Pan-specific	Protein principal and a second protein and a second protein pr	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	2161 1380	2914	2990 972	2758 1251	3291
872 537 860 562	NK214 NK113-1 NP030 PN055-1	NMDAR1	Pan-specific	Mammalian STE20-like protein-serine kinase 1 (KRS2)  Dual specificity protein phosphatase 3  N-methyl-D-aspartate (NMDA) glutamate receptor 1 subunit zeta	0, 0	0, 0	0,0	0, 0	0, 0	375 5131 657	449 2401 309	499 6770 702	578 7300 796	912 9322 610
562 636 148	PN055-1 PN061 NK031-5	PED15 (PEA15)	S896 S116 Pan-specific		0, 0	0, 0	0, 0	0, 0 1, 0 0, 0	0, 0	999	309 1059 1151	702 1531 1498	796 1680 1280	
148 611 754	NK031-5 NN085-1 NK161-3 NN051	CDK8 PARP1 RON	Pan-specific Pan-specific Pan-specific Pan-specific	Cyclin-dependent protein-serine kinase 8 Poly (ADP-ritose) polymerase 1 (ADPRT) Macrophage-stimulating protein receptor alpha chain Hep70Hsc70 interacting protein (ST13)	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	1220 11418 12290 7803	1151 7291 8850 7468	9789 6974 7652 4354	1280 15914 12713 8631	2135 11636 8005 6900
343 705 784	PN185	PRKDC (DNAPK) Smad2	Pan-specific T220	DNA-activated protein-serine kinase	0, 0	0,0	0,0	0,0		768	7468 7306 473	1121	6631 4721 803	945
696 36	NP019 NN122 NK179	Smad2 PP4/A'2 APG2 TrisB	Pan-specific Pan-specific	Mothers against decapentaplegic homolog 2 Protein-serine phosphatase 4 - regulatory subunit (PPXIA'2) Hap 70-related heat shock protein 4 (HSP70RY) SMICE MT3816 proceeder, breche pick ferone	0, 0	0,0	0, 0	0, 0	0,0	7954 1482	6663 1533 1067	9165 1663	8369 1704	9807 1925
840 353 721	NK179 NK072 NP036	Hpk1 PTPD1	Pan-specific Pan-specific Pan-specific	BNDF/NT3/4/5 receptor- tyrosine kinase Hematopoetic progenitor protein-serine kinase 1 Protein-tyrosine phosphatase non-receptor type 21	0, 0	0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	1554 1210 2098	1057 2046 2323	1927 1620 1565	1966 1449 1712	2149 2257 1380
51 813	NK008-5 NN105 NP006-2	Aurka Statsa Dusp1 (MKP1)	Pan-specific Pan-specific	Aurora Kinase A (serine/threorine protein kinase 6) Signal transducer and activator of transcription 5A MAS Honey Appendix A (CL 100, MAS)	0, 0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0	3372 2180	3452 2193	2688 1356 27109	2819 2274	2685 1802
203 684 368	PN143 NN059-3	PLCg2 Hsp60	Pan-specific Y753 Pan-specific	MAP kinase phosphatase 1 (CL100, VH1) 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-2 Heat shock 60 kDa protein 1 (chaperonin, CPN60)	0, 0	0, 0 0, 0 0, 0	0,0		0,0	505 1462	31922 383 1008	713 2267	18872 866 2748	22426 497 2699
259 222	NK231-2 NP041-2 NN053 NK235-3	ErbB3 DUSP7	Pan-specific Pan-specific Pan-specific	Tyrosine kinase-type cell surface receptor HER3 Dual specificity protein phosphatase 7 Heme oxygenase 2	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	42403 10505 5991 9576	43431 11282 6710 11827	32776	39160 11851 7138 9740	32420 11298 6824 9918
263	NK235-3	HO2 ErbB4	Pan-specific	neme oxygenaeu z Receptor tyrosine-protein kinase erbB-4	0, 0	0,0	0,0	0,0	0,0	9576	11827	7974 5431	7138 9740	6824 9918

Average - Smaller	S. Dev Smaller	%S.Dev. Smaller
1052 2002	165 660	16 33
2002 229 1023	80 220	35 21
1023 698 6170	99	21 14 32
5170 228	1656 234	32 102
4515 4589	736 758	16 17
2748 9204 19287	362 579 7796	13 6
19287 4938	7796 402 9438	40 8 21
44637 1573		
7365 14131 513	467 2000 2504	30 27 18
513 679	110 156	21
23634 12602	4192 2809	18 22
5186 796 1658	1198	23
	215 435 1282 1432	27 26
7432 14197 867	1432 183	10 21
1900 7328	673 1359	35 19
2807	440	16
655	59	9
119 1497	32 327	27 22
15070 5521	5057 525	34 10
1665 1254 1296	214 125 336	13 10
1296 3565	336 394 1196	26 11
2698 1082	233	44 22
2250 5505	876 1110 490 108	39 20
2042	490 108	24 33
328 10149 12078 5864	1715	17 15
5864 6312 1081	1795 443 1124 382	8
1081	382	18 35 29
1420	614	43 9
6681 6996	622 1575	23
6996 1140 3681	316 301	8
1114	227 1212	20 53
2300 6473 12115	827 1919	13 16
331 430	1919 68 100	21 23 57
15460 1058	8873 134	57 13
	656 232	15
613 176 3681	29	38 17 22
1716 7661	295 1015	17
2244 9188 1420	359	16 18
1420	1628 369 1299	26
257	59	23
5517 8530 5153	1001 1785 1065	18 21 21
5153 5946 469	1065 1471 136	21 25 29
4458	136 744	17
6836 1309	744 669 434	10 33
521 11295	125 3409	24 30
2636 5819	688	26 18
5819 1073 7035	1038 539	18 50
7935 6444 6783	1992 1148 1566	25 18 23
6236 1551	1475	23 24 39
1551 1085 11100	900 355 2985	39 33 27
11100 858	2985 267	27 31
9622 2383	812 972	12 41 62
392 2823	244 374	13
1596 562	510 187	32 33
562 6185 615	187 2318 165 281	33 37 27 21
1368	281 358	21 25
11210	2819	25 24
7291 6407	450 1994	6
822	1884 214	29 26
8391 1661	1075 155	13 9
1661 1731 1716 1816	388	22 22
1816 3003	384 346 338	19 11
1961 25989	344 4754	18 18
593 2037	173 691	29 34
38038	4661 770	12

					Normalized Median 1597	Normalized Median 1688	Normalized Median 1753	Normalized Median 1745	Normalized Median 1646
Flag- Patient 1-	Flag- Patient 2-	Flag- Patient 3-	Flag- Patient 4- Bigger	Flag- Patient 5-	Globally Normalized - Patient 1- Bigger	Globally Normalized - Patient 2- Bigger	Globally	Globally Normalized - Patient 4- Bigger	Globally Normalized - Patient 5- Bigger
1- Bigger 0, 0	Bigger	Bigger	Bigger	Bigger	Bigger 1078	Bigger	Patient 3- Bigger	Bigger 1100	Bigger
0, 0	0,0	0, 0	0, 0	0, 0	1078 1315	1494 1292	2751	3492	943 2483
0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 1, 1 0, 0	0, 0	0, 0	0, 0	0, 0	237 574	420 968	416 951	111 969	109 2321
0, 0	0,0	0, 0	0, 0	0,0	628 4258	1044 4254	1170 6650	390 7326	711 6722
0, 0	1, 1 0, 0 0, 0	0, 0	1, 1 0, 0 0, 0	0,0	438 5092 4603	11 4128 4486	17 5788 5905	784 5744 6649	41 4703 4223
0, 0	0,0	0, 0	0, 0	0,0	2113 6645	2315 7326	3361 13077	2849 11705	4223 4841 13110
0, 0	0, 0	0, 0	0, 0	0, 0	23205	22423	21382	17447	24009
0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0	4624 42769	5276 45960	7178 44994	6150 47453	4456 68378
0, 0	0, 0	0,0	0, 0	0,0	1696 9388 13645	2538 9278	1841 8381 17525	47453 1477 8363 18625	1234 5734 15911
0, 0	0,0	0, 0	0, 0	0,0	13645 529	13198 596	17525 527	18625 775	15911 425
0, 0	0,0	0, 0	0, 0	0,0	22082 19384	29315 16014	29902 13127	26589 8247	23545 13299
0, 0	0.0	0.0	0.0	0.0	8421 431 1268	8179 618 1725	5930 886 2168	3139 1143 2256	3075
0, 0	0,0	0, 0	0, 0	0, 0	1268	1725 7021	2168 10040	2256 10500	1328 1762 7805
0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0	15500	13867	13739 1317	18183 1217	17291 1182
0, 0	0,0	0, 0	0, 0	0,0	3133 5613	2098 7137	1070	2675	1534
0.0	0,0	0.0	0, 0	0,0	3199 4583	2305	2936 4372	3715 4909	3356 5450
0, 0	0, 0	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	922	1107	745	421	413
0, 0	0,0	0, 0	0, 0	0,0	94 1902 23396	104 2524 20911	190 1970 12561	132 950 15721	138 895 10314
0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	23396 5145 1467	20911 5148 2348	12561 6052 2313	15721 6037 1504	10314 7963 1487
0, 0	0,0	0, 0	0, 0	0,0	759 1572	3042 1713	990 1642	954	1122 1006
0, 0	0,0	0,0	0, 0	0,0	3539 1846	3783 3105	5002 3433	1156 4548 4384	2581 1955
0, 0	0,0	0, 0	0, 0	0,0	719	901	1295	1342	1646
0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0, 0	0, 0	0, 0	1864 6573 2611	1860 5369 2252 783	2764 5056 2238	2670 6305 2463	3103 6670 1554
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	312 10150	783 11619	300 11159	199 11996	192 9962
0, 0	0,0	0.0	0, 0	0,0	15600 6029 7679	13656 5382	14970	7784	13270 7937
0, 0	0,0	0, 0	0, 0	0, 0	7679 560	6796 698	7138 1359	3061 1685	9387 1524
0, 0	0,0	0, 0	0, 0	0,0	13155 698 6560	13919 859 7356	7422	3901 1939	4013 2162 5905
		0, 0 0, 0 0, 0			6560 7990	7356 6631	1964 8741 7818	1939 7294 8695	5905 6239
0, 0	0,0	0, 0	0, 0	0, 0	823 4320	460 3084	1694 3778	1814 5462	1294 2986
0, 0	0, 0	0, 0	0, 0	0, 0	1304 871	1512 645	1534 2531	818 2763	761 5430
0, 0	0,0	0, 0	0, 0	0, 0	6951 12168	6983 12648	7839 12502	3645 15724	8988 11273
0, 0	0, 0	0, 0	0, 0	0, 0	397 394	500 666	344 498	333 473	185 249 9671
0, 0	0,0	0, 0	0, 0	0, 0	32588 460	18951 1074	11157 1218	1037	1817
0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	0, 0	0,0	4997 326	4385 447	4348 667	5622 980	3878 825
0, 0	0, 0	0, 0	0, 0	0,0	223 3980	321 4692	61 4527 1528	215 3321	109 2943 2431 7726
0, 0	0,0	0, 0	0, 0	0, 0	1566 8565	1975 9591	9231	1570 5362	2431 7726
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	2285 6834 970	3417 10104 1310	2839 11136 2216	1719 10519	1578 9825 1174
0, 0	0,0	0, 0	0, 0	0, 0	970 7910 145	1310 7194 275	2216 7015 335	1812 7484 301	1174 4962 298
0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0	0,0	5651	6318	7108	6185	3739
0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	8673 6306 4822	7598 4826	8110 5870	10108 7340 7189	10319 2679 7254
0, 0					375	5588 256	6270 705	475	643
0, 0	0,0	0, 0	0, 0	0, 0	4771 7200 731	4650 6485 1307	5317 6750	5494 8044	3089 7282 1915
0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	731 521 16654	1307 741 15874	1495 722	1386 386 6698	1915 352 7584
0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0,0	0, 0	0,0	2780	4184	722 11962 2381	2806	1554
0, 0 0, 0 0, 0 0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	0,0	8061 2089 9999	8922 1755	6702 505	3140 628	3267 571
0, 0	0,0	0, 0 0, 0 0, 0	0, 0	0, 0	9999 8918 9725	8211 6714 8793	8292 5986 7809	9623 5690 4036	4867 5960 4606
0, 0	0,0	0, 0	0, 0	0,0	9725 9819 2531	8793 8573 1570	7809 5628 846	4036 2941 1637	5163
0, 0	0,0	0, 0	0, 0	0,0	1249 16578	1622 15359	1125 10909	850 6013	1404 741 8300
0.0	0,0	0, 0	0, 0	0, 0	653	1019	1053	998	686
0, 0	0,0	0, 0 0, 0 0, 0	0, 0	0, 0	7717 1500 616	7064 1418 512	7855 2337 673	6608 2599 50	4717 4341 150
0, 0	0,0	0.0	0, 0	0,0	3023	3329 2055	4004 1592	2680 1011	1384
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0, 0	1782 367 2766	525 3798	732 5655	519 6618	1710 729 12712
0, 0	0,0	0, 0	0, 0	0,0	349 867 1368	688 1375	697 1532	654 1784	746 1409
0, 0 0, 0 0, 0 0, 0	0, 0	0,0	1, 0 0, 0 0. 0	0,0	1368 8475	1271 9370	1704 14587	1450	1611 13837 11712
0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	10299 7069	9615 7356	7186 7128	10663 8264	11712 7101
0,0	0,0	0, 0	0, 0	0,0	8858 533	7958 783	6101 1213	4760 767	4726 857
0, 0	0,0	0,0	0, 0	0,0	8864 1377	8817 1486	11147 1834	7148 1007	6422 2688
0, 0	0,0	0, 0	0, 0	0,0	1382 1568	1639 1747	2152	1663 1682	1905 2141
0, 0	0,0	0, 0	0, 0	0,0	1711 2943	2756 3582	2571	1054	1074
0, 0 0, 0 0, 0	0, 0	0.0	0.0	0, 0	2866	2599 26638	3035 2012 24954	2631 1336 22135	2970 1078 27523
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	29814 301 1849	468 1242	24954 1224 2172	22135 509 2493	27523 483 2498
0, 0 0, 0 0, 0 0, 0	0,0	0, 0	0, 0	0,0	38720 10684	38392 10693	40311 10993 5770	36339 6585	37623 15867
0, 0	0,0	0,0	0, 0	0,0	6309	5884	5770	8056	8717

Average (Average Average (Average Average Aver	S. Dev Larger Larger 1988 1988 1988 1989 1989 1989 1989 198	%S.Dev. Larger Larger 17 38 39 59 59 100 110 110 110 110 110 110 110 110 11		NGCPC  NGCPC	Student leaf product of the state product of the st
2.500 2.500	853 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	53 52 52 53 53 54 54 55 55 55 55 55 55 56 56 57 57 58 58 58 58 58 58 58 58 58 58 58 58 58		13	161 161 161 161 161 161 161 161 161 161
1107 1107 1107 1107 1107 1107 1107 1107	138 601 601 601 601 601 601 601 601 601 601	62   62   62   63   64   64   64   64   64   64   64		13	559 686 686 686 687 478 478 485 485 485 485 485 485 485 48
781	283 283 283 284 284 284 284 284 284 284 284 284 284	50 100 100 101 101 101 101 101 101 101 1		133 133 133 133 133 132 122 122 122 122	559 686 686 686 687 478 478 485 485 485 485 485 485 485 48
5001   1000	601 1 940 940 940 940 940 940 940 940 940 940	130 12 18 18 19 27 11 11 11 12 12 11 11 12 12 13 13 15 15 15 16 17 17 18 18 19 19 25 18 19 25 19 25 19 25 19 25 19 25 19 25 19 25 25 25 25 25 25 25 25 25 25 25 25 25		13 13 13 13 13 13 12 12 12 12 12 12 12 12 11 11 11 11 11	
500 500 500 500 500 500 500 500 500 500	2294 2491 2594 2595 2595 2595 2595 2595 2595 2595	311 27 111 110 110 110 110 110 110 110 110 11		13 13 12 12 12 12 12 12 12 12 12 11 11 11 11	453 455 .563 .341 .568 .637 .295 .062 .382 .561 .311 .428 .572 .994 .495 .293 .090 .453 .593 .594 .495 .495 .495 .495 .495 .495 .495
\$7600   \$7600	2294 2491 2594 2595 2595 2595 2595 2595 2595 2595	111 118 119 125 166 163 265 163 275 163 275 286 40 37 19 22 286 385 385 386 387 19 287 287 288 288 288 288 288 288 288 288		12 12 12 12 12 12 12 12 11 11 11 11 11 1	.563 .341 .568 .637 .295 .082 .382 .561 .311 .428 .572 .994 .495 .293 .090 .441 .529 .004 .451 .529 .641 .451 .641 .641 .641 .641 .641 .641 .641 .64
1991   1992   1993   1994   1995   1994   1995	441 1320 2116 1320 2116 116 189 3083 3671 3226 3227 334 377 746 1623 472 1724 34 631 4927 1028 414 842 283 839 650 600 2769 859 859 859 859	25   25   26   27   27   27   27   27   27   27		12 12 12 11 11 11 11 11 11 11 11 11 11 1	.637 .295 .082 .382 .561 .311 .415 .572 .694 .495 .293 .000 .000 .483 .529 .441 .495 .587 .604 .441 .495 .495 .495 .495 .495 .495 .495 .495
8-229 8-229	1320 2116 116 116 119 3083 3083 30871 3292 354 1794 1798 347 746 1623 472 472 472 472 472 472 472 34 631 631 503 657 362 278 889 890 800 800 800 800 800 800 800 80	16 16 13 20 20 25 25 26 20 26 26 28 26 22 25 26 26 27 27 27 27 27 27 27 27 27 27 27 27 27		12 11 11 11 11 11 11 11 11 11 11 11 11 1	
571 1 200 1	116 119 3083 3083 30871 2226 3397 3397 1794 17786 1623 347 746 1623 4472 4411 2774 34 427 1028 4414 822 283 839 961 331 503 667 362 218 800 2799 859 2077 452	250 255 255 265 266 267 277 277 277 277 277 277 277 277		11 11 11 11 11 11 11 11 11 11 11 11 11	.382 .561 .311 .428 .572 .694 .495 .293 .090 .483 .529 .426 .411 .414 .414 .414 .414 .607 .566
18014 1802 1802 1802 1802 1802 1802 1802 1802	329 329 364 1794 17786 347 746 1623 472 471 274 491 4927 1028 414 842 233 839 667 3667 3667 3667 3667 3667 3667 367 3	26		11 11 11 11 11 11 11 11 11 11 11 10 10 1	.311 .428 .572 .694 .495 .293 .090 .483 .529 .026 .441 .193 .587 .604 .458 .298 .461 .414 .414 .607 .567
881 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	329 329 364 1794 17786 347 746 1623 472 471 274 491 4927 1028 414 842 233 839 667 3667 3667 3667 3667 3667 3667 367 3	40 40 37 19 222 11 11 36 61 22 22 32 22 11 11 66 67 7 21 41 30 39 39 39 30 30 30 30 30 30 30 30 30 30 30 30 30		11 11 11 11 11 11 11 11 11 11 10 10 10 1	.572 .994 .495 .293 .990 .483 .529 .026 .441 .193 .587 .604 .458 .498 .461 .411 .607 .507
1832 1835 1835 1835 1835 1835 1835 1835 1835	1794 1798 347 746 1623 472 472 472 472 474 34 4927 1028 414 4927 1028 414 283 839 961 331 502 276 867 867 867 867 867 867 867 867 867 8	19 19 22 11 11 35 26 38 30 17 23 61 20 22 28 28 21 116 61 7 7 21 14 30 39 39		11 11 11 11 11 11 11 10 10 10 10 10 10 1	
960   960	746 1623 472 411 274 34 631 4927 1028 414 842 283 839 961 331 503 667 362 218 800 2769 2077 452 4324	36 36 35 20 15 20 15 9 38 38 30 17 22 32 22 32 22 11 16 61 7 7 21 14 30 39 39 39 39 39 39 39		11 11 11 11 10 10 10 10 10 10 10 10 9 9	.529 .026 .441 .193 .587 .604 .458 .298 .461 .414 .811 .607
3102 3102 3102 3102 3102 3102 3102 3102	472 411 411 34 431 432 444 444 444 444 283 836 367 331 567 362 2769 2769 277 452 432 432 444 800	26 38 30 17 23 61 20 22 32 28 21 11 66 61 7 21 14 30		11 10 10 10 10 10 10 10 10 9 9	.587 .604 .458 .298 .461 .414 .811 .607 .566
721 131 131 131 131 131 131 131 131 131 1	274 34 631 4927 1028 4144 842 283 951 331 503 657 362 218 800 2769 2077 452 4324	26 38 30 17 23 61 20 22 32 28 21 11 66 61 7 21 14 30		10 10 10 10 10 10 10 9 9	.587 .604 .458 .298 .461 .414 .811 .607 .566
196581 196581 196581 196581 1964 11874 11873 1418 13901 1418 2945 1180 2945 1180 2945 1180 2945 1180 2945 1180 1180 1180 1180 1180 1180 1180 118	34 631 4927 1028 414 842 283 899 961 331 503 657 362 218 800 2769 859 2077 452 4324	26 38 30 17 23 61 20 22 32 28 21 11 66 61 7 21 14 30		10 10 10 10 10 10 9 9	.298 .461 .414 .811 .607 .566 .712
1824 1373 1418 1373 1418 1418 1418 1418 1418 1418 1418 141	4927 1028 414 842 283 839 961 331 503 667 362 218 800 2769 859 2077 452 4324	30 17 23 61 20 22 32 28 21 11 16 61 7 21 14		10 10 10 9 9	.298 .461 .414 .811 .607 .566 .712
1824 1373 1418 1373 1418 1418 1418 1418 1418 1418 1418 141	414 842 283 839 961 331 503 667 362 218 800 2769 859 2077 452 4324	23 61 20 22 32 28 21 11 16 61 7 21 14 30 39		10 9 9 9	.414 .811 .607 .566 .712
3891 2945 21452 21	839 951 331 503 657 362 218 800 2769 859 2077 452 4324	22 32 28 21 11 16 61 7 21 14 30 39		9	.566 .712
2452 2452 2995 2224 357 10977 10977 10977 10977 10977 10977 10976 1306 6336 6336 6336 6336 6336 6336 633	331 503 667 362 218 800 2769 859 2077 452 4324	28 21 11 16 61 7 21 14 30 39			.712
2224 2234 357 10977 10977 11976 6336 6336 6336 6336 6336 6336 6336 1196 119	362 218 800 2769 859 2077 452 4324	16 61 7 21 14 30 39			.466
10977 13056 6336 6812 1165 8482 1162 1171 1277 1217 1217 1217 1217 121	800 2769 859 2077 452 4324	7 21 14 30 39		9	.508 .506
13056 6336 6812 1165 8482 1524 7171 7475 1217 3026 1198 6881 12448 6881 1283 352 456 456 6881 1283 362 1648 456 6891 1283 1384 456 456 1886 1886 1886 1886 1886 1886 1886 18	2769 859 2077 452 4324	30 39		9 9	.626 .808 .288
6812 1165 8482 1524 7777 7475 1217 7475 22448 6881 1283 352 448 6881 1283 352 456 456 456 456 1883 3892 1884 8891 1886 8891 1886 8891 1886 8891 1886 8891 1886 8891 8891	2077 452 4324	30 39		8	.288 .462 .477
1524 7777 7475 1217 3926 1186 2448 6881 12863 352 456 16383 11321 4646 649 188 3892 1814 8095 2388				8	.622
7475 1217 3926 1186 2448 6881 12863 352 456 16383 1121 4646 649 186 3992 1814 8095 2368		51 40 13		7 7 7	.626 .727 .472
3926 1186 2448 6881 12863 352 456 16383 1121 4846 649 188 3892 1814 8095 2368	948 907 513	13 12 42		7	.472 .552
6881 12863 352 456 16383 1121 4646 649 186 3892 1814 8095 2368	909	23		7	.552 .686 .667
352 456 16383 1121 4646 649 186 3892 1814 8095 2368	334 1717	28 70		6	.720 .766
649 186 3892 1814 8095 2368	1780 1508	26 12 29		6	.663 .490 .687
649 186 3892 1814 8095 2368	136 8812	30 54		6	.564
186 3892 1814 8095 2368	8812 434 604	39 13		6	.749 .462
2368	239 91 675	37 49 17		6	.802 .825 .379
2368	349 1507	17 19		6	.538 .622
1496	689	29		6	.577
6913	1492 454 1021 66	15 30 15 24		5	.689 .175 .788
271 5800	66 1131	24 20		5	.788 .279
8961 5404	1079 1583	12 29		5	.697 .791
6224 491	934 166 849	15 34 18		5 5	.639 .730
7152 1367	533 381	7 28		5	.426 689
544 11754 2741	163	30 35	l E	4	.795 .756
2741 6018 1110	852 2405 673	31 40 61	E	3 3	.811 .846 .907
1110 8198	673 1810	61 22 18		3	.665
6654 6994	1182 2272	32	l ⊨	3	.718 .814
6425 1598 1117	2470 543 312	38 34 28	l E	3 3	.808 .854 .832
11432	4033 174	35	F	3	.804
11432 882 6792 2439	4033 174 1131 1056	20 17 43	l þ	3 2	.727
400 2884 1630	252	63		2 2	.938 .913
1630 574	345 139 3475	21 24	E	2	.874 .873
6310 627	142	23	ΙE	2	.908
1394 1481	300 158	22 11	l þ	2 2	.778 .870
11385 9895 7384	2422 1515 452	21 15		1 1	.929 .909
7384 6481 831	452 1675 220	26 26	F	1 1	.835 .958
8480 1678	1636 569	19	l E	1	.937 .946
1748 1734	261 218	15	l F	1	.922 .892
1833 3032 1978	721 308 692	39 10 35	E	1	.957 .853 .963
1978 26213 597	692 2572 322	35 10 54	ΙÉ	1	.963 .910
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38277 10964 6947 9322	1306 2945	3 27			.930 .976

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					F1	Flor	F1	F1	Flor	1545	1490	1864	1726	2278
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag- Patient 1- Smaller	Flag- Patient 2- Smaller	Flag- Patient 3- Smaller	Flag- Patient 4- Smaller	Flag- Patient 5- Smaller	Globally Normalized - Patient 1- Smaller	Globally Normalized - Patient 2- Smaller	Globally Normalized - Patient 3- Smaller	Globally Normalized - Patient 4- Smaller	Globally Normalized - Patient 5- Smaller
168	PN148	Connexin 43	S367	Gap junction alpha-1 protein	0, 0	Smaller 0, 0	0,0	0, 0	0,0	852	585	Smaller 1551	1838	Smaller 1345
544 146 465	NK116-4 PK165 PK893	mTOR CDK6 MAPKAPK5	Pan-specific Y13 T186	Mammalian target of rapamycin (FRAP) Cyclin-dependent protein-serine kinase 6 MAP kinase-activated protein kinase 5	0, 0 0, 0 0, 0	0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	17900 360 12740	18402 162	23303 401 10550	27726 421 10277	20821 473
681 800	PK132 NK172-3	PKR1 Src	T446 Pan-specific S142	MAY kinase-acrivated protein kinase 5 Double-stranded RNA-dependent protein-serine kinase Sic proto-oncogene-encoded protein-tyrosine kinase	0, 0	0,0	0,0	0, 0	0,0	12740 295 507	513 1493	873 504	525 604	480 1474
321 496 156	PN196 PK052 PK578	GATA1 MEK4 CNr1	S142 S257/T261 S317	Erythroid transcription factor MAPK/ERK protein-serine kinase 4 (MKK4) Cherkmoint rontein-serine kinase 1	0.0	0, 0 0, 0 0, 0	0.0	0.0	0, 0 0, 0 0, 0	518 1826 2220	398 1649 2086	852 2302 3918	1125 1582 2606	858 2309 3819
672 742	PK578 NK140 PN070 NK114	PKCt Rb	Pan-specific T821	Checkpoint protein-senne kinase 1 Protein-senine kinase C theta Retirioblastoma-associated protein 1	0, 0 0, 0 0, 0	0,0	0,0	0, 0 0, 0 0, 0	0,0	764 1173	573 1812	3918 388 32	2606 574 886	539 1754
539 387 626	NK114 NK075-6 NN141-1	MST2 IkB Kinase alpha PDI	Pan-specific	Mammalian STE20-like protein-serine kinase 2 (KRS1) Inhibitor of NF-kappa-B protein-serine kinase alpha (CHUK) Protein disulfide-isomerase	0, 1 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	1, 1 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	7518 4448 6533	8255 3582 7566	14311 3627 9450	13513 2648 9502	9939 4504 7846
604 333 72	NK122 PK648 PK003	PAK1 GSK3a BMX (Etk)	Pan-specific Pan-specific Pan-specific T19+pS21	Protein disultriae-isomerase p21-activated kinase 1 (alpha) (serine/threorine-protein kinase PAK 1) Glycogen synthase-serine kinase 3 alpha	0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	404 8087	1022 8864	9450 442 7292	9502 272 5920	7846 570 10690
72 630 114	PK003 NN180-1	BMX (Etk) PDK2 Cdc25A	Y40 Pan-specific Pan-specific	Bone marrow X protein-tyrosine kinase Pyruvate dehydrogenase kinase isoform 2 Cell division cycle 254 phosphatase	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0		0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	77 4406 9875	52 4199 7598	155 4849	140 5603 10340	132 5963 6149
602 122	NN180-1 NP038-2 NP008 NK024 PP003	PAC1 Cdr2l 5	Pan-specific Pan-specific	Cell division cycle 25A phosphatase Dual specificity MAP kinase protein phosphatase Cell division cycle 2-like protein-serine kinase 5	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	1526 1168	1921 886	11609 1879 2009	1587 1259	6149 2993 2105
715		PTEN Fos	9380/9382/9385 Pan-specific T183/Y185	Phosphatdylinositol-3.4.5-trisphosphate 3-phosphatase and protein phosphatase Fos-c FBJ murine osteosarcoma oncoprotein-related transcription factor	0.0	1,1			0,0	1175 3503	1183 2911	706 996	1273 1479	895 1501
426 667 88	PK035-2 PK085 PK555	Fos JNK 1/2/3 PKCh CaMK2a	T183/Y185 T655 T286	Fos-c FBJ murine osteosarcoma oncoprotein-related transcription factor. Jun N-seminus protein-serine kinase (stress-activated protein kinase (SAPK)) 17. Protein-serine kinase C eta. Calcium/calmodulin-dependent protein-serine kinase 2 alpha.	1, 1 0, 0 0, 0	0, 0	0, 0	1, 1 0, 0 0, 0 0, 0	0, 0 0, 1 0, 0	317 2555 8862	586 2175 7741	858 3190 6936	552 2992 8225	543 4100 6808
580	NK248-3	p38b MAPK CDK2 B-Raf			0, 0	0,0	0,0	0, 0	0,0	7659	8934	7798	4802	6369
136 74 867 285	NK026-6 NK156-4 NK253-3 PK625	B-Raf WNK2 ERK5	Pan-specific Pan-specific Pan-specific T219+Y221	Cyclin-dependent protein-serine kinase 2 RafB proto-oncogene-encoded protein-serine kinase Serine/fitnecrine-protein kinase WMK2 Extracellular regulated protein-serine kinase 5 (Big MAP kinase 1 (BMK1))	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	0, 0	0,0	1427 13835 11768 5385	1266 11664 9806 3281	1964 6747 14972 5815	1403 12662 16054 5168	2599 9832 13102 4891
658	NK136-2	PKCe PKCI	Pan-specific T555/T563	Extracelular regulated protein-senine kinase 5 (Big MAP kinase 1 (BMK1))  Protein-senine kinase C epsilon  Protein-senine kinase C lambdallota	0, 0	0,0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	1373 1162	975 359	1349 1297	1557 1148	2090 2097
669 167 288 448	PK087 PN020 PN174	Cofflin 2 Earin Krs-2	S3 TC07	Coffin 2 Cytovilin 2 Mammalian STE20-like protein-serine kinase 1 (KRS2)	0.0		0.0		0.0	2149	1255	2762 252	3069 281	3379 194
500	PN174 NK113-3 NK104-5 PN091 NK063-3	MEK5	Pan-specific Pan-specific S400 Pan-specific	MAPK/ERK protein-serine kinase 5 (MKK5)	0, 0	0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0	1123 8497	1250 8465	1394 7675	1514 5548	2063 5765
827 305 415 307	NK063-3 NK085-2	Tau FGFR2 JAK2 FGFR3	Pan-specific Pan-specific Pan-specific	Microtubule-associated protein tau Fibroblast growth factor receptor-tyrosine kinase 2 (BEK) Janus protein-tyrosine kinase 2	0, 0	0, 0	0,0	0, 0	0, 0	2249 18448 48320	927 14161 55677 8486	2007 20692 47720	1994 19426 60269	1711 11142 74340
124	NK085-2 NK236-2 NK026-3 NK026-3 NK052 NK121-2	CDK2	Pan-specific	Fibroblast growth factor receptor 3 Cyclin-dependent protein-serine kinase 2	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	48320 12456 1054 7792 7570	744	12311 793	9130 806	6495 538
351 582 574		HO1 p38d MAPK p38a MAPK	Pan-specific Pan-specific Pan-specific	Heme oxygenase 1 Mitogen-activated protein-serine kinase p38 delta (MAPK13) Mitogen-activated protein-serine kinase p38 alpha	0, 0	0, 0	0,0	0,0	0,0	3881	7942 5261 3873	11366 4736 3251	10757 2947 1747	9264 3656 2725
323	PN034	GFAP PDK1	S8 Pan-specific	Gliaf förliary acidic protein Pyruvate dehydrogenase kinase isoform 1 Cell division cycle 25A phosphatase	0, 0 0, 0 0, 0 0, 0	0.0	0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 1, 1 0, 0	0.0	6247	2662 10537	4947 7752	6083	6228 7995
115 63 55 431	NN179-2 NP038-3 NN006 PK530	Cdc25A Bcl2 AurKB	Pan-specific Pan-specific S227	Cell division cycle 25A phosphatase B-cell lymphoma protein 2 alpha Aurora Kinase B (serine/threonine protein kinase 12)	0, 0	0,0	0,0	0, 0 1, 1	0,0	4175 799 17174	2620 493 15629	5349 1541 13328	5763 2022 9785	3641 1145 11556
431 505	PK530 NK189-2 NK107-3	INK2	Pan-specific Pan-specific	Luc M terreforus protein carina kinana (etrans activated protein kinana (CADVI), 2	0, 0	0, 0	0,0	0, 0	0, 0	30795	15629 26570 1875	31030	9785 27101 2056	38880 2537
505 339 359	NK107-3 NK107-3 NN169 PN042-3 NK056-4 PK151	MEKK-NT HDAC4 Hsp25 ERK2	Pan-specific	OBSTRUCTURE AND ADMINISTRATION OF THE STATE	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	2164 577 740	1875 414 577	2400 777 753	2056 839 768	814 665
277 297 797		FAK SPHK1	Pan-specific Y576+Y577 Pan-specific	Exhibitionian regulation protein-serine kinase 2 (942 kee* kinase) Focal adhesion protein-tyrosine kinase Sphingosine kinase 1		0,0	0,0		0,0	1379 1604	33266 505 1315	1342 2784	26484 1283 1999	1486 4113
555 152	NN070 NK034	NFkappaB p50 Chk1	Pan-specific Pan-specific	NF-kappa-B p50 nuclear transcription factor Checkpoint protein-serine kinase 1	0, 0	0, 0	0,0	0, 0	0,0	652 2044	1594 2964	417 1547	573 1594	621 2708
266 247 404	NK055-3 PN193 PK033	ERK1 eIF4G IR/IGF1R	Pan-specific S1232 Y1162/Y1163	Extracellular regulated protein-serine kinase 1 (p44 MAP kinase)  Eukaryotic translation initiation factor 4 gamma 1  Insulin receptor / Insulin-like growth factor 1 receptor	0, 0	0, 0	0, 0	0, 0	0,0	19379 972 107	496 635	16064 1394 606	19764 1497 591	12377 2031 344
205	NP047-2 NN060-2	DUSP10 Hsp70	Pan-specific Pan-specific	Dual specificity protein phosphatase 10 Heat shock 70 kDa protein 1	0, 0	0, 0	0,0	0, 0	0, 0	3511 8242	3273 4407	3795 10684	4347 13571	3896 9606
790 142 480	NK251-1 NK028-4 PK048-2	SNF1IK CDK5 MEK1	Pan-specific Pan-specific T386	Serinethreonine-protein kinase SIK1  Cyclin-dependent protein-serine kinase 5  MAPK/ERK protein-serine kinase 1 (MKK1)	0, 0	0, 0	0,0	0,0	0,0	34 1041 2523	9 994 1680	32 1070 1979	193 1281 2152	2781 2487
433	NK197-2	JNK3	Pan-specific	Jun N-terminus protein-serine kinase (stress-activated protein kinase (SAPK0)) 3 SH2 domain-contairing transforming protein 1 Serine/threcnine-protein kinase TBK1 MAP kinase phosphatase 1 (CL100, VH1)	0,0	0,0	0,0 0,0 0,0 0,0	0, 0	0,0	10533	13780 2025 2506 12431	12972	14616	18588 1263
834 204 137	NK220-2 NP006-3 NK026-7	TBK1 DUSP1 (MKP1) CDK2	Pan-specific Pan-specific Pan-specific	Serine/threonine-protein kinase TBK1 MAP kinase phosphatase 1 (CL100, VH1) Cyclin-dependent protein-serine kinase 2	0, 0	0,0	0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	2158 15922 1154	2506 12431 1292	2640 16908 1855	1837 8165 1373	4058 9195
466 389	PN050-1 NN064-2 PK156 NK055-1	MARCKS IkBa	S152/S156 Pan-specific	Myristoylated alarine-rich protein kinase C substrate Inhibitor of NF-kappa-B alpha (MAD3)	1, 1	0, 0	0, 0 0, 0 0, 0 0, 0	0,0	0,0	275 868	312 2046	38 605	1179	557 1545
597 264 706	PK156 NK055-1 NK048-6	p70 S6K ERK1 PRKDC (DNAPK)	S424 Pan-specific	Ribosomal protein S6 kinase beta-1 Extracellular regulated protein-serine kinase 1 (p44 MAP kinase) DNA-activated protein-serine kinase	0, 0	0,0	0,0	0, 0	0,0	631 14798 24730	384 11884 31387	930 11396 34774	1033 13801 32314	733 11950 38790
93 854	NK022	CaMKK VEGFR2	Pan-specific Pan-specific Y1214 Pan-specific Pan-specific	Calciuminalmodulio, dependent protein, serine kinase kinase		0, 0		0.0		4212 323	2905 487	4404 598	4247 698	4100 1452
586 450	PK133 NK059-1 NK092-2	p38g MAPK Lok		Vascular endothelial growth factor receptor-tyrosine kinase 2 (Fik1) Mitogen-activated protein-serine kinase p38 gamma (MAPK12) Lymphocyte-specific protein-tyrosine kinase	0, 0 0, 0 0, 0	0, 0	0,0	1, 1 0, 0 0, 0 0, 1	0, 0 0, 0 0, 0	1335 1152	657 1842	1483 1313	2044 1361	1884 2280
158 392 836	NK035 PN168 PK829	Chk2 lkBe TEC	Pan-specific S22 Y519	Checkpoint protein-serine kinase 2 NF-kappa-B inhibitor epsilon Tyrosine-protein kinase Tec	0, 0 0, 0 0, 0	0, 0	0,0	0,0	0, 0	1253 396 1230	930 204 950	1327 511 1228	1134 425 1964	1387 350 1271
454 508	PK149 NK110-2 PK522	Lck Met	Y394 Pan-specific S377	NF-kappa-B inhibitor epsilon Tyrosins-protein kinase Toc Lymphocyte-specific protein-tyrosine kinase Hepatocyte growth factor (HGF) receptor-tyrosine kinase	0,0	0, 0	0,0	0, 0	0, 0	1695 20733	1262 19167	2043 21165	2147 19226	2372 13429
32 824 616	NK175-5 PK756	AMPKa2 TAK1 PCTK2	Pan-specific S180	5-AMP-activated protein kinase catalytic subunit alpha-2 TGF-beta-activated protein-serine kinase 1 Cet division protein kinase 17	0, 0 0, 0 0, 0	0,0	0,0	0,0	0,0	10991 731 5788	8236 1070 4934	10778 1226 5209	994 5061	13069 1251 6237
191 757	NND32 NK163-3 NK236-3	Cyclin G1	Pan-specific Pan-specific Pan-specific	Cyclin G1 Orosomucoid 1 receptor-tyrosine kinase	0, 0	0,0	0,0	0, 0	0, 0	2210 8361 4178	2165 11301 2942 1766 109	3295 7222	2448 6135	2174 5934
308 529 481	PK045-PN007	FGFR3 MLC MEK1 + R23/NPM1	Pan-specific S19 S217+S221	Fibroblast growth factor receptor 3 Myosin regulatory light chain 2, smooth muscle isoform B23 (nucleophosmin, numatrin, nucleolar protein NO38)	0, 0	0, 0	0,0	0,0	0,0	4178 979 138	2942 1766	4769 1328 160	4089 1237 221	3970 1853 136
133	PK565 PN509 NP015	CDK11A eEF1A1	T583 Y141	B23 (Indecoprosimit, Furnishin, industrial Protein NO36) Cell division cycle 2-like 2 protein kinase Elongation factor 1-alpha 1	0, 0	0,0	0,0	0, 0	0,0	7124 3009	5619 3730 7315	6602 4199	5215 3039	6725 5093
694 229 341	NP015 NK052-4 PN188	PP2B/Aa EGFR	Pan-specific Pan-specific S498	Protein-serine phosphatase 2B - catalytic subunit - alpha isoform Epidermal growth factor receptor-tyrosine kinase	0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0,0	8908 37537	7315 33667 718	9417 26425 1612	6587 28324 1931	6472 29833 2724
254 262	NK054-2 NK235-1	HDAC5 ErbB2 ErbB4	Pan-specific	Historie deadesylase 5 ErbB2 (Neu) receptor-tyrosine kinase Receptor tyrosine-protein kinase erbB-4	0, 0	0,0	0,0	0, 0	0,0	4582 6860 5042	3522 6627	1581 4808	1830 4283	2734 1540 5463 3658
758 822 151	NK163-4 NN171 PK575	Ros Synapsin 1 CDK9 CDK1	Pan-specific Pan-specific Pan-specific T186	Receptor tyrosine-protein kinase ert.B4  Orosomucoid 1 receptor-tyrosine kinase  Synapsin 1 isoform la	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	5042 1440 5242	3769 1208 5862	3158 1183 4359	3897 1778 4173	3658 1634 5143
126 278	NK025-1	CDK9 CDK1 ERK3	Pan-specific Pan-specific	Cyclin-dependent protein-serine kinase 9  Cyclin-dependent protein-serine kinase 1  Extranelli far renulated protein-serine kinase 3	0,0	0,0	0,0	0,0	0,0	1833 1551	1453 1728	1827	1726	5143 1271 2027
579 189 187	NK248-2 NK031 PN190 NK227-2 NN059-2	p38b MAPK	Pan-specific Pan-specific S147	Cyclin E1  Cyclin B1	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0,0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	7875 7321 385	5951 5410 186	7370 7093 296	4216 4707 538 17512	5520 3832 666
187 458 367	PN190 NK227-2 NN059-2	Cyclin E Cyclin B1 LKB1 Hsp60	Pan-specific Pan-specific	Cyclin B1 Serine/threonine-protein kinase 11 Heat shock 60 kDa protein 1 (chaperonin, CPN60)	0, 0	0, 0 0, 0 0, 0	0,0	0,0	0, 0 0, 0 0, 0	365 17263 16860	186 10722 12153	296 9608 20415	538 17512 18908	666 11081 19258
214 119 59	NP030-4 NP003 NN000	DUSP3 Cdc25C	Pan-specific Pan-specific Pan-specific		0, 0	0,0	0,0			4734 1570 619	9422 1805	6116 1457	5045 1563 807	4090 2086 1100
59 282 432	NN000 NK206-4 NK197	Bak ERK5 INK3	Pan-specific Pan-specific Pan-specific	Dual specificity protein phosphatase 3 Cell division cycle 25C phosphatase Bct2 homologous artagonist/kiler (BCK2L7) Extracebillar regulated protein-aerine kinasa 5 (Big MAP kinase 1 (BMK1)) Jun N-terminus potein-serine kinase (stress-activated protein kinase (SAPK0)) 3	0, 0	0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	619 11486 3014	1184 7635 4264	990 8249 3607	807 10950 3046	1100 7840 3237
234	PK123	JNK3 EGFR COT	Y1110	Jun N-terminus protein-serine kinase (stress-activated protein kinase (SAPKb)) 3 Epidermal growth factor receptor-tyrosine kinase Osaika thyroid oncogene protein-serine kinase (Tpl2)	0, 0	0, 0	0.0	0.0		988	585	1030	1371	1552
171 287 128 445	NK042-2 PN198 PK563	Estrongen Receptor CDK1	Pan-specific S104 Y19	Estrogen receptor alpha Cyclin-dependent protein-serine kinase 1	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	0, 0	0, 0	4152 1289 1603	4164 598 1596	5206 1792 2781	4535 1813 2305	5709 1772 3198 1014
2	PK037 PN001 NK248-1	Kit 4E-BP1 n38h MAPK	Y730 S65 Pan-specific	Mast/stem cell growth factor receptor Kit  Eukaryotic translation initiation factor 4E binding protein 1 (PHAS1)  Mitronen,activated motein,serine kinase n/8 heta	1, 0	0,0	0,0	1,0	1.0	1266 805 1696	155	1163 110 3419	902 93 1970	/8
578 324 195 627	NK248-1 PN178 PK591 NK126-2	p38b MAPK GluR1 DDR1 PDK1	Pan-specific S849 Y796+pY797	Mitogen-activated protein-serine kinase p38 beta Glutamate receptor 1 Epithelial discoldin domain-containing receptor 1	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	1696 1249 3501	3058 698 2518 1982	3419 1975 4646 1066	1970 1907 2905 1109	2701 1100 3386
627	NK126-2	PDK1	Pan-specific	3-phosphoinositide-dependent protein-serine kinase 1	0, 0	0,0	0,0	0, 0	0,0	995	1982	1066	1109	3386 1979

Average - Smaller	S. Dev Smaller	%.S.Dev. Smaller
1234	457	37
21630 363	3604	17
10401	107 1505	
537 916	187 465	14 35 51
750 1934	261 314	35 16
2930	786	16 27
568 1131	120 651	21 58
10707 3762	2743 680	26 18
8179		14
542 8170	258 1592	48 19
111 4944	40 601	36 12
4944 9114	601 1970	12 22 27
1981 1485 1046	529 483 212	33 20
1046 2078	212 958 172	
571 3002	172 652	30
7714		22 10
7714 7113 1732 10948	1413 495	20 29 23
10948		17
13141 4908 1469	2229 868 364	17 18 25
1469	364 552 753	25 46
2523 190	71	37
1469 7190	325 1288	22 18
1778 16774	458 3570	26 21
16/74 57265	3570 9739 2300	21 17
9776 787	2300 165	24 21
9424 4834	1445 1589	15
3095 5234	800	26 26
8826	1060	12
4310 1200	1141 539	26 45
13494	2670	20
2206	237	11
684 701	164 71	24 10
30561 1199	5740 353	19 29
2363 771	1005 419	43 54
2171	575	26
16289 1278	2929 517	18 40
457 3764	204 384	45 10
9302	364 3011 66 681	32 106
1433	681	48
14098	2627	15 19
17/4 2840 12524	762 3489	26 29 28
12524	3489 658	28 38
245	193 508	
742	228	79 41 31
12766 32399	1305 4611	10
3973 712	543 391	14 55
1481	486	33
1590 1206 377 1328	415 162 101	26 13
	338	25
4004	388 2774 1719 188	20 15 17
18744 10380	1719	17
1055 5446	188 492	18 9
2458 7791	431 1958	18 25
3990 1433	592 329	15
1433	38	23 25
6257 3814	780	20
7740 31157	1208 3979	16 13
1598	713	45 47
2611 5608 3905	1228 1002 622	18
1448 4956	233 618	16 16 12
4956 1622 1790	618 223 155	12 14
1789 6186	1314	9 21
5673 410	1351 171	24 42
13237 17519	3424 2918	26
5881	1888	32
940 9232 3434	226 204 1642 466	13 22
9232 3434	1642 466	18 14
1105 4753	335	30 13
4/53 1453 2297	470 635	32
2297 1202	635 263	28 22
248 2569	280 648	25

					Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
					1597	1688	1753	1/45	1040
Flag- Patient 1- Bigger	Flag- Patient 2- Bigger	Flag- Patient 3- Bigger	Flag- Patient 4- Bigger	Flag- Patient 5- Bigger	Globally Normalized - Patient 1- Bigger	Globally Normalized - Patient 2- Bigger	Globally Normalized - Patient 3- Bigger	Globally Normalized - Patient 4- Bigger	Globally Normalized - Patient 5- Bigger
0, 0	0, 0	0, 0	0, 0	0, 0	614 19306	1175 17571	1514 22024	1469 22587	1406 26725
0, 0	0, 0	0, 0	0, 0	0, 0	183 12378	314 11383	370 10676	428 10978	520 6449
0, 0	0, 0	0, 0	0, 0	0, 0	398 806	454 1356	704 764	635 748	483 883
0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	257 2591 2006	380 2653 1928	1297 2030	1051 1370 4169	747 955
0, 0	0, 0	0, 0	0, 0		491	535	2824 735 1745	535	2626 520
0, 1	0, 1	0, 0	1, 1	0, 0	1215 9916	753 9400	1745 12473	881 10593	1015 10719
0, 0	0, 0	0, 0	0, 0	0, 0	3534 7526	5019 7391	3687 7841	3706 9227	2704 8550
0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0	431 11552	1037 8580	456 7739	343 4587	418 7922
0, 0	0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	67 4157 7590	98 4498	141 5356	95 5659 9319	148 4756
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0	7590 1478 1578	9313 2152 1182	5356 11083 1794 1309	9319 2297 1998	4756 7700 2060 1264
0, 0	0, 0	0, 0	0, 0	0, 0	1578 880	1182 702	1309 1491	1998 864	1264 1226
0, 0	0,0	0, 0	0, 0	0,0	2983 549	2459 428	1189 638	2124 743	1496 458
0, 0	0, 0	0, 0	0, 0	0, 1	2925 9031	3116 8334	2979 7037	2845 9089	2916 4411
0, 0	0,0	0, 0	0, 0	0,0	9772 1253	7770 1815	6225 2043	5890 2019	5263 1372
0, 0	0, 0	0, 0	0, 0	0, 0	1253 11975 9840	10878 11810	2043 6825 15176 4309	2019 12975 15206	11053
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0	9840 5414 1238	3981 1372	4309 1504	15206 6241 1486	12407 4112 1599
0, 0	0,0	0, 0	0, 0	0,0	678	473 1983	914 2882	2129	1750 2612
0, 0	0,0	0, 0	0, 0	0, 0	133 1247	169 2134	208 1570	253 1244	168 990
0, 0	0, 0	0, 0	0, 0	0, 0	6987	7361 930	8550	6666	5568 2866
0, 0	0,0	0, 0	0, 0	0,0	1387 16352 42998	930 17163 47565	1366 20997 59731	2128 11485 45759	2866 15502 80921
0, 0	0, 0	0, 0	0, 0	0, 0	8009 808	9864 991	10920 906	9507 586	8976 514
0, 0	0,0	0,0	0, 0	0,0	8563 6138	7756	9300 4800	9807	10127
0, 0	0,0	0, 0	0, 0	0,0	4844 2671	3429 4881	2803 5336	1621 4274	2242 8078
0, 0	0,0	0, 0	0, 0	0,0	11351	10673 3647 615	7979 5526	6179 4343 671	6301
0, 0	0,0	0, 0	1, 1	0,0	3406 465			4343 671	3820 2409
0, 0	0, 0	0, 0	0, 0	0,0	29800 1762	14107 24445 1929	11531 28329 2630	23097 2754	13161 42277
0, 0	0,0	0, 0	0, 0	0,0	434 507	19/29 522 655	701	680 592	936 741
0, 0	0,0	0, 0	0, 0	0,0	29592	31623	24214 1131	26059 1504	34454 1418
0, 0	0, 0	0, 0	0, 0	0,0	788 1998	883 1304	2536	1504 3097	2346
0, 0	0, 0	0, 0	0, 0	0, 0	1061 2343	982 3049	422 1772	690 1168	522 2015
0, 0	0, 0	0, 0	0, 0	0, 0	14223 551	17504 955	14738 1318	15027 1361	16072 1898
0, 0	0, 0	0, 0	0, 0	0, 0	127 3146	625 3425	534 4110	547 4053	341 3167
0, 0	0,0	0, 0	0, 0 1, 1 0, 0	0,0	5289 12 877	3425 5979 13	8637 15	4053 8103 236	16175 20
0, 0	0, 0	0, 0	0, 0	0, 0	877 2234	1187 2353	1709 2067	1368 2064	1658 1546
0, 0	0,0	0, 0	0, 0	0,0	12170	11922	12256 1994	13455 1496	17055 983
0, 0	0, 0	0, 0	0, 0	0,0	1507 14950 1212	2688 13322	2712 12003	3043 8751	2554 10135
	0,0		0, 0	0,0	1212	1938	1859	1928	1209
0, 0	0, 0	0, 0	0, 0	0, 0	190 941 423	78 1773 434	154 1213	48 864 1117	687 1099
0, 0	0, 0	0, 0	0, 0	0, 0	13028 19366	11192 28254	8599 37522	15713 30994	11660 36461
0, 0	0,0	0, 0	0,0	0,0	3932 351	3494 516	3218 450	5144 1231	2907
0, 0	0,0	0, 0	0, 0	0,0	736 1417	699 1625	1488 1358	1231 1501 1610	2534 1445
0, 0	0, 0	0, 0	0, 1	0,0	754 161	1042	1321	905	1634
0, 0	0,0	0, 0	0, 0	0,0	731	824 4204	427 1447 1902	496 1682 2012	459 1533 2327
0, 0	0,0	0, 0	0, 0	0,0	1284 14566 9929	1381 19483	19840	15821	2327 18077 13564
0, 0	0,0	0, 0	0, 0	0, 0	9929 814 5790	8490 1102	10823 1289 6370	5689 786 4097	13564 932 3478
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0		2059	2416	6370 3361 4194		3478 1729 3779
0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	12473 3358	8839 3313	4194 5220	1901 7042 3201	3779 3502
0, 0	0, 0	0, 0	0, 0	0, 0	1326 77	1441 158	1468 141	1377 194	1063 142
0, 0	0, 0	0, 0	0, 0	0, 0	6685 3836	5979 3191	7263 3780	4160 2835	5012 4084
0, 0 0, 0 0, 0	7638 31353 656	8004 37879 1060	8539 20819 1602	6335 24355 1730	5438 30185 2366				
0, 0 0, 0 0. 0	0, 0	0, 0 0, 0 0. 0	0, 0	0, 0	656 4081 7739	1060 2566 5440	1602 1192 4828	1730 2790 2736	2366 1471 5219
0, 0	0,0	0, 0	0, 0	0, 0	7739 3560	5440 4204	4828 2891	3841	5219 3544
0, 0	0,0	0, 0	0, 0	0,0	703 6339	985 5345	1832 4282	1200 2480	1969 4429
0, 0	0, 0	0, 0	0, 0	0, 0	1459 1635	2221 1804	1491 1992	1289 1559	1026 1257
0, 0	0, 0	0, 0	0, 0	0, 0	5442 5783	5547 6529	5956 6393	5937 4054	5628 3381
0.0	0.0	0, 0	0, 0	0,0	170 13574	233	388 7612	310	789 10578
0, 0	0,0	0, 0	0, 0	0,0	14023	13243 14590 5456	16462	15934 15027 5432	20509
0,0	0,0	0, 0	0, 0	0,0	7521 1467 588	2053 1033	4951 1996 921	985 875	1313 897
0, 0	0,0	0, 0	0, 0	0,0	9000	9141	7085	11195	5936
0, 0	0, 0	0, 0	0, 0	0,0	4800 683	809	2951 1340	1693 744	2221 1487
0, 0	0, 0	0, 0	0, 0	0, 0	4818 708	3117 642	4393 1839	5239 1474	4209 1982
0, 0	0, 0	0, 0	0, 0 1, 0	0,0	2083 1095	1038 1272	2781 1220	3206 1326	1394 581
1, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	1, 0 0, 0 0, 0	164 2509 733	313 3289 1005	143 2320 1598	82 1833 1356	431 1778 1632
0, 0	0, 0	0, 0	0, 0	0,0	733 3323	1005 2865	1598 3572	1356 3285	1632 2401

Average - Larger	S. Dev Larger	%S.Dev Larger	%CFC - Average Larger from Average Smaller	Student 1 test p value
1236	332	27	omaner	.994
21643 363 10373	3127 113	14 31		.995 .992 .953
10373	2044 115 227	20		.953
535 911		25	-1	.963 .978
746	392	53	-1	.975
1920 2909	727 87 347	25	-1	.970
563 1122	87 347	16 31	-1	.970 .968 .986
10620	1042	10	-1	.934
10620 3730 8107	742 689	20 8	-1	.961
537	253	47	-1	.900
8076 110	2220 30	27 28	-1	.932
400E	551	11	-1	.824
9001 1956 1467	551 1282 290 297	14 15 20	-1	.824 .891 .931 .955
1467 1033	297 286	20 28	- 1	.955 .958
2050	647 116	32	-1	.903
563 2956	116 91	32 21 3	-1	.932
2956 7580	91 1749	23	-2	.902 .830
6984 1700	1620 329	23 19	-2	.868
1700 10741	329 2096 2064 876	20	-2	.929 .712 .721 .849
12888	2064 876	16 18	-2	.721
1440	124	9	-2	.856
1189 2472	640 492	54 20	-2	.934
186	41 394	22 27	-2	.862 926
7026	969	14	-2	.769
1735 16300	684 3054	39 19	-2	.911
55395	13988	25 10	3	.721 805
9455 761	963 183	10 24	-3	.805 .797
9111	859 905	9	-3	.599 .723
4673 2988 5048	1105 1763	19 37 35	-3	.723 .717 .875
5048	1763 2161	35 25	4	.875
4148	754	18	4	.723
1155	746 2347	65 18	4	.919
12968 29590 2111	2347 6800	18 23	4	.432 .368
654	497 172	24 26 18	4	.766
654 670 29188 1145	120 3697	18	4	.692
1145	282	25	-5	.691 .765
2256 735	594 250	26 34	-5 -5	.832 840
735 2070	623	34 30	- 5	.840 .628
15513 1217	1164 449	8 37	-5	.708 .690
435	180	41	-5	.244
3580 8836	421 3878	12 44	-5 -5	.383
59 1360	88 308	149	- 5	.811 .814
2053	276	13	-5	.693
13371 1680	1916 457	14 27	-5 -5	.907
2501 11832	522 2207	21 19	-5	.774
1629	343	21	-6	.834
231	234 321	101 27	-6	.848 .729
700	288 2331	41	-6	.720
12038 30519	2331 6543	19 21	-6	.410
3739 669	779	21 47	-6	.619 .834
1392 1491	669	48 7	-6 -6	.715
1491	669 107 313	7 28	-6	.715 .654
353	136 389	39 31	-6	.724
353 1243 1781	389 393	31 22 11	-6 -6 7	.591 .226
17517	2013 2600	11 27	-7	.537
985 5084	189 1102	19 22	-7 -7	.439 .633
5084 2293	1102 580	22 25	-7 -7	.633
2293 7265	580 3201 757	25 44 20	-7	.333 .716
3719 1335	757 145	20	-7	.659
1335 142	145 38	11 26	-7 -7 -7	.659 .596
3545	1119 461	19 13	-7	.376 .427
7191	1139	16	-7	.194
28918 1483	5903 586	20 40	-7 -7	.321 .428
2420 5192	1032 1594	43 31	.7 .7	.584
3608	431	12	-8	.404
1338 4575	488 1281	36 28	-8	.698 .449
1497	398	27	-8	.609
5702	246	4		.529
5228 378	1277 218	24 58	- 8	.362 .687
12188 16122	2850 2337	23	-8	.887
16122 5407	2337 1239	14 23	-8	.360
1559	414	27	- 8	.608
863 8471	148 1816	17 21	-8	.176
3148 1013	1149 333	37 33	-8	.633 .621
			- 8 - 8 - 9	
4355 1329 2100	714 559 814	16 42 39	-9	.432 .442
1099	814 270	25	- 9	.550
227	127	56	.9 .9	.904
2346				
2346 1265	548 348 412	23 27	-9	.620 .390

Block	Row	Column	Refseq	Uniprot Link
5	6	7	NP_000156.1 NP_004949	P17302
10	6	7	NP_004949 NP_001250	000534
5 8	10	5	NP_003659.2 NP_002750	Q8/W41
11	10	7	NP_002750 NP_005408	P19525 P12931
12	,	10	NP_002040.1 NP_003001 NP_001265	P15976 P45985
6	6	9	NP_003001 NP_001265 NP_006248	014757
14	9	3	NP_006248 NP_000312	P06400
4	9	4	NP_006272 NP_001269	Q13188 Q15111
6	9	5	NP_001269 NP_000909.2	P07237
15	8	2	NP 063937	Q13153 P49840
14 6	6	6	NP_001712 NP_002602	P51813 Q15119
4 7	7	1 5	NP_001780.2	P30304
3	6	8	NP_003709	Q14004
15 3	10	3	NP_000305 NP_005243	P01100
3	8	8	NP_002741 NP_006246	P45983 P24723
5	6	9 5	NP_006246 NP_057065.2 NP_002742.3	Q9UQM7
7	6	11	NP_002742.3 NP_001789	P24941
9	6	1 11	NP_004324 NP_001269323.1	P15056 Q9Y3S1
9	10 7	11 7	NP_001269323.1 NP_002740.2	Q13164
9	9	9 7		P41743
8	6 7	7 8 7	NP_002731 NP_068733 NP_001104547.1 NP_006273	Q9Y281 P15311
2	8	7	NP_006273 NP_660143	Q13043
6	10	8	NP_005901	P10636
8	8	1 5	NP_005901 NP_000132.3 NP_004963	P21802 060674
4	8	2	NP_000133.1 NP_001789	P22607
2	8	1	NP_002124 NP_002745	P09601
8	9	4	NP_001306	Q16539
14	7 9	11 5	NP_002046 NP_001265478.1	P14136 Q15118
8 14	7	1 4	NP_001780.2 NP_000624	P30304 P10415
14 15	6	2 8	NP_004208 NP_002744 XP_042066	Q96GD4
7	8	9	XP_042066	Q13233
14	8	2	NP_006028.2 NP_003521	P56524 P84243
9	7	5 10	NP_002736 NP_005598	P28482 005397
11	10	- 6	NP 892010	Q9NYA1
14	8	10	NP_003989 NP_001265 AAA36142.1	P19838 O14757
5	7	3	AAA36142.1 NP_004944	P27361 Q04637
12	8	8	NP_000866 NP_009138.1	P06213
5	7	10	NP 005336	P08107
16 11	10 7	10	NP_775490.2 NP_004926	Q00535
13 6 4	8	3	NP_002746 NP_002744.1 NP_003020	Q02750 P53779
14	10 10 7		NP_003020 NP_037386	P29353 Q9UHD2
8	7	9 5	NP_004408.1 NP_001789	P28562
9	8	5	NP_002347 NP_065390	P29966
8	9	9	NP 003152	P25963 P23443
13	7 10	2	AAA36142.1 NP_001075109.1	P27361 P78527
9	6	6	NP_006540	Q8N559
5	9	3	NP_002960	P53778
10	oo 60	10	NP_005347 NP_009125	P06239 096017
4 6	8	5 10	NP_004547.2 NP_003206.2	000221 P42680
10	8	7	NP_005347 NP_000236.2	P06239
15	6	11	NP_006243.2	P54646
6 15	10	7 8	NP_663306 NP_001163935.1	Q43318 Q00537
8	7	2	NP_001163935.1 NP_004051 NP_002935	P51959 P08922
8	8	2	NP_000133.1	P22607
10	8	9	NP_291024 NP_002511	P19105 P06748
15 15	6 7	10	NP_076916.2 NP_001393.1	09U088 P68104
3	9	10	NP_000935	Q08209
10	7	9	NP_005219 NP_001015053.1 NP_004439	Q9UQL6
14	7	7	NP_001036064.1	Q15303
5 14	10	3	NP_002935 NP_008881	P08922 P17600
14	6	8	NP_001252.1 NP_001777	P50750
1	7	6	NP_001777 NP_002739 NP_002742.3	Q16659
4	7	5 2 1	NP_002742.3 NP_001229 NP_114172	P24864
9	7 8 7	1 3 10	NP_114172 NP_000446.1 NP_002147	P14635 Q15831
1 16	7	10	NP_002147 NP_004081.1	P10809 P51452
15	6	7 3	NP_001781 NP_001179	P30307
9	7	6	NP_001179 NP_620602 NP_002744.1	Q18611 Q13164
12	10	5	NP 005219	P53779 P00533
1	6 7	8	NP_005195 NP_000116.2 NP_001777	P41279
11	6	9	NP_000116.2	P06493
14	8	5	NP_006566 NP_004086	P10721 Q13541
12	9	5	NP_002742.3 NP_000818.2	Q15759 B43381
8	7	3	NP_001189450.1	008345

Serial   Antibody   Target Protein   Place	Flag- Patient 5- Smaller	Globally Normalized Median 1545 Globally Normalized -	Globally Normalized Median 1490	Globally Normalized Median 1864	Globally Normalized Median 1726	Globally Normalized Median 2278
1712   NY 1973-2   D.SEP3   Pro-specific   Louis specificity protein	Flag- Patient 5- Smaller	Globally Normalized -	Clabelle			
1712   N9933-2   CLSPS	5- Smaller		Normalized -	Globally Normalized -	Globally Normalized -	Globally Normalized -
1712   N9933-2   CLSPS	0.0	Normalized - Patient 1- Smaller	Globally Normalized - Patient 2- Smaller	Normalized - Patient 3- Smaller	Patient 4- Smaller	Patient 5- Smaller
118         N90033 00:258         Plan-specific Cell division cycle 328 (programates         0.0	0,0	14950 30344	21099 15726	15066 25787	11459 32413	10805 23536
847   NK181-4 TYK2   Pan-specific   Protein-tyrosine kinase 2 (Jakrelated)   0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0	7226 14076	8527 8717	6152 12228	5576 5827	6507 5775
847   NK181-4 TYK2   Pan-specific   Protein-tyrosine kinase 2 (Jakrelated)   0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0	5195 740	8045 562	5664 962	6354 754	4812 1618
811 NN117 STAT4 Pan-specific Signal transducer and activator of transcription 4 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	1645 5554 3094	895 3939 2919	1395 4779 957	1298 5585 1182	1303 5340 1213
472         NK099-3         MEX1         Pas-specific         MAPKERK protein-serine kinase t (MKX1)         0,0	0,0	5175	4926	4369	4918	1213 4718 3056
172   1909-3 MERT   Pro-specific	0, 0 0, 0 0, 0 0, 0	7306 7151 9740	2800 4181 7181	10144 9251 11258	7253 6087 8590	7806 5954 12289
665         NWCD-2         PMC/LOC         Ms-specific         Percentage of the property of the percentage of the	0, 0	9740 1482 1706	7181 8937 1088 1144	11258 1864 1956	8590 2917 1933	12289 3091 1711
	0,0	1706 6335	1144 2449	1956 6774	1933 9099	1711 5317
103   West   Cambrid   Pro-squeek   Cambrid   Pro-squeek   Cambrid   Pro-squeek   Cambrid   Pro-squeek   Pr	0, 0 0, 0 0, 0 0, 0	9066 145	2449 7062 186	10811 75	10854 26	5317 10400 126
440 NP004 KAP Pan-specific Cyclin-dependent kinase associated phosphatase (CDK inhibitor 3, CIP2) 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0,0	4315 1109 10968	6278 1656 8958	814 11446	5558 1022 10330	6152 1780 10829
238 PK603 EGFR Y998 Epidermal growth factor receptor-tyrosine kinase 0, 0 0, 0 0, 0 0, 0 0, 0 360 PM6072 Hord Stories (April 1998) PM607 S15 Hord short 27 kina contain beta 3 (Hord 1) 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0	0,0	3510 4085	2887 2146	3954 4797	2620 6052	4150 4665
689 NP033 PP2A B' (B56) Pan-specific Protein-serine phosphatase 2A - B regulatory subunit - B56 alpha isoform 0, 0 0, 0 0, 0 0, 0	0, 0 1, 0 0, 0	7178 1071	6986 1257	8556 1541	6578 1733	8961 3577
	0, 0 0, 0 0, 0	2111 17735 10688	1777 19505 13899	2727 16428 8198	1890 12761 7967	3063 10903 6409
65   MCCCC 2   gibt MMY   Pre-specific   Minigan exhausted primare in transp gibt data (MAYCCC)   6.0   6.	0,0	10688 4871 10925	13899 5563	8198 5034 13424 16941	7967 3549 6546	6409 5499 10112
286 PK626 ERK5 Y22 Extracellular resident protein-penting includes (Big MAP kinase 1 (BMK1)) 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0	0, 0 0, 0 0, 0 0, 0	10925 24007 467	5563 9295 19316 372	13424 16941 605	19861 984	10112 19417 648
	0,0	2087 1724 27038	751 1169 17473	1960 2630 22378	1563 1533 22264	2081 2180 19872
1514   PRET 9   \$1,575.4.   \$510	0,0	27038 940	17473 829	22378 1287	996	1402
299   NND42   FAS   Pan-appeolis   Tumor necrosis factor superfamily member 6 (Apo1, CD95)   0, 0	0,0	940 785 9080 5220 4065	466 7899	892 9636	976 10179	1022 10598
346         PHILES         HISDOR PG         5 TO         PRINCE         0,0	0,0	5220 4065 6450	4874 3307	5523 4879	5786 3258 7487	6439 5826
423 NK086-4 JAK3 Pan-specific Janus protein-tyrosine kinase 3 0, 0 0, 0 0, 0 0, 0	0,0	6450 7029	5286 7875 1557	5165 4896 1449	7487 7118 1141	6248 9701 1893
443 PRODE PK 17703 Bilaninalmi resupulmi rakum recipium N 0, 0, 0 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0	0,0	557 5832	910	432	310	212 5035
423   M008-4   JMC3	0, 0 0, 0 0, 0 0, 0	5832 2580 808	4455 2274 505	5050 3213 563	6326 2945 926	3921 338
367 NAMES Married Day country Married Married Control of Control o	0, 0 0, 0 0, 0	808 6277 679 1665	505 5909 561	563 9046 687	926 5335 967	338 7514 1610
	0,0	1065	1913 1108	2018 395	2367 509	2840 392
107   PR011 Carron 2   SH   Carrol 2   Car	0,0	3461 3986	2238 3287	3880 4467	4565 3097	3482 4422
16   NK129   Mot ( (Khai)   Pairspecinic (Mot appraisatement process masses   0,0	0,0	7562 12817 5777	4838 7812 13842	6181 6007 8897	4069 10825 7160	4988 7754 5442
486 PK049 MEK2 T394 MAPK/ERK protein-serine kinase 2 (MKK2) 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0,0	784 1180	699 1000	752 774	530 1133	420 1409
798 NNT01 SPHK2 Man-Specific Sphinipposine knalse 2 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 374 NNT65 Hapf00b Pan-Specific Heat shock 90 K0a protein beta 0, 0 0, 0 0, 0 0, 0 0, 0	0,0	1676 3951	1336 2910	2894 2904	1807 4225	3455 3385
	0, 0 0, 0 0, 0	1630 2336 4594	1951 1777 3444	2997 3131 4431	1946 2489 3374	4262 3109 2972
256   7955   2053a   1267-126   2053a	0,0	4594 20426	3444 19436 650	4431 14863 1905	3374 19851	2972 18248 1795
186         MC233.3         SSG1         Perspection         antidating protein issues C relevanting protein         0.3         0.6         0.0         0.0         0.0           646         MC123         MC2         Perspection         Profession invasor C settlement on an of a protein control of a protein on a control or an of a protein or	0,0	20426 1864 1072	1018	1905 1905 4115	1376	2610
MNUSSA   MRC2   Passagent   MAPCRR protesses transp 2 (MACCR)   0.0	0,0	5241 2755 2673 1674	3843 3800 2712 1772	3683 3427 2309	3859 3293 3271 1530	3620 4209 5787 2954
	0,0	1674 1633	1772 961	2309 1076	1530 1826	2954 1780
	0,0	4343 1160	2647 848	2283 1272	3133 1037	2936 1029
55   M054-2   NOP-0	0,0	9855 3309 5793	6838 2168 4437	4361 4158	5471 2474 5309	3975 3404 6654
688         NPO11         PPI-LQ (PP1g1)         Pan-specific         Protein-serine phosphatase 1 - catalytic subunit - panma isoform         0, 0         0         0         0, 0         0	0,0	5793 1260 34356	4437 677 22426	7965 888 31106	5309 1523 20710	6654 1519 18163
211         New Old - 1005**2         Presspecific Quantification of the complete of	0,0	4056 11661 1474	3008 8205	902	1047	1412
167   1693   15742   Pre-specific Signal resolution and of the monogene 2   8.0	0,0	1474 1627	1161	1483	11018 982 1494	13514 1890 2451
160         PH0222 -2         Contaction         Y466         Outstation forestation (mouse)           100         NeW201         CM54         Phase-specific         Local (mouse)         0,0 <td>0, 0 0, 0 0, 0 0, 0</td> <td>1627 293 728 1381</td> <td>928 317 480</td> <td>2041 398 800</td> <td>1494 274 1025 1275</td> <td>2451 196 437</td>	0, 0 0, 0 0, 0 0, 0	1627 293 728 1381	928 317 480	2041 398 800	1494 274 1025 1275	2451 196 437
PRINCES   PRIN	0,0	9989	1680 7414	2318 11766	5268	2315 6921
100   16/12   1972/Alash   Phas-specific   Technologies 2A A regulatory schools - appea and held subhoris   0.0   0.0   0.0   0.0	0,0	843 293	1263 158	982 404	815 482	2287 218
708         NK151         PRKVMW4         Pan-specific         Putable protein-serine Missae WNM4         0,0	0,0	1209 685 1291	895 708 508	2857 648 1152	1456 827 1477	3974 1434 1360
116         NP002         Cdc258         Pan-apecific         Celd division cycle 258 phosphatase         0,0	0,0	2029 5169	1077 3022	3038 4810	3660 6243	3305 3766
ACO   N/K096   JAKS   Pa-specific   Januar protein-hyrosine kinase 3   0,0   0,0   0,0   0,0	0,0	3440 6502	2767 3011	5775 9103	4168 6409	5374 4749
470         NNPSS         MEF-2         Pau-specific         Myelin expression factor 2 (MYEF2)         0,0 </td <td>0.0</td> <td>1670 645 3593</td> <td>986 427 4211</td> <td>1630 240 4004</td> <td>1863 337 2398</td> <td>2551 366 4125</td>	0.0	1670 645 3593	986 427 4211	1630 240 4004	1863 337 2398	2551 366 4125
70   PHIGE   RCGAT GROUNDWARD AT   Resignating the X-bind Spirit   RCGAT GROUND AT   RCGAT GROUND A	1,1 0,0 0,0	3593 3410 6626	4211 2921 4310	4004 2841	2398 3138 5436	4125 3904
	0.0	336	418	4119 255 1393	552	3963 300 1391
129   PRODS   CEXT2	0,0	972 821 1051	737 1064 1111 4832	1393 639 1502	701 484 918	1391 917 1967
	0, 0 0, 0 0, 0 0, 0	1051 7291 3524	4492	1502 6490 4640 5174	6568 4041	1967 6244 4725
10   10   10   10   10   10   10   10	0.0		5287 15025	25662	5813	6031 32528
570         NN081-NN120 (pd5         Pan-specific         CDKS regulatory suburit p25 and p35         0,0	0,0	22391 3276 5223	2481 8721	2298 7229	19661 3302 5721	3197 6008
	0,0	613 1389 877	330 864	565 884	422 1520 656	424 1646
	0,0	877 1221 9235	1059 1080 6777	648 1497 7238	656 1581 9439	1430 1598 8216
Nrt	0,0	796	450	1002	889	1560
436 PN048-1 Jun S73 Jun prote-propted AP1 transcription factor 0.0 0.0 0.0 0.0	0,0	494 2345 740	305 1616 1003	518 2559 883	2517 820	720 3707 1413
100   100	0, 0 0, 0 0, 0	740 1657 8269	1000 4669	3018 7408	820 2180 4865	1785 5549
270         PK864         ERK1         Y204         Extracellular regulated protein-serine kinase 1 (p44 MAP kinase)         0, 0         0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0         0, 0	0,0	2001 440	1518 515	2571 728	1805 533	2776 363
511         PK7077         Met         T1355+Y1356         Hepatocyte growth factor (H3F) receptor-tyrosine kinase         0, 0 <td>0,0</td> <td>6324 1440</td> <td>5868 1366</td> <td>6515 1226</td> <td>5148 1405</td> <td>7033 1656</td>	0,0	6324 1440	5868 1366	6515 1226	5148 1405	7033 1656

Average - Smaller	S. Dev Smaller	%S.Dev. Smaller
14676 25561	3655 5843	25 23
6798 9325	1017 3353	15 36
927	1138 368	19 40
1307 5039 1873	242 622 931	18 12 50
1873 4821 2230	931 269	6
7298 7125	1893	26 26
10163 2088	1405	14
1690 5995	293 2163	38 17 36
9639 112	56	15 50
5466 1276	729 375	13 29
10506 3424 4349	852 592 1275	8 17 29
4349 7652	1275 933	29 12 49
1836	900 498	22
15466 9432 4903 10060	3179 2621	21 28 15
10060	727 2236 2289	15 22 11
611 1689	202 506	33 30
1847 21805	509 3176	28 15
1091	217 198	20 24
9478 5568 4267	940 531 978	10 10 23
4267 6127	978 849	14
7324 1422	1548 297	21 21
465 5340 2987	210 659 565	45 12 19
2987 628	565 212	19 34
901 2160	379	19 42 19 47
694	408 324 750	
3852	568 1221	21 15
5528 9043 8223	2442 3062	22 27 37
637 1099	139 210	22 19
2234 3475	803 537	36 15
2557 2568 3763	970 509 635	38 20 17
3763 18525	635 1959 627	
1596	597	36 37
3548	575 493 1146	14 14 32
3574 2048 1455	524 384	32 26 25
3069 1069	699	23 13
6100 3103	142 2125 710	35 23
6031 1173	1204 340 6261	20 29 25
25352 2085 10934	6261 1238 1737	25 59
10934 1398	311	22
1708 296	514 65 216	30 22 31
894 1794 8271 1238	216 447 2313	31 25 28
1238	447 2313 548 119	44 38
2078 860	1161 293	56 34
1158	341	29
4602 4305 5955	944 1118 1135 2026	36 24 26
1740	502	29
403 3666	135 669	34 18
3243 4673	385 673	12 14
372 1039 785	105 303 204	28 29 26
785 1310 6285	204 382 806	26 29 13
4285 5774	447 507	10
23053 2911 6580	5882 431 1258	26 15
6580 471	1258 104	22
1256 934	331 291	31
1395 8181	208 1054	15
939 496	361 134 671	38 27 26
2549 972	227	
1928 6152	664 1434 471	24 34 23
2134 516	122	22 24

					Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
					Median 1597	Median 1688	Median 1753	Median 1745	Median 1646
Flag- Patient	Flag- Patient	Flag- Patient	Flag- Patient	Flag- Patient	Globally	Globally	Globally Normalized -	Globally Normalized -	Globally
Patient 1-	2.	3.	4.		Normalized - Patient 1-	Normalized - Patient 2-	Normalized - Patient 3-	Normalized - Patient 4-	
Patient 1- Bigger	Bigger	Bigger	Bigger	Bigger	Patient 1- Bigger	Patient 2- Bigger	Patient 3- Bigger	Patient 4- Bigger	Patient 5- Bigger
	0, 0	0, 0	1, 0 0, 0	0, 0	19710 22220	18115 21097	10102 25828	10056 27794	8726 19149 5207
0, 0	0, 0	0, 0	0, 0	0,0	6909 8503	8043 9387	6574 9601	4078 7817	6893
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0	7132 1021	6380 773	5514 744 1587	4923 899	3264 759
0, 0	0,0	0, 0	0, 0	0, 0	1387 4077	886 4147	1587 4662	900 6332	1149 3496
0.0	0,0	0,0	0, 0	0.0	2591 5063	2283 4195	833 4349 1790	1487 5151	1244 2936
0, 0	0, 0	0, 0	0, 0	0,0	1898 6623 6779 8402	3237 5408	7235	1565 7372	1517 6101
0, 0	0, 0	0, 0	0, 0	0, 0	6779 8402	6954 8780	7937 7963	5599 9120	4629 11092
0, 0	0.0	0, 0	0, 0	0,0	796 1225	1465 1415	1834 1411	2485 1973	2737 1514
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	3567 7153	3584 7906	3592 9402	7002 9440	8981 9045
0, 0	0,0	0, 0	0, 0	0, 0	91 6466 1452	173 5393 1315	32 4992 948	81 3869 877	121 3606 1088
0, 0	0, 0	0, 0	0, 0	0,0	7935	8945	10405	877 8724	10665
0, 0	0, 0	0, 0	0, 0	0, 0	3692 2731	2771 2904	3662 5152	2/38 4464	2342 4055
0, 0 0, 0 0, 0	0,0	0, 0	0, 0	0, 0 1, 0	8014 1476	8301 1688 2194	8279 1804 2144	3489 1872	5796 1281
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0, 0	20371	2194 17076 9304	2144 10274 7556	1968 9944 7204	10684 6629
0, 0	0,0	0,0	0, 0	0,0	10983 5342 10827	9304 5678 9643	7556 4218 11099	2731 4948	3687 7913
0.0	0, 0	0, 0	0, 0	0, 0	19261	21539 262	14879	19840 634 1805	12372
0, 0 0, 0 0, 0 0, 0	0,0	0, 0	0, 0	0,0	184 1161	988	859 1709	634 1805 2059	669 1786 1251
0, 0	0,0	0, 0	0, 0	0,0	1718 18379 746	1233 15484	1859 17007	2059 19994 1106	1251 24945 1012
0, 0	0,0	0, 0	0, 0	0,0	424	858 707 9502	1068 897	1106 629 4907	977 10942
0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	6919 4331 4110	8502 5792 3513	10419 5390 3717	4907 3794 4784	10843 5116 2580
0, 0	0,0	0, 0	0, 1	0, 0	5843	5806	4485	5995	4725
0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	7372 1254 599	8158 1180	7880 1242 452	3715 1495 27	4960 1058 125
0, 0	0, 0	0, 0	0, 0	0,0	4965	833 5573	4879	4740	3188
0, 0	0,0 1,1 0.0	0, 0 1, 1 0, 0	0, 0	0,0	2262 828 7202	2144 292 5168	3521 642 5923	3345 954 6497	1765 25 4952
0, 0	0,0	0, 0	0, 0	0,0	823	581	720	770	1034
0, 0	0, 0	0, 0	0, 0	0, 0	1788 681	2485 805	738	1235 451	1405 341
0, 0	0, 0	0, 0	0, 0	0, 0	2344 4115	2625 3222	2772 4059	4100 2981	3474 2287
0, 0	0, 0	0, 0	0, 0	0, 0	4213 9412	4630 8394	5091 4731	5647 8354	4312 8153
0, 0	0, 0	0, 0 1, 1 0, 0	0, 0 0, 0 0. 0	0,0	11257 650 721	8503 867 1370	5766 502 658	6453 559 940	3490 166 1035
0, 0	0,0	0, 0	0, 0	0,0	1798 2699	1478 2581	1866 2891	2935 3600	1522 3160
0, 0	0, 0	0, 0	0, 0	0, 0	1334	1546	2278	3674	2120 1930 2425
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0	2280 3437	1643 3409	1871 3449	3267 3364	
0, 0	0, 0	0, 0	0, 0	0, 0	15219 1056	15004 761 977	14485 1727 1227	14982 2093 1660	19420 1886
0, 0	0,0	0, 0	0, 0	0,0	1788 3563 2640	977 3320 3709	1227 3410 3436	1660 4121 2512	1149 3193 2785
0, 0	0, 0	0, 0	0, 0	0,0	2431 1707	2981 1710	3436 3986 1425	2512 2233 2167	2785 3552 1689
	0, 0	0, 0	0, 0	0,0	772	1/10 864	852	1350	2337
0, 0	0,0	0, 0	0, 0	0, 0	2582 811	3668 1365	2220 1026	2997 725	1549 602
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0	0, 0	5794 2575 6589	8498 2313 4820	4380 2479	4776 3466 3275	2386 2280 3683
0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	6589 809 18518	4820 882 21684	2479 7121 1105 27681		3683 1463 18000
0, 0	0,0	0, 0	0, 0	0, 0	18518 3113 7601	21684 2219 9381	27681 696	699 21232 1545	18000 1234 10724
0, 0	0,0	0, 0	0, 0	0,0	7681 1488	1277	12183	6206 995	10724
0, 0	0,0	0, 0 1, 1	0, 0	0,0	1920 236	1257 334 705	1251 155	1702 198	1075 322
0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0, 0	0,0	387 1714 6902	705 1154 6952	797 1377	705 1946 6680	331 1358 5648
0, 0	0,0	0, 0	0, 0	0, 0 0, 0 0, 0	6902 805 261	6952 1228 219	8614 1018 275	6680 1033 290	5648 1124 263
0, 0	0,0	0, 0	0, 0	0,0	261 1733 560	219 809 866	275 1221 892	290 2423 612	263 2543 683
0, 0	0,0	0, 0	0, 0	0,0	548	776	1019	1199 2209	1319
0, 0	0,0	0, 0	0, 0 0, 0 0, 0	0, 0	1719 3335	1985 4006	2262 4909	2208 3644	2829 3371
0, 0	0,0	0, 0		0,0	2847 4092	3734 4752	3865 6023	3915 4647 1322	3855 5404
1, 1	0, 0 1, 1 0, 0	0, 0 0, 0 0, 0	0, 0 1, 1 0, 0	0, 0	1387 108 3331	1504 160 4445	1364 436 3047	1322 324 1891	1699 656 2608
0, 0 1, 1 0, 0 0, 0 0, 0	0,0	0, 0	0,0	0,0	2920 3622	3354 4137	2842 4391	2088 4051	2336 3282
0, 0	0,0	0, 0	0, 0	0,0	352	299	335 786	252 1031	312 714
0.0	0.0	0.0	0.0	0.0	1230 589	1078	573	375	647
0, 0	0,0	0, 0	0, 0	0,0	1472 5032 3561	1241 4741 4172	1013 4476 3575	967 5681 3256	745 6128 3156
0, 0	0,0	0, 0	0, 0	0,0	6036 14833	41/2 5321 18613	35/5 4183 20054	3256 3628 17099	4664 24514
0, 0	0,0	0, 0	0, 0	0,0	2150 7502	2531 6081	1869 4710	2557 5275	2899
0, 0	0,0	0, 0	0, 0	0,0	296	455 4059	515 601	334 4067	339
0, 0	0,0	0, 0	0, 0	0,0	954 661 764	1058 1036	601 666 1176	1067 556	1483 919
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	764 7461 718	1048 6406 474	1176 6456 798	1498 6729 936	1230 6454 916
0, 0	0,0	0, 0	0, 0	0,0	718 260 1284	474 419	798 415	936 369 1749	916 564 2878
0, 0	0,0	0, 0	0, 0	0,0	1284 691 1189	1846 1163	2651 764	1749 655	2878 693
0, 0	0, 0	0, 0	0, 1	0, 0	4356	4558	2003 5682	1319 5264	1824 5130
0, 0	0, 0	0, 0	0, 0	0, 0	1788 276 5332	1359 555	1419 398	2305 639	1793 225
0, 0	0, 0	0, 0	0, 0	0,0	1034	5887 1331	6405 1115	3963 1251	3472 1019

Globally Globally Globally Globally

Average - Larger	S. Dev Larger	%S.Dev Larger	%CFC - Average Larger from Average Smaller	Student T test p value
13342	4603	35	-9	.461
23217	3156	14	-9	.370
6162 8440	1380	22 12	-9 -9	.142
5443	1323	24	-9	.451
839		13	-10	.698
1182	273	23	-10	.284
4543 1687	968 654	21	-10 -10	.375
4339 2001	797 634	18 32	-10 -10	.253 .543
6548	729	11	-10	.346
6380 9072	1148 1081	18 12	-10 -11	.035
9072	1081 700		-11 -11	.168
1863		38 17		.303
5345	2249 908 47	42	-11 -11	.648
8589	908	42 11	-11	.096
99		47	-11	.556
4865	1043 217 1039	21 19	-11 -11	.497
1136 9335	1039	11	-11	.481
3041	541 923	18	-11 -11	.354
3861		24	-11	.349
6776	1891 218	28 13	-11 -12	.354 .349 .411 .707 .450
1624 2046	218 197	13	-12	.707
13669				
8335	4262 1597	31 19	-12 -12	.285
4331 8886	1079	25	-12 -12	.227
8886 17578	2267 3407	26 19	-12 -12	.099
	2407			.230
540 1490	240 345	45 23	-12 -12	.539 .408
1624 19162	330 3254	20	-12 -12	.459
19162	3254	17	-12	.310
958	136	14	-12	.216
727 8318 4885	197 2210	27 27	-12 -12	.423
4885	725 724	15	-12 -12 -12	.245
3741	724	19	-12	
5371 6417 1246	633 1761	12	-12	.113
6417	1761	12 27 11	-12 -12	.552
1246 407	143		-12	.448
4669	298 793	73 17	-12 -13	.391
2608	696	27	-13	.460
548	344 834	63	-13 -13	.359
5948 786	1/10	14	-13	.378
1883	148 530	28	-13 -13	.420 .545
603	177	29	-13	.515
3063 3333	639 688	21 21	-13 -13	.196
3333	688	21	-13	.277
4//9 7900	1600	11	-14	.399
7094	2626	37	-14	.568
549 945	228 254	42 27	-14 -14	.342
945				.346
1920 2986	529	28 12	-14 -14	.585
2986 2190		12 37	-14	.085
	820 572 397			388
2198 3217	397	26 12	-14 -15	.081
15822	1815	11	-15	.105
1504	509	34	-15 -15	.219
3521	310 323 470	23 9		
3016	470	16	-15 -15	.121
3037 1740	661 239	22 14	-15	.346
1740	239 588	14	-15	.417
1235	588		-15	.399
2603	714	27	-15	.405
5167	2000	39	-15	.380
2623	435	17	-15	200
5098	1531	30	-15	.259
992 21423	270 3447	27 16	-15 -15	.418 .267
1761	990	16		.267
1761 9235	836 2122	47 23	-16 -16	.275
1180	180	15	-16	.284
1441	317 70	22	-16	.484
249	70	28	-16	.488
585 1510	188 283	32 19	-16 -16	.359
6959	953	14	-16	.200
1042	140	13 9	-16 -16	.469 .371
262	24	9	-16	.371
1746	140 24 670 134	38 18	-16 -16	.557 .476
972	134 280	18 29	-16	.326
2200	368	17	-16	.335
3853	580	15	-16	.313
3603 4984	389 666	11	-16 -16	.252
	666 136	13	-16 -16	.353
		59	-16	.685
1455 337			-16 -16	.685 .114
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337 3064 2708 3896 310 865 662 1088 5212 3544 4766 19022 2401 5388	448 395 34 236 232 248 609 355 844 3245 357 1321	17 10 11 27 36 23 12 10 18 17 15 24	-17 -17 -17 -17 -17 -17 -17 -18 -18	.455 .065 .486 .079 .058 .055 .132 .063 .291
337 3064 2708 3896 310 865 652 1088 5212 3544 4766 19022 2401 5427	448 395 34 236 232 248 609 355 844 3245 357 1321	17 10 11 27 36 23 12 10 18 17	-17 -17 -17 -17 -17 -17 -17 -18 -18 -18	.455 .065 .486 .079 .058 .055 .132 .063
337 3064 2708 3896 310 885 652 1088 5212 3544 4766 19022 2401 5427 388 1033 768	448 395 34 236 232 248 609 355 844 3245 357 1321 83 282 282	17 10 11 27 36 23 12 10 18 17 15 24	-17 -17 -17 -17 -17 -17 -17 -18 -18 -18 -18 -18	.455 .065 .486 .079 .058 .055 .132 .063 .291
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337 3064 2708 3896 310 885 652 1088 5212 3544 4786 19022 2401 5427 388 1143 6701 769 405 2062 7793 1568	448 335 34 236 232 248 609 355 844 3245 367 1321 83 282 282 180 396 98 504 188 305	177 100 111 277 386 122 110 118 177 155 24 211 227 223 221 6 222 224 29	-17 -17 -17 -17 -17 -17 -17 -18 -18 -18 -18 -18 -18 -18 -18 -18 -18	.455 .085 .486 .079 .055 .055 .132 .063 .291 .305 .130 .038 .023 .248 .248 .248 .248 .248 .248 .248 .248
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										Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
					Fine.	Floor.	F1	Fine.	Fla.	1545	1490	1864 Clabello	1726	2278 Claballs
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag- Patient 1- Smaller	Flag- Patient 2- Smaller	Flag- Patient 3- Smaller	Flag- Patient 4- Smaller	Flag- Patient 5- Smaller	Globally Normalized - Patient 1- Smaller	Globally Normalized - Patient 2- Smaller	Globally Normalized - Patient 3- Smaller	Globally Normalized - Patient 4- Smaller	Globally Normalized - Patient 5- Smaller
584	NK121-4	p38d MAPK	Pan-specific	Mitogen-activated protein-serine kinase p38 delta (MAPK13)	Smaller 0, 0	Smaller 0, 0	Smaller 0, 0	Smaller 0, 0	Smaller 0, 0	Smaller 3300	Smaller 4312	Smaller 4388	Smaller 3777	Smaller 4580
787 273 388	NK233-1 NK055-NK056-2 NN064	SMG1 ERK1/2	Pan-specific Pan-specific Pan-specific	Lambdariota protein kinase C-interacting protein Extracellular regulated protein-serine kinase 1 (p44 MAP kinase) + Extracellular re Inhibitor of NF-kappa-B alpha (MAD3)	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	32722 7053 2322	33525 5500 1965	22433 6704 858	31109 6491 449	36787 7119 2552
388 271 776	NN064 PK866 NK249-1	IkBa ERK1 SIK2	Pan-specific Y204+T207 Pan-specific	Inhibitor of NF-kapa-B alpha (MAD3) Extracellular regulated protein-serine kinase 1 (p44 MAP kinase) Serine/threonine-protein kinase SIK2	0, 0	0, 0	0, 0	0, 0	0,0	2322 6290 2602	1965 4233 4297	858 5262 3626	7171 3283	2552 5827 4014
143 67 585	NK028-5 PK538 PK743	CDK5 Bar	Pan-specific Y177 Y182	Cyclin-dependent protein-serine kinase 5 Breakpoint diuster region protein	0, 0	0, 0	0,0	0, 0	0, 0	1917 2078 3594	1465 1524 6237	1968 2752 4971	1844 1482 3424	5123 3658 4022
585 656	PK743 PK077-2	p38d MAPK PKCd EDK1	Y182 Y311	Mitogen-activated protein-serine kinase p38 delta (MAPK13)  Protein-serine kinase C delta  Extracel for growthste gotten serine kinase 1 (nd MAP kinase)	0, 0	0, 0	0,0	0,0	0,0	3594 2860 2666	6237 2499 2110	4971 2217 2026	3424 2445	4022 2225 3402
563 703 778	PN054 NK149-2 NK249-3	NMDAR2B PRK2 SIK2	Y1472 Pan-specific	Extracential regulated protein-sentite kinase i (pre-kinase) N-methyl-D-aspartate (NMDA) glutamate receptor 28 subunit Protein kinase C-related protein-serine kinase 2	0, 0	0,0	0,0	0,0	0,0	217 437 6445	133 486 5129	276 506 6508	345 442 4753	389 1435 5322
778 739 588 487	NK249-3 PN068	Dh	Pan-specific Pan-specific S807 Pan-specific T394	Protein kinase C-related protein-serine kinase 2 Serine/threonine-protein kinase SIK2 Retiroblastoma-associated protein 1	0, 0 0, 0 0, 0	0, 0 0, 1 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	6445 835	5129 1402 7865	6508 1177	4753 669 7051	5322 1181
487 200	PN068 NK059-4 PK049-2 PN027-2	p38g MAPK MEK2 human Dok2	T394 Y142	MAPK/ERK protein-serine kinase p.o. gamma (WAPK 12)	0, 0	0,0	0,0	0,0	0,0	442 1541	1008 1311	364 1613	643	366 1429
200 478 213 692	PN027-2 PK046-1 NP030-3 NP032	Dok2 MEK1 DUSP3	T292 Pan-specific	Docking protein 2 MAPK/ERK protein-serine kinase 1 (MKK1) Dual specificity protein phosphatase 3	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0	2852 3803 7892	2220 4841 7538	2992 5580	820 2251 5399 7124	2639 4578 11582
692 495 769	NP032 NK103-2 NN133	PP2A/Bg2 MEK4 SG2NA	Pan-specific Pan-specific	Protein-serine phosphatase 2A - B regulatory subunit - gamma isoform MAPK/ERK protein-serine kinase 4 (MKK4)	0, 0 0, 0 0, 0 0, 0	0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	7892 2866 2614	7538 3310 3129	12033 3019 3572	7124 2226 2469	11582 3855 3074
609 687 246	NK122-4 NP010 PN031	PAKa PP1/Cb (PP1b) eIF4G	Pan-specific Pan-specific S1108	Striatin-3 p21-activated kinase 1 (alpha) (serine:threorine-protein kinase PAK 1) Protein-serine phosphatase 1 - catalytic subunit - beta isoform Eukaryotic translation initiation factor 4 gamma 1	0, 0	0,0	0,0	0, 0	0,0	779 3922 2499	785 2408 1506	671 4385 2844	801 2393 3513	1462 3704 2662
272	NK055-NK056	ERK1/2	Pan-specific	Extracellular regulated protein-serine kinase 1 (p44 MAP kinase) + Extracellular re	0,0	0,0		0,0	0,0	3958	1506 2880 485	3859	3557	4374
551 265 81	NK117-4 NK055-2 PK549	Nek2 ERK1 BRSK1	Pan-specific Pan-specific T189	NIMA (never-in-mitosis)-related protein-serine kinase 2 Estraceliklar regulated protein-serine kinase 1 (p44 MAP kinase) BR serine/threceine-protein kinase 1 MAPKIERK protein-serine kinase 1 MAPKIERK protein-serine kinase 1	0, 0	0, 0	0,0	0,0	0, 0	628 5995 9615	4930 5486	790 5908 8201	873 6412 6803	1785 7285 8688
81 471 350	PK549 NK099-1 PN101-2	MEK1 Histone H3	Pan-specific T189 Pan-specific T3	MAPK/ERK protein-serine kinase 1 (MKK1) Histone H3.3	0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 1, 1 0, 0	0, 0	9615 3401 1325	622 858	8201 1030 1178	6803 1946 1666	8688 3081 1832
709 531 697	PN104 PK056	Progesterone Recepto MLK3 PP4C (X/C)	S294 T277+S281 Pan-specific	Progesterone receptor Mixed-lineage protein-serine kinase 3 Protein-serine phosohatase X - catalytic subunit (PPXIC)	0, 0	0, 0	0,0	1, 1	0,0	221 2273 8573	142 2281 7434	243 2239 9363	241 1866 5061	816 3326 12297
697 366 475	NP020 NN059-1 NK099-9	PP4C (X/C) Hsp60 MEK1	Pan-specific Pan-specific Pan-specific	Protein-serine phosphatase X - catalytic subunit (PPXIC) Heat shock 60 kDa protein 1 (chaperonin, CPN60) MAPK/ERK protein-serine kinase 1 (MKK1)	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	8573 2639 11055	7434 1397 6333	9363 2911 9902	5061 3633 12619	12297 4712 9608
89 842	NK019-2 NK180	CAMK2d TTK GCK	Pan-specific Pan-specific	Calcium/calmodulin-dependent protein-serine kinase 2 deta  Dual specificity protein kinase	0, 0	0,0	0,0	0, 0	0,0	11055 1545 998 3037	1057 588 3030	2116 1982 4140	1689 898 2246	2437 1998 5112
322 289 452	NK066 PN175 PK039	Ezrin Lok	Pan-specific Y353 S158	Germinal centre protein-serine kinase Cytovillin 2 Lymphocyte-specific protein-tyrosine kinase	0, 0 0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	1085 1314	684 1315	1609 1403	1600 967	1118 1399
206 315	NP045-2 PN033	DUSP11 Fos	Pan-specific T232	Phosphaśdylinositol-3,4,5-trisphosphate 5-phosphatase 2 Fos-c FBJ murine osteosarcoma oncoprotein-related transcription factor	0, 0		0,0	0,0	0,0	8026 573	7089 742	10697 913	7953 930	7176 561
182 652	PK587 NK135	CSF1R PKCd BRGA1	Y699 Pan-specific S1423 T180+pY182 Pan-specific	Macrophage colony-stimulating factor 1 receptor Protein-serine kinase C deta  Front open type 1 support his type of the control of the contro	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0		640 2711 1440	507 1904 585	1088 1874 1507	798 2238 1889	1492 2673 1781
78 581 113	PN116 PK741 NP038-1	p38b MAPK Cdc25A	T180+pY182 Pan-specific	Macrophage colony-stimulating factor 1 receptor Protein-serins kinase C debta  Breast cancer type 1 susceptibility protein Mitogen-activated protein-serins de innase p38 beta Cell division cycle 25A phosphatase	0, 0	0, 0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	8450 2397	7820 4882	10403 2669	8067 3270	8137 2616
327	PKU25	GRK2 Hsp90a ERK1	Pan-specific S670 Pan-specific T202+Y204	G protein-coupled receptor-serine xinase 2 Heat shock 90 kDa protein alpha	0,0	0.0	0,0	0,0	0,0	5187 1060	4807 552	5529 1351 4375	3486 1294	5666 1776 4884
268 8 395 162	PK621 NK001-2 PK154 NK037-1	EHK1 Abi IKKa	Pan-specific T23	Extracellular regulated protein-serine kinase 1 (p44 MAP kinase) Abelson proto-oncogene-encoded protein-tyrosine kinase Inhibitor of NF-kappa-B protein-serine kinase alpha (CHUK)	0, 0	0, 0	0,0 0,0 1,0 0,0 0,0 0,0	0,0	0,0	5899 5120 1209	3901 4348 711	6265 1494	3867 3208 1347	5744 1770
394		CK1e IKKa	Pan-specific Pan-specific	Casein protein-serine kinase 1 epsilon Inhibitor of NF-kappa-B protein-serine kinase alpha (CHUK)	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0	0,0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	15709 3809	11450 3027	19852 5908	13383 4271	18731 4256
95 464	NN021 NN011 PN049-PN112-2	Caterin b Caspase 1 MAPKAPK2	Pan-specific Pan-specific T334	Catenin (cadherin-associated protein) beta 1 Caspase 1 (Interleukin-1 beta convertase) Miscose cardistand proteins history and interest distributed protein sizes of the convertase of the convertage of the conve	0, 0	0, 0 0, 0 0, 0	0,0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	1315 2485 754	2730 2091 641	804 2139 587	1229 1515 600	3821 2721 332
13 382	PN003-PN004 NN025	Adducin a/g IAP1	S662 Pan-specific S473	Adducin alpha (ADD1)  Cellular inhibitor of apoptosis protein 1 (baculoviral IAP repeat-containing protein	0, 0	0,0	0,0	0, 0 0, 1 0, 0	0,0	1277 1430	756 961	1197 1366	914 1585	876
773 677	PK072-1 NP045-1	Akt1 (PKBa) SHIP2 PKG1	S473 Pan-specific	RAC-alpha serine/threonine-protein kinase Phosphatidylinositoi-3,4,5-trisphosphate 5-phosphatase 2 cGMP-dependent protein kinase 1, alpha iscoyme	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0,0 0,0 0,0	0,0	0, 0 0, 0 0, 0	1144 5528 1380	767 6692 1000	2103 8419 1498	1960 6015 2059	1717 5520 2520
612 393	NP045-1 NK143 NN086 NK075-2	Paxilin IKKa	Pan-specific Pan-specific	CLMM*-dependent protein kinase 1, aspna isczyme Paxillin 1 Inhibitor of NF-kappa-B protein-serine kinase alpha (CHUK)	0, 0	0,0	1, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0,0	74 894	65 918	1498 52 895	2059 55 897	152 2137
657 11 566	NK075-2 NK136 NK002 NN083	PKCe ACK1 p107	Pan-specific Pan-specific	Protein-serine kinase C epsilon Activated CDC42 kinase 1	0, 0 0, 0 0, 0	0,0		0, 0	0, 0 0, 0 0, 0	532 1643 1110	730 1972 979	414 2210 776	580 1409 777	1221 3186 1029
777 161	NK249-2 NK236 NK227-4	p107 SIK2 CK1d LKB1	Pan-specific Pan-specific Pan-specific Pan-specific	Froten-serine Keisser ungstellt in der Versichten (2014) (1988) (	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	1110 2204 1111	979 3290 1466	776 3668 1188	777 2936 1050	1029 3511 2453
460 592 459	NK227-4 PN159 NK227-3	p53	S37	Serine/threonine-protein kinase 11 Tumor suppressor protein p53 (artigenNY-CO-13) Serine/threonine-protein kinase 11	0, 0	0, 0	0,0	0,0	0,0	10083 2853 9324	8388 2105 6662	12727 3334 7656	10876 3315 9671	10611 2294 7332
459 292 75	NK227-3 PK020-3 NK156-5	LKB1 FAK R.Raf	Pan-specific 8722 Pan-specific	Serine/threonine-protein kinase 11 Focal adhesion protein-tyrosine kinase Battl protein-protein-tyrosine kinase	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 1	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	9324 648 1741	973 1377	7656 969 973	9671 851 1719	7332 551
85	NN136-2 PN172	Calnexin eIF4R	Pan-specific 8422							11270	6294 202	9018 494	9851 40	7951 591
242 841 759 693	PK160 NK164 NP013-NP014	TrkB RSK1 PP2A/Ca	Y705 Pan-specific Pan-specific	Calnexin  Elikaryotic translation initiation factor 4B  BNDF/RTS445 receptor: Pyrosine kirase  BNDF/RTS445 receptor: Pyrosine kirase  Ribboomal S6 prodein-serine kirase  Protein-serine phosphatase 2A - catalytic suburit - alpha isoform	0, 0 0, 0 0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	562 797 1005	265	669 656 812	502 914 801	712 1265 787
494	NK103	PPZA/Ca MEK4 Akt1 (PKBa)	Pan-specific		0, 0	0,0	0,0	0,0	0,0	1005 1325 1888	615 1838	812 1306	801 883 1328	1533
685 517 546	PK517 NN156 PK051-4 PN186	PLCg2 (PLC R) MKK3	Pan-specific S189 S373	RAC-alpha serine/threorine-protein kinase 1-phosphatidy/inosibid-15-kisphosphate phosphodiesterase gamma-2 MAPK/ERK protein-serine kinase 3 beta isoform (MKKS beta) Mive prote-oncosense protein	0, 0	0, 0 0, 0 0, 0	0,0	0, 0	0, 0 0, 0 0, 0	892 635 870	1297 974 638 525	766 879 951	782 1299 1085	2224 2208 1184 1006
752	PN186 NK159-2 NK021-3	Myc ROKa CaMK4	Pan-specific	Rho-associated protein kinase 2	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	870 1259 3590	525 733 3393	984	1085 1789 3104	1006 2016 4854
90 812 844 568	PM083.1	CaMK4 STAT5 TYK2 p21 CDKI1	Pan-specific Y694 Pan-specific	Calcium/calmodulin-dependent protein-serine kinase 4 Signal transducer and activator of transcription 5A Protein-tyrosine kinase 2 (Jak-related)	1.0	1, 0	1.1	1.1	0.0	2049 710	813 1541 758	4225 2418 695 1181	3105 1581 1156	1940 1903 1900
594	NK181 NN078 PN160	p21 CDKI1 p63	Pan-specific Pan-specific S6	Protein-tyrosine kinase 2 (Jak-related) cyclin-dependent kinase inhibitor 1 (MDA6) Tumor suppressor protein p63 (antigenNY-CO-13)	0, 0	0, 0	0,0	0,0	0,0	1143 1260	785	1796	1156 1432 1775	1981
83 210 185	NN174 NP008-2 NN028	DUSP2 Cyclin A	Pan-specific Pan-specific Pan-specific	Carbonic anhydrase 9 Dual specificity protein phosphatase 2 Cyclin A1	0, 0	0, 0	0,0	0,0	0, 0	2606 46477 7269	1490 49799 4210	3372 38572 6872	2531 41024 6099	2765 40835 7380
730 655	NK155-4 PK077-1	Cyclin A Raf1 PKCd	Pan-specific Pan-specific Y311	Raf1 proto-oncogene-encoded protein-serine kinase Protein-serine kinase C delta	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0 0, 1 0, 0	0, 0 0, 1 0, 1 0, 0 0, 0	700	823 1737	851 2064	6099 1245 1277	1366 1712
257 607	NK155-4 PK077-1 PK134 NK123 NK130-4	ErbB2 PAK3 Akt2 (PKBb)	T686 Pan-specific Pan-specific	ErbB2 (Neu) receptor-tyrosine kinase p21-activated kinase 3 (beta) (serine/threonine-protein kinase PAK 3) RAC-beta serine/threonine-protein kinase	0,0	0,0	0,0	0,0		1941 7913 779	6259 991 2279	8237 777	4841 672	8761 1975
24 135 196		ARZ (PKBb) CDK2 DGKZ	Pan-specific Pan-specific	HAL-Ceta serinertreconne-protein kinase Cyclin-dependent protein-serine kinase 2 Diacylglycerol kinase zeta Protein-serine kinase C beta 2	0, 0 0, 0 0, 0 0, 0 0, 0	0.0	0,0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	677 1657	2279 1111 1126	714 2889	637 1698	1920 3413
196 651 659	NK219 PK076-2 PK081-1	PKCb2 PKCe	Pan-specific Pan-specific T641 S729	Protein-serine kinase C epaion	0,0	0,0	0,0	0,0	0, 0 0, 0 0, 0 0, 0	1657 858 508	1126 423 326	906 1089	943 855	3413 1082 997
399	PK663	InsR FGFR1 RSK1/2		INSR insulin receptor Fibroblast growth factor receptor-tyrosine kinase 1 Ribosomal 56 protein-serine kinase 1/2	0,0	0,0	0,0	0,0	0,0	2602 5176 1139	2860 8331 962	3876 6896 589	3299 6499 839	3825 5683 767
764 376 76	PK100-2 PN176 PK534 NK212	Hsp90b B-Raf	Pan-specific 8363/8369 8254 8446+8447	Insert insulan receptor  Fibroblastig rowin factor receptor-tyrosine kinase 1 Ribocamai SS protein-serine kinase 1/2  Ribocamai SS protein-serine kinase 1/2  Heat shock SI Oka protein beta  RaffS proto-oncogene-encoded protein-serine kinase	0, 0 0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0 1, 1 0, 0 0, 0 1, 1 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0 0, 0	0,0	78 8248	119 6394	71 6636	101 8485	111 8496
561 573 330	NK212 NK120-5 NN048	NIK p38a MAPK Grp78	Pan-specific	Sernettreonne protein knase N.K. Mitogen-activated protein-serine kinase p38 alpha	0, 0	0, 0	0, 0	0, 0	0, 0	463 10496 5658	269 7456 5013	570 10366 6080	636 11036 4373	1281 11494 11182
330 402 170	PN044 NK042	Grp78 Integrin b1 COT	Pan-specific S785 Pan-specific	Glucose regulated protein 78 Integrin beta 1 (fibronectiin receptor beta subunit, CD29 antigen) Osaka thyroid oncogene protein-serine kinase (Tpl2)	0, 0	0,0	0,0	0,0	0,0	1260 4692	1135 2366	1986 5041	1426 3268	1518 5135
26 403	NK130-7 PK032-1	Ald2 (PKBb) IR	Pan-specific Y972	RAC-beta serine/threonine-protein kinase Insulin receptor	0, 0	0, 0	0,0	0,0	0,0	693 804	658 1045	772 989	837 754	2796 589
283 485 397	NK206-5 NK100-6 NK078-2	ERK5 MEK2 II K1	Pan-specific Pan-specific Pan-specific	Extracellular regulated protein-serine kinase 5 (Big MAP kinase 1 (BMK1)) MAPK/IERK protein-serine kinase 2 (MKK2) Interorin-liked protein-serine kinase 1	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0.0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	11008 18108 1424	6866 14063	9843 14770	7845 15660	7367 11095 1764
82 668	NK014 NK138-1	Btk PKCI	Pan-specific Pan-specific	integrin-linked protein-seinne knaate 1 Bruton's agammaglobulinemia tyrosine kinase Protein-serine kinase C lambdaliota	0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	0,0	0,0	1424 1239 929	1010	959 1462	1519 1102	1764 1536 2832
560 771 639	NK207 PN161	NIK Shc1 PITSLRE	Pan-specific Y349	NF-kappa beta-inducing kinase SH2 domain-containing transforming protein 1	0, 0	0,0		0, 0	0,0	526 465 338	417 586 699	718 1000 413	832 637 524	1567 945 1103
639 589 94	PN161 NK213 NK059-5 PN505	PITSLRE p38g MAPK Casul	Y349 Pan-specific Pan-specific Y166	NR "Program communication of security and security of the Security of Security	0, 0 0, 0 0, 0 0, 0	0, 1 0, 0 0, 0 0, 0	0, 0 0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0 0, 0	338 4591 3098	699 4772 1814	413 7724 3749	524 5357 2464	1103 6394 3885
	1 14303		100		ν, υ	ν, υ	υ, υ	υ, υ	ν, υ	J-/30	10.14	5/49	2404	Jun 20

Average - Smaller	S. Dev Smaller	%S.Dev. Smaller
4071 31315	469 4811	12 15
6573 1629	584 828	9 51
5757 3564	985 591	17 17
2463 2299	1342 821 1042	54 36 23
4450 2449 2489	1042 235 505	23 10 20
2489 272	91	33
5631	388 714	59 13
1053 7606 564	264 993 244	25 13 43
1343 2591	281 311	21
4840 9234	633 2120	13 23
3055 2971	535 394	18
899 3363	285 816	32 24
3363 2605 3726	816 649 497	24 25 13
912 6106	456 764	50 13
7759 2016	1455 1093	19 54
1372 333	347 244	25 74
2397 8546 3059	490 2372 1098	20 28 36
9903	1098 2075	21
1769 1293	476 585	27 45
3513 1219 1280	1002 350	29 29
8188 744	1312	16 21
905	352 360	39 16
1441 8576	459 936	32
3167 4935 1207	936 905 783 401	29 16
1207 4585	401 754	33 16
4937 1306 15825	1076 351	22 27 20
15825 4254	351 3155 942	22
1980 2190	1126 409 138	57 19
583 1004	138 199	24 20 24
1538	506	33
1691 79	1081 536 37	32
1148 695	494 282	47 43 40
2084 934 3122	615 135	30 14
3122 1454	521 520	17 36
10537 2780	1396 508	13 18
8129 798	508 1168 171 365	14 21 23
1570 8837	365 1666	23 19
338 542	198 157	59 29
804 1277	210 123	24 15 23
1925	595 547	31
1124 927 887	547 274 194	49 30 22
1356 3831 1760	481	35 16
1760 1201	630 544 471 376	16 31 39 29
1283 1519	439	29
2553 43342	608 4145 1168	24 10
43342 6366 997	4145 1168 260 268	18 26 15
7202	1447 479	20 46
1039 2779 1012 2157	393 485	14
2157	853 222	40 26
842 755 3293 6517	292 508 1089	39 15
6517 859	1089 185	21
96 7650	19 933	20 12
644 10170	342 1415	53 14
6461 1465	2431 292	38 20 27
1465 4100 1151	292 1096 825 165	27 72 20
836 8586	1577	18
14739	2278	15
1512		
1512 1253 1401	314 244 760	19 54

					Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
					Median 1597	Median 1688	Median 1753	Median 1745	Median 1646
Flag- Patient 1- Bigger	Flag- Patient 2- Bigger	Flag- Patient 3- Bigger	Flag- Patient 4- Bigger	Flag- Patient 5- Bigger	Globally Normalized - Patient 1- Bigger	Globally Normalized - Patient 2- Bigger	Globally Normalized - Patient 3- Bigger	Globally Normalized - Patient 4- Bigger	Globally Normalized - Patient 5- Bigger
0, 0	0, 0	0, 0	0, 0	0, 0	3805 25946	3677 18891	3027 18281	3052 22425	2928 41241
0, 0	0, 0	0, 0	0, 0	0, 0	4945 3329	5898 1273	4947 586	6172 377	4650 1023
0, 0	0,0	0, 0	0, 0	0,0	4689 3051	4488 3314	4056 3033	5384 2448	4626 2544
0, 0	0,0	0, 0	0, 0	0,0	1996	1904 1359	2381 1597	1137	2521 2296
	0.0	0.0	0.0	0.0	1989 5308 1962 2193	4573 2487 1939	2926 1940 839	2027 3092 1912 2581	2296 2027 1565 2477
0, 0	0,0	0, 0	0, 0	0,0	2193 120	1939 140	839 209	2581 190	2477 437
0, 0	0,0	0, 0	0, 0	0,0	300 4277	432 4952	490 5216	397 4861	1040 3349
0, 0	0, 1	0, 0	0, 0	0,0	987 8150	761 6652	890 5071	912 5870	685 4785
0, 0	0, 0	0, 0	0, 0	0,0	508 1454 2340	815 1312 2494	379 981 1753	386 975 2383	173 659
0, 0	0, 0	0, 0	0, 0	0, 0 0, 0 0, 0	2340 3311 10187	2494 4413 7885	1753 4128 8155	2383 4121 5599	659 1411 3395 5084 1703
0, 0	0, 0	0, 0	0, 0	0, 0	2662	3200	2619	2025	1703
0, 0	0, 0	0, 0	0, 0	0, 0	2550 613	2798 806	2092 695	2783 795	1648 683
0, 0	0, 0	0, 0 0, 0	0, 0	0,0	2852 1794	2431 1435	3015 2989 1334	2949 1182	2172 2993
0, 0	0,0	0,0	0, 0	0,0	587	572 4790		644 6421	1078 5130
0, 0	0, 0	0, 0	0, 0	0,0	587 3944 8252 652	572 4786 5366 988	742 4911 3088 935	644 5421 7908 2224	6076 3174
0, 0	0, 0	0, 0	0, 0	0,0	531	1095	1469	825	1500
0, 0	0, 0	0, 0 0, 0 0, 0	1, 1 0, 0 0, 0	0, 0	180 1707 9110	181 2213 7667	239 2046 6873	460 1607 5740	252 1876 4289
0, 0	0, 0	0, 0	0, 0	0,0	2417 6820	2370 8197	2864 9323	2333 8970	2068 5695
0, 0	0,0	0, 0	0, 0	0, 0	1627 797	937 480	876 1061 2971	1927	1595 963
0, 0	0, 0	0, 0	0, 0	0, 0	3103 600	3200 1003	1011	2270 1180	2250 989
0, 0	0,0	0, 0 0, 0 0, 0	0, 0	0,0	1329 7304 432	1048 6796 398	950 7864 755	1032 5251 253	661 4888
0, 0	1, 1	0, 0	0, 0	0, 0	432 764	398 389	755 669	253 1026	4888 1075 696
0, 0	0, 0	0, 0	0, 0	0,0	1597 837	2229 783	1513 1251	1566 1404	2013 1350
0, 0	0, 0	0, 0	0, 0	0, 0	7561 3161	7926 2613	6584 2477	6223 2320	5178 1781
0, 0	0, 0	0, 0	0, 0	0, 0	4978 893	4760 779	3994 1075	3043 1050	2473 907
0, 0 0, 0 0, 0	0, 0	1, 0 0, 0 0. 0	0, 0 0, 0 0. 0	0,0	4330 3231 444	3353 3976 1046	2557 5612 996	3859 3307 1205	3756 3090 1390
0, 0	0, 0	0, 0	0, 0	0, 0	11274	1046 11306	996 15020	1205 7639	1390 16242
0, 0	0, 0	0, 0	0, 0	0, 0	2759 3197	3356 1251	4258 521	3056 1115	3098 1605
0, 0	0,0	0, 0	0, 0	0, 0	1617 625	1664 478	2174 518	1491 538	1557 98
0, 0 0, 0 0, 0	0, 0	0, 0	0, 0 0, 1 0, 0	0, 0	718 913 651	917 966 991	770 1096 1416	805 1228 1331	679 1541 1564
0, 0	0,0	0, 0	0, 0	0,0	5401 688	6095 849	4669 1463	5535 1745	3191 1793
0,0	0,0	1, 0	0, 0	0,0	53 885	71	42 831	64 768	77 844
0, 0	0,0	0, 0	0, 0	0,0	483	699	638	380	487
0, 0	0, 0	0, 0	0, 0	0,0	1609 835 2184	2371 889 2671	1917 489 1976	941 805 3480	1201 582 1700
0, 0	0, 0	0, 0	0, 0	0, 0	2184 1190 7759	2671 1108 8240	1976 1021 7753	3480 1176 9287	1091 7455
0, 0	0, 0	0, 0	0, 0	0, 0	1920 5523	2242 6347	1830 5261	2673 7138	2017 6945
0, 0	0,0	0, 0	0, 0	0, 0	731 1211	890 1275	548 988	562 1222	332 1319
0, 0 0, 0 0. 0	0, 0	0, 0 0, 0 0, 0	0, 0 1, 1 0, 0	0,0	7601 243 280	6907 312	4392 24 379	8969 169 463	5899 541 581
0, 0	0, 0	0, 0	0, 0	0, 0	280 607 759	356 309 790	379 333	463 668 581	581 1418 588
0, 0	0, 0	0, 0	0, 0	0, 0	759 930	790 1446	329 1164	581 795	588 873
0, 0	0,0	0, 0	0, 0	0,0	1781 725	1089 840	1145 464	1820 1274 755	1410 927
0, 0	0, 0	0, 0	0, 0	0, 0	318 377 622	514 611 627	987 836 951	719 1274	914 792 1615
0, 0	0,0	0, 0	0, 0	0,0	3371 1271	2327	2645 1503	3474 1687	2533
0, 0	0, 0	0, 0	0, 0	0, 0	856 817	1108	957 890	855 1127	711 1183
0, 0	0,0	0, 0	0, 0	0,0	888 1570	871 2030	1341 2110	1329 1862	1242 1950
0, 0		0, 0 0, 0 0, 0	0, 0	0, 0	33251 5210	28376 4799	30128 4428	26671 5320 1237	43185 3953
0, 0	0, 0	0, 0	0, 1	0, 1	436 1483	938 1585	499 925	1237 1389	595 1091
0, 0	0,0	0, 0	0, 0	0,0	6347 680	6137 1088	5928 658	3522 691	4751 731
0, 0	0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	1658 697	2163 855	2542 870	1903 600	2028 724
0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	0, 0	0, 0 0, 0 0, 0	0, 0 0, 0 0, 0	2007 477	1040 559	1890 629 721	1747 710	1290 735
0, 0	0, 0	0, 0	0, 0	0,0	255 2490	316 2455 5048	721 2502	628 2533	866 2170
0, 0	0, 0	0, 0 1, 1	0.0	0, 0	5979 660 57 5730	934 934 45 5543	4825 147	4764 782	3385 640
0, 0	0,0	0, 0	0, 0	0,0			5530	6280	140 5062 719
0, 0	0,0	0, 0	0, 0	0, 0	413 6676	355 7901	395 7166 5303	483 8374	7158
0, 0	0,0	0, 0	0, 0	0, 0	5666 833 3126	5050 1143 2360	5303 1340 2938	2555 1181	5105 870 2900
0, 0	0,0	0, 0	0, 0	0.0	586 626	650 918	2938 984 535	539 575	1452 384
0, 0	0,0	0, 0	0, 0	0,0	6770 15001 1357	7403 7799 993	6121 9047 849	6642	4242 11850 1097
0, 0	0,0	0, 0	0, 0	0,0	1357 657	993 1026	849 863	9825 1168 877	1097
0, 0	0,0	0, 0	0, 0	0,0	1002	724 422	842 534	1313	1165 847
0, 0	0, 0 0, 1 0, 0	0, 0	0, 0	0, 0	489 334 322	362 575	652 394	668 382	586 528
0, 0	0,0	0, 0	0, 0	0,0	4012 2081	4314 1714	4656 1961	4321 2862	3269 2080

ally ized - nt 3- ger	Globally Normalized - Patient 4- Bigger	Globally Normalized - Patient 5- Bigger	Average - Larger	S. Dev Larger	%S.Dev Larger	%CFC - Average Larger from Average	Student T test p value	Block	Row	Column	Refseq	Un L
7 81	3052 22425	2928 41241	3298 25357	367 8404	11 33	Average Smaller -19	.106	12	9	6	NP_002745 NP_055907.3	015
17 6 6 13	6172 377	4650 1023	5322 1317	598 1054 429	11 80	-19 -19	.085	1 8	7 8	5 4	36142.1, NP_002 NP_065390 AAA36142.1	P27
13 11	5384 2448 1137	4626 2544 2521	2878 1988	329 484	11 24	-19 -19 -19	.097	12	10	7	NP_056006.1 NP_004926	Q91
9 9	2027 3092	2296 2027	1854 3585	333 1187	18 33	-19 -19	.279 .294	14 16	9	6	NP_004318.3 NP_002745.1 NP_006245	P1 01
9	1912 2581 190	1565 2477 437	1973 2005 219	295 625 114	31 52	-19 -19 -19	.036 .147 .220	13 9	9 7 9	2	NP_000825	P2 Q1
6 ) 1	397 4861 912	1040 3349 685	532 4531 847	262 666 109	49 15	-20 -20	.136 .075 .304	7 4 10	10 10	8 9	NP_006247 NP_056006.1 NP_000312	Q1 Q9
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					Globally Globally Normalized Normalized Median Median 1545 1490	Median	Globally Globally Normalized Normalized Median Median 1728 2278				Normalize Median 1597	Median	Median	Globally Globally formalized Normalized Median Median 1745 1646						
Serial Antibody Target Protein No. Codes Name	Phospho Site (Human)	File Full Target Protein Name Paties	p- Flag- Flag- nt Patient Patier 2- 3- ler Smaller Smalle	Flag- Flag- t Patient Patient 4- 5-	Globally Normalized - Patient 1- Smaller Globally Normalized - Patient 2- Smaller Smaller		Globally Globally Normalized - Normalized - Patient 4- Patient 5- Smaller Smaller	Average - Smaller	S. Dev %S.Dev. Smaller Smaller	Flag- Patient Patient Patient 1- 2- 3- 4- Bigger Bigger Bigger Bigger				Globally ormalized - Patient 4- Bigger Bigger	Average - Larger	S. Dev %S.Dev. Larger Larger	%CFC - Average Larger fro	Student T	Block Row	Column Refseq Uniprot
No. Codes Name  603 NND84 PACSIN1		Protein kinase C + casein kinase substrate in neurons motein 1 0 0	0.0 0.0	0.0 0.0	Patient 1- Patient 2- Smaller Smaller	1940	1142 2743			1- 2- 3- 4- Bigger Bigger Bigger 0.0 0.0 0.0 0.0	Bigger Bigger	410	904	Patient 4- Patient 5- Bigger Bigger 1646 1142	4000	442	%CFC - Average Larger fro Average Smaller	n test p value		
593 PND57-2 p53 550 NK117-3 Nek2 575 PK060-1 p38a MAPK	S392 Tu Pan-specific Ni	umor suppressor protein p53 (antigenNY-CO-13) 0, 0	0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0	888 724 570 443	902 595	871 572 659 1364	791 726	727 48 127 16 327 45 336 19	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 616 0, 0 293	734 365	557 379	522 384 956 583	563 515	115 20 241 47 304 25 549 46 520 25	-29 -29 -29	.026 .292 .090	16 9 14 9	5 NP_065855 Q0BY11 7 NP_000537 P04637 3 NP_002488 P51955 3 NP_001306 Q16530 2 NP_004324 P15058 11 NP_659732 P46734 6 NP_004653
73 NK156 B-Raf 490 NK101-3 MEK3	Pan-specific M	IATRI proto-oncogene-encoded protein-senne whase U, U  MAPK/ERK protein-serine kinase 3 beta isoform (MKK3 beta) 0, 0	0,0 0,0	0,0 0,0	1373 1025 3201 3928 1703 1639	1306 2391 2944	1491 3222 2734 2753 2164 3287	1004	784 47	0,0 0,0 0,0 0,0	0, 0 968 0, 0 2374	935 979 3026 1513 578	606 1726	1172 2225 1814 1657 1862 1573	1190 2119 1655	549 46 520 25 204 12	-29 -29	.039	9 6 12 8	2 NP_004324 P15056 11 NP_659732 P46734 8 NP_001561.3 O43187
406 NK081 IRAK2 679 NK148 PKN 467 PK694 MARK1	Pan-specific Pr	rotein kinase C-related protein-serine kinase 1 0, 0	0,0 0,0	0, 0 0, 0 0, 0 0, 0	1703 1639 447 464 16864 11317	593 17612	2164 3287 486 1591 14060 10416	716 14054	441 61 2873 20	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 1401 0, 0 354 0, 0 11699	1513 578 12382 6106 470	513 7028	1862 1573 500 575 11105 7094	504 9861	204 12 81 16 2322 24 1113 20 193 29	-29 -30 -30	.358	4 10 13 8	8 N°_001961.3 Q4318/ 1 NP_002732 Q16512 5 NP_001273053 Q9P042 7 NP_000876 P13612 9 NP_003152 P23443 11 NP_006249.1 P14619
401 PN043 Integrin a4 596 PK166 p70 S6K 678 NK203 PKG1b-NT	S988 In S411 Ri	ttegrin alpha 4 (VLA4) 0, 0 8bosomal protein S6 kinase beta-1 0, 0	0,0 0,0	0,0 0,0	7158 799 497 3305 4506	9817 1341 5575	488 1591 14060 10416 5603 5795 973 1143 4093 4167			0,0 0,0 0,0 0,0	0,0 6907 0,0 448	6106 470 3276	5492 680 2778	5220 3557 762 967 3467 2088			-30 -30 -30	.036 .056	8 8 12 9 16 9	7 NP_000876 P13612 9 NP_003152 P23443 11 NP_006249.1 P14619
381 NN131 (2PP2A (PHAPII)	Pan-specific Pr Pan-specific Py Pan-specific Co	CMP-dependent protein resista 1, tela source 0.0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 1 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	7590 4394 1029 1602	7035	6796 10487	7261	1949 27 626 40 244 31	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0, 1 5316 0, 0 1291 0 0 800	3276 4999 1438 338 1026	2680 900 298	6459 5840 1014 808 647 641	5059 1090 545	1288 25 238 22 194 36	-30 -30	.036 .056 .070 .104 .283	9 8 15 7	2 NP_003002 Q01105 9 NP_002028 P06241 11 NP_004374 P41240
184 NK044-2 Csk 783 PN184 Smad2 571 NK120-2 p38a (MAPK 14)	S467 M Pan-specific M	tothers against decapentaplegic homolog 2 0, 0 fitogen-activated protein-serine kinase p38 alpha 0, 0		0,0 0,0	853 547 1409 1006 5786 3480	1837 4661	604 1225 1662 1306 4501 5431	1444 4772	244 31 288 20 802 17			1026 3218	942 1769	1326 992 4270 3465 145 146	3315	194 36 191 19 851 26	-30 -31	.050	8 10 9 9	9 NP_001003652 Q15796 3 NP_001306 Q16539
491 PK051 MEK3/6 97 NN016 Caspase 6 295 PK017 FAK	Pan-specific Co Y397 Fo	RePMCHER protein-senine kinase 3 beta isotorm (MKK3 beta)     U, U     aspase 6 (appoptotic proteinse Mch2)     Cocal adhesion protein-tyrosine kinase     O, 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0	112 93 675 396 7613 7730 1354 1485	198 1074 9852	170 138 656 570 8627 7185	674 8201	38 27 223 33 949 12 409 27 663 46	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 60 0, 0 315 0, 0 6471	3218 56 448 5785 1289	604 5699	145 146 550 421 6240 4219 770 1247	467 5683 1054	40 40 101 22 785 14 197 19	-31 -31 -31	.050 .050 .093 .090 .008 .043	16 8 16 6 12 7	7 NP_001217 P56212 10 NP_005598 005397
295 PK017 FAK 461 NK095 Lyn 281 NK208-3 ERK5 565 NN725-5 NT5E 111 NK025-5 Cdc2 p34	Pan-specific Ex Pan-specific Ex Pan-specific Ex	res-related protein-tyrosine kinase 0, 0 chracellular regulated protein-serine kinase 5 (Big MAP kinase 1 (BMK1)) 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	1354 1485 1046 1212 4470 2672 521 401	1148 1052 4695	8627 7185 1313 2311 1042 2711 4706 4990 628 2340	1522 1413 4307	409 27 653 46 834 19 710 73	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 1051 0, 0 946 0, 0 3226	1289 1035 2342 395	948	1011 940		39 4	-31	.262	5 8 5 7 9 9	11 NF 7003241 71417 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
354 NN054 Hsc70	Pan-specific C Pan-specific Hi Pan-specific Pr	Oyolin-dependent protein-serine kinase 1         0,0           (eat shock 70 kDa protein 8         0,0           orotein-serine kinase C mu (Protein kinase D)         0,0	0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	924 817	751 900	628 2340 1813 3225 846 2369	967 1506 1289	942 63	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 523 0, 0 496 0, 0 1003	395 723 907	547 863 722	849 1012 1584 1501 737 1038	665 1033 881	433 42	-31 -31 -32	.032 .335 .220 .207 .295	8 6 14 8 12 9	11 NP_001777 P06493 1 NP_778225 P33778 11 NP_002733 Q15139
615 NK125 PCTK1 673 PK089.1 PKC1 310 NN172 FH.2 779 NK250-1 SIK3	Pan-specific Pi S676 Pr Pan-specific Fo	year-supportables processive for window?	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0 0,0 0,0	955 975 999 755 1121 484	2290 1473 1138	1813 3225 846 2369 1190 2699 1214 1311 1363 1587	1150	250 22 250 22	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 1126 0, 0 585 0 0 441	723 907 534 599	1152 900 1017	1584 1501 737 1038 1786 946 938 910 924 1032 4485 3540	1109 787 775	404 36 159 20 267 35	-32 -32 -32	.295	11 9 12 9 16 8	8 NP_148978 Q00538 10 NP_006248 Q04759 2 NP_001034581 1_Q14192
779 NK250-1 SIK3 398 PK662 ILK1	Pan-specific Se Y351 In		0,0 0,0	0,0 0,0	5677 5739 964 855		6387 5500 1979 1404	5880 1290	319 5 342 26 794 39 148 17 234 36	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 4231 0, 0 1098	5053 636		1171 592	4001 875		-32 -32	.013	8 10 12 8	8 NP_001269677.1 <u>Q0Y2K2</u> 6 NP_001547 <u>Q14920</u>
398 PR962 ILK1 15 NN003 AK2 190 PN191 Cyclin E 384 PK153 IGF1R 749 NK158 RIPK 23 PK148 AM1 (PKBa)	T395 C) Y1165/Y1166 In	contrigue kinase 2 0, 0  0, 0  0, 0  nsulin-like growth factor 1 receptor protein-tyrosine kinase 0, 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0 0,0 0,0	1021 650 458 348	1773 2704 810 1027	1430 3236 945 1050 715 671	895 644	148 17 234 36	0,0 0,0 0,0 0,0	0, 0 1842 0, 0 460 0, 0 241	853 568 352	553 479	1850 1212 634 813 558 544	1372 606 435	234 27 404 29 118 19 122 28	-32 -32	.020 .085	13 7 16 8	1 NP_001616 P34819 1 NP_001229 P24864 3 NP_000866 P08069
	Pan-specific Ri Y474 Ri Pan-specific Fr	keceptor-inferacting protein-serine kinase 1 0, 0 MAC-alpha serine/threonine-protein kinase 0, 0 Potrio tyre-A morentor 1 mortein-tyrosine kinase 0.0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	5849 1916 1308 953 1271 1079	9082 2391 2503	9583 9244 2110 2354	6534 1823 1697	2780 43 585 32 672 40 344 43 525 49	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 3820 0, 0 846 0, 0 1418	2458 950	4180 1229	4068 7539 1350 1776 1772 974	435 4413 1230 1144 543 722	1681 38 328 27 409 36	-33	.094 .035 .282	13 9 16 6 6 7	11 NP_003795 <u>Q13548</u> 5 NP_005154 <u>P31749</u> 5 NP_005223 <u>P21709</u>
405 NK080-2 IRAK1 87 NK016-2 CaMK1d 104 NN167 Cayeolin 1	Pan-specific In Pan-specific Co Pan-specific Co	Interfación i receptor-associated kinase 1 (Pelle-like protein kinase) 0, 0 o actividen a l'encommonale dependent protein-antine kinase 1 delta 0, 0 o alavacción 1 0, 0 o commonale del commonale d	0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	564 657 788 551 456 376	604 1251 642	1103 2530 718 1485 770 2021 835 597 629 834	1076	344 43 525 49 159 27	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 432 0, 0 679 0, 0 301	703	826	666 /36	543 722 389	227 42 57 8 100 26	-33 -33 -33	.020 .085 .094 .035 .282 .016 .230 .046	8 8 1 6	8 NP_001560 P51617 5 NP_003647 Q8IU85 9 NP_001166366.1 Q03135
104 NN167 Caveolin 1 250 PN170 Elk1 674 PK090-1 PKC1 649 NK133 2 PKC5	\$389 E1 \$695 Pr	TS domain-containing protein Elk-1 0, 0  rotein-serine kinase C thota 0, 0  notein porine kinase C thota 1	0,0 0,0		333 378	601	508 453		159 27 242 45 95 21	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 1, 1 0, 0 0, 0	0,0 219 0,0 179		283	338 354		100 26 152 42 68 22		.126 .038 .212 .115	14 7 16 9	2 PF_001034581: 014192 8 PF_001034587: 014192 8 NF_001547 01420 9 NF_001547 01420 11 NF_001229 P2484 13 NF_000068 (1990) 11 NF_001766 01456 15 NF_000154 27176 15 NF_000154 27176 15 NF_000154 27176 15 NF_000154 27176 16 NF_000154 27176 17 NF_000154 27176 18 NF_000154 27176 19 NF_00164564 003155 18 NF_000154 27176 10 NF_000164564 003155 10 NF_00016464 003155 10 NF_000164664 003155 10 NF_00016464 00315
648 NK133-2 PKCb 91 PK556 CaMK4 806 PN079-PN136 STAT1 530 NK208 MLK3 108 PN171 C-Cbi	T200 Ci Y701 Si	Total Francisco Communication (Communication Communication	0,0 0,0 0,0 0,0 1,1 0,0	0,0 0,0 0,0 0,0 0,0 0,0	4491 3524 3741 2138 1524 892	5560 4365 1585	2837 5903 2543 4219 1597 2832 424 955	3401 1686	1166 26 900 26 630 37 270 62	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 3610 0, 0 2171 0, 0 544	2107 536 259 536	1722 1658 1259	4674 2602 2885 2493 1471 1767 243 439	29/1 2263 1115	68 22 1052 35 410 18 497 45 77 27 246 31	-33 -34	.212 .115 .039	13 9 13 6 15 10	10 NP_00248 Q04759 4 NP_002729 P05771 5 NP_001735.1 Q16566 8 NP_003330 P42224 10 NP_002410 Q16584 10 NP_005179.2 P22681
108 PN171 c-Cbi 745 PN151 RelB 301 NK061 Fes	Y700 Si S562 Tr	Ambount-commodure-cognisms protest-senims with senims 4 0, 0 (ingred transduction protest-senims with senims 4 0, 0 (ingred transduction and activation of transcription 1 alpha 0, 0 (ingred transduction protein clinase 3 0, 0 (ingred transduction protein CBL 0	1,1 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	258 216 1043 683 1038 585	1320 1253			270 62 306 26 638 44 599 31	0, 0 1, 1 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 233 0, 0 552 0, 0 660		709	980 1162	788 949	246 31 145 15 398 31	-34 -34 -34 -34	.006	12 6 13 9	10 NP_002410 U16584 10 NP_005179.2 P22681 10 NP_006500.2 Q01201
301 NK061 Fes 86 NN137-1 Calreticulin 781 NN095 Smac/DIABLO 25 NK130-6 AH2 (PKBb)	Pan-specific Co Pan-specific Co Pan-specific So	ranscription factor ReiB 0, 0, 0 earFps probin-lyrosine kinase 0, 0 alreitosin 0, 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	1535 1332 16801 8094 600 350	2297 12085 1211	2023 2316 1592 2944 13130 15358 1121 1045	1940 13093 865	599 31 2996 23 333 38 1008 79	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 1803 0, 0 8814 0, 0 254	1007 800 8798 383	988 6629 572 706	1688 1087 9800 8854 931 694	1273 8579 567	398 31 1046 12 237 42 353 42	-34 -34 -34 -35	.176 .040 .054 .274	12 7 13 6 16 10	10 NP-0051792 P22881 10 NP-005902 Q1291 11 NP-001996 P07332 4 NP-004341 P7-0332 8 NP-02303 QNP28 1 NP-001976 QNP28 1 NP-002825 Q09124 1 NP-002825 Q09124 1 NP-002825 Q09124 1 NP-0038011 Q15202 9 NP-98001 QNP28 6 NP-008245 Q09566 6 NP-008245 Q09566
25 NK130-6 AM2 (PKBb) 774 NP026-2 SHP2 680 NK144-1 PKR1				0,0 0,0	578 545 1492 1409 604 469		739 3219 1381 3970 767 2279					481 1124 592	706 1051 717	898 1480 1846 1355 798 528			-35 -35	.274 .243 382	11 6 8 10 12 10	1 NP_001617 P31751 7 NP_002825 <u>006124</u> 1 NP_002750 P19525
864 NP037 Wip1 554 NK119 Nek7 654 PK080 PKCd	Pan-specific Pr Pan-specific Ni	rotein phosphatase 1D 0,0  IIIMA (never-in-mitosis)-related protein-serine kinase 7 0,0  rotein-serine kinase C delta 0,0	0,0 1,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0	1372 1117 1175 670	1815 1710 343	1232 1806 930 2257 651 240	1469 1348	657 66 291 20 570 42 143 34	0, 0 0, 0 1, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 1273 0, 0 1080	383 481 1124 592 717 380	694 632	1229 846 1303 959	952 871	99 15 250 26 328 38 264 98	-35 -35	.243 .382 .083 .200	8 10 13 8	11 NP_003611.1 <u>015297</u> 9 NP_598001 <u>Q870X7</u>
671 PK093-1 PKCm (PKD) 489 NK101 MEK3	S916 Pr	rotein-serine kinase C mu (Protein kinase D) 0, 0	0,0 0,0	0,0 0,0	3018 2511 719 593	3103 603	2723 1986 562 1046	2668	401 15 179 25	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 1712 0, 0 636	2028 311	1487 288	1958 1360 451 564	1709	259 15	-36	.011 .025 .365 .164	8 9 8 8	10 NP_002733 Q15139 11 NP_659732 P46734
599 PK146 p70 S6K 876 NK188-1 ZIPK 298 PK629 FAK	Pan-specific ZI Y577 Fe	Per-Norte Protest-General Walker 2 deep reported (1997) (0.00 Per Nortes (1997	0,0 0,0 0,0 1,1 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0 0,0 0,0 0,0 0,0	200 35 492 742 2750 1797	76 1051 2431	89 97 805 1307 2008 2537	99 880 2305	55 55 278 32 350 15	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 25 0, 0 327 0, 0 1755	50 425 1304	83 315 1354	198 1360 451 564 96 60 1105 598 1653 1181 213 162 700 1103	63 554 1449	137 30 25 39 293 53 218 15 43 29 145 17 142 23 197 54	-37 -37 -37	.385 .164 .010	4 9 13 10 16 7	9 NP_003152 P23443 11 NP_001339 O43293 10 NP_005598 O05397
298 PK629 FAK 105 PN147 Caveolin 1 112 NK025-6 Cdc2 p34 139 NK027-2 CDK4	Y14 Ci Pan-specific Ci Pan-specific Ci				122 143 1020 1207 429 576	943 629	227 322 994 2594 482 2906	237 1352 1004	350 15 98 41 628 46 953 95		0, 0 77 0, 0 795 0, 0 429	145 898 638	147 735 710	213 162 700 1103 528 838	149 846 629	43 29 145 17 142 23	-37 -37 -37	.118 .110 .425	16 6 12 6 7 7	9 NP_001166366.1 003135 11 NP_001777 P06493 1 NP_00066 P11802
576 PK060-3 p38a MAPK	T180/Y182 M S363/S369 Ri	fitogen-activated protein-serine kinase p38 alpha 0, 0 libosomal S6 protein-serine kinase 1/2 0, 0	0,0 1,1 0,0 0,0 0,0 0,0 0,0 0,0	1,1 1,1 0,0 0,0	890 348 1064 788 531 651 1303 1279	28 1511	1131 538 1106 1273		390 66 239 21 90 16 186 16	0, 0 0, 0 1, 1 1, 1	1,1 20 0,0 530	145 888 638 599 561 354 675 1100 213	501 683 264	333 384 793 1005	367 714	197 54 173 24 59 17 124 17	-37 -38	010 1110 1110 425 462 018 015 058 215 186 081 132 107 215	12 9 1 10	11 NP 569732 P46734 9 NP 003152 P22443 11 NP 007339 Q4323 11 NP 007339 Q4323 11 NP 007558 Q05337 9 NP 00116856 Q03135 11 NP 0007577 P0443 11 NP 007506 Q11535 11 NP 007506 Q11535 11 NP 007506 Q11535 11 NP 007506 Q11541 11 NP 007506 Q11541 11 NP 007507 Q1541
763 PK100 R5K172 290 NK060 FAK 488 PK050 MEK2 mouse 738 PN131-1 Rb 750 NK160 ROCK-IFROKb	T394 M S795 Ri	terinodasiona-associated protein i	0,1 0,0	0,0 1,1	1064 788 531 651 1303 1279 1457 1025	1237 2395	1131 538 1106 1273 420 658 816 1290 2145 1242 275 691	1185 1653	186 16 528 32 169 46	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0, 0 892 1, 1 665	675 1100	718 1080	845 545 1299 957 243 168	735 1020	209 20		.027	4 8 14 10	11 NP_075627 P36507 4 NP_000312 P06400
430 NK088-2 JNK2 79 PN014 BRCA1 666 NK218 PKCh	Pan-specific Ju S1497 Br	once protein-semin viniase beau 0,0 un N-terminus protein-semine kinase (stress-activated protein kinase (SAPK)) 1 preast cancer type 1 susceptibility protein frotein-semine kinase C eta 0,0	0,0 0,0 0,0 1,1 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0	347 348 833 391	347 1516 652	456 1456 1095 1308 526 999	590 1029	435 74 391 38 181 27	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 280 0, 0 428	348 559 566 505	266 618	250 676 727 834 291 504	364 633 405	78 34 159 44 139 22 112 28 74 14 499 18	-38 -38 -38	.186	2 8	1 NP 000099 (3):484 (4):58 (4)
666 NK218 PKCh 274 PK170-PK171 ERK1/2 138 NK027 CDK4 775 PP004 SHP2		rotein-serine kinase C eta  kinase C eta  kinase S etine kinase C eta  kinase 1 (p44 MAP kinase) + Extracellular rr 0, 0  y-clin-dependent protein-serine kinase 4  0, 0	0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	489 623 788 527 3618 3135	1548 6351	3164 5794	4413	1378 31	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 374 0, 0 492 0, 0 3443	566 505 2140	288 560 2420	291 504 481 680 3152 2393	544 2710	159 44 139 22 112 28 74 14 499 18	-38 -38 -39	.034 .132 .107	1 9 13 7 12 6	4 NP_006246.2 P24723 4 36142.1, NP_002 P27361 7 NP_000066 P11802
675 NK141 PKCz	S576 Pr Pan-specific Pr Pan-specific Dr				627 1062	680 664 2779	523 597	695	239 102 189 27 845 38	0, 0 0, 0 1, 1 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 13 0, 0 494 0, 0 1981	13 551 925 369 1027 1425 286	482 325 1087	31 181 413 333 1612 1192	144 423 1359		-39	.215 .021 .169	4 10 8 9 16 7	7 NP_002825 Q06124 11 NP_002735 Q05513 4 NP_004217 Q94768
325 NN045 GNB2L1 188 NN030-1 Cyclin D1 502 NK106-2 MEK7	Pan-specific G Pan-specific O Pan-specific M	Suanine nucleotide-binding protein beta (receptor for activated C kinase 1 (RACH 1, 0 )cyclin D1 (PRAD1) 0, 0 0,0 0,0 0,0 0,0 0,0 0,0 0,	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0	1530 836 2185 1544 1018 1232	1954 3055 1173	54 116 523 597 1679 3637 1003 2529 1433 3610 787 3755 482 1207 1064 3554	1570 2366 1593	189 27 845 38 621 40 849 36 1092 69	1, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 1222 0, 0 1954 0 0 1000	369 1027 1425	760 648 925	1561 868 1942 1572 621 834	1429	407 43 516 36	-39 -40 -40	.021 .169 .183 .166	11 7 9 7	11 NP 006089 P63244 1 NP 444284 P24385 3 NP 005034 014733
12 CN001 ACTA1 (Alpha -actir 186 NN029 Cyclin B1	/ I sirapcone A	ctin, alpha skeletal muscle 0, 0 cyclin B1 0, 0	0,0 0,0	0,0 0,0	503 462 1476 1021	884			292 42	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0, 0 559 0, 0 950	286 1068	317 991		424 1174	265 28 107 25 240 20	-40 -40	075	16 6 5 7	3 NP_001091.1 P68133 1 NP_114172 P14635
378 NK193 HSTK12 (Aurora 2) 564 NN074 NME7 801 NK172-4 Src	Pan-specific No. Pan-specific St	ycan B1 0, 0  uurora Kinase B (serine/threonine protein kinase 12) 0, 0  uurora Kinase B (serine/threonine protein kinase 12) 0, 0  irc proto-oncogene-encoded protein-tyrosine kinase 0, 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0 0,0 0,0 0,1 0,0	1799 1378 1155 825 256 254	3081 1625 377	1954 3554 1412 3765 1024 2112 452 2093	1348 686	964 42 464 34 707 103	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 1975 0, 0 1173 0, 0 235	1068 636 404 298	253	1841 1496 1155 915 762 515	811 413	516 37 342 42 201 49	-40 -40	.136 .458	5 9 15 10	1 NP_037462 Q9Y588 7 NP_005408 P12931
447 NK090-2 Krs-1 92 NK211 CamKi 590 NN082 p53	Pan-specific Pr Pan-specific Co Pan-specific To	Totein-senine kinase suppressor of Nas 1 U, U  Calcium/calmort/lin_dependent nortein_serine kinase 1 alnha 0 0	0,0 0,0	0,0 0,0	616 353 838 494 1317 2129 16758 13358	1167	1325 3560	1477	274 41 1080 73 420 21	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0.0 634	340 630 1426 12267	429 1166 1041	518 401 860 1098 1212 859	398 877 1164 16148	74 19 225 26 197 17 5817 36	-40 -41 -41			
590 NN082 p53 296 PK017-1 FAK 279 NK058 ERK3 735 PN113 Rb 275 PK168-PK169 ERK1/2		umor suppressor protein p53 (artigenWY-CO-13)         0.0           ocul adhesion protein-lyvosine kinase         0.0           transcellular regulated protein-senior kinase         0.0           teletrioblasiona-associated protein- 1         0.0           teletrioblasiona-associated protein- 1         0.0           transcellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated protein- senior kinase 1 (p44 MAP kinase) + Extracellular regulated kinase	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 1 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	16758 13358 1226 727 26 5	2518 27963 1993	1671 2172 31598 47065 875 1981 22 48 966 1068	27349 1360 24	420 21 11959 44 537 39 14 58 466 39	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0, 0 1073	12267 464 5 329	610	897 962	801	197 17 5817 36 228 28 11 75 205 30	-41 -41 -41	.109	16 7 13 7 1 9	8 NP_00537 P04637 8 NP_00538 Q0537 5 NP_002738 P31152 10 NP_000312 P06400 4 361421, NP_002 P27361
497 NK104 MEK5 870 NK186 Yes	Pan-specific M Pan-specific Ya	Zirtracellular regulated protein-serine kinase 1 (p44 MAP kinase) + Extracellular n     0.0       MAPK-IERK protein-serine kinase 5 (MRKS)     0.0       Jamaguchi santorma proto-oncogene-encoded tyrosine kinase     0.0       Iromodomain-containing protein-serine kinase 2     0.0	0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	1378 566 361 346 22 12	1961 439 32 2482	986 1068 442 1917 37 28 1515 3275	1188 701 26	466 39 609 87 9 33 853 45	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 762 0, 0 294 0, 0 10	329 303 13 683	620 308 17	924 813 463 658 21 14	690 405 15	205 30 141 35 4 26 287 26	-42 -42 -42		9 7 16 9 2 10	4 36142.1, NP_002 P27361 2 NP_660143 Q13163 11 NP_005424 P07947
80 NK013 BRD2 338 NK071 Haspin 197 NK048 DNAPK	Pan-specific Br	tromodomain-containing protein-serine kinase 2 0, 0 laploid germ cell-specific nuclear protein-serine kinase 0, 0 MA priliarbate portein-serine kinase 0, 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 1 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	1348 923 1939 1145	2482 2793 1548	1515 3275 1122 3480 1308 1572	1909 2096 1392	853 45 925 44 281 22	0,0 0,0 0,0 0,0	0,0 1/69	683 630	828 782	1372 1374 1489 1300 842 815	1096 1194	287 26 428 36 165 22	-43 -43		5 6 14 7	3 NP_005095 P25440 8 NP_114171 Q8TF76 2 NP_008935 P79527
99 PN162 Caterin a	9641 Ci 933 Ci	Caterin (cadherin-associated protein) alpha 0, 0 Caterin (radherin-associated protein) heta 1 0, 0	0,0 0,0		407 357 588 458 794 790		653 543 1144 866	649 854	335 52 297 35	0, 0 0, 0 0, 0 0, 0	0, 0 273 0, 0 260	252 375	347 729	451 511 483 549 895 946	367 479	100 27 159 33		.164	8 6 16 6	8 NP_001277236.1 P35221 8 NP_001895 P35222
101 Prints Calentin B 462 NK097 MAPKAPK2 14 NN002 AJF 595 NK223 970 58K 534 NK111 Mrs2 866 PK855 WNK1	Pan-specific Ap	Iltogen-activated protein kinase-activated protein kinase 2 0, 0 poptosis inducing factor (programed cell death protein 8 (PDCD8)) 0, 0 libosomal protein S6 kinase beta-1 0, 0	0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0	794 790 827 836 4456 5686	923 7333	739 3677 6147 6498	1242 1401 6024	502 40 1140 81 952 16	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 434 0, 0 755 0, 0 3180	252 375 779 836 3901 400	754 3188	689 868 3515 2870	696 780 3331		-44 -45	.002 .164 .017 .072 .321	13 8 8 6 16 9	4 NP_004/50 P49137 4 NP_004199 <u>095831</u> 9 NP_003152 <u>P23443</u>
534 NK111 Mnk2 866 PK855 WNK1 418 PK034-1 JAK2	Pan-specific M S382 Se Y1007+Y1008 Ja	MAP kinase-interacting protein-serine kinase 2 (calmodulin-activated) 0, 0	0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0 0,0 0,0 0,0 0,0	686 463 20 10 38 14	673 34 25	787 2333 30 55 26 119	989	680 69 15 51	0,0 0,0 0,0 0,0	0.0 3/3	400 10 16	21	558 806 15 24 10 57	541 16 23	154 29 6 35	40	.1//	14 8 3 10 15 8	10 NP_060042 <u>OSHBH0</u> 11 NP_001171914.1 <u>Q9H4A3</u> 4 NP_004963 <u>O60674</u>
815 NN108 STAT5B 875 NK187-2 ZAP70 786 PN125 SMC1		lignal transducer and activator of transcription 5B 0, 0 cea-chain (TCR) associated protein-tyrosine kinase, 70 kDa 0, 0 tructural maintenance of chromosomes protein 1A 0, 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	13 9 18 8 43 8	18 23 29	29 60 15 71 20 102	26 27 41	38 86 18 71 22 83 33 80	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	0, 0 5 0, 0 6 0, 0 14	7 7 10	13 20 18	18 24 12 23 15 43	13 14 20	7 52 7 49 12 58	-49 -50 -50	.119 .108 .202	2 10 1 10 4 10	5 NP_036580 P51692 11 NP_003168 P43403 10 NP_006297.2 Q14683
786 PN125 SMC1 792 NN145 SOCS2 877 NK188-2 ZIPK					20 5 37 10	19 33	13 75 35 108	26 44	25 93	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0		6 12 250	12 19	8 26 21 45	13 21	7 54 12 58	-51 -52	.202	7 10 9 10	4 9147.1 PP 00 127.1 11 11 11 11 11 11 11 11 11 11 11 11 1
7 NK001 Abi NK185 Wee1 863 NK185 Wee1 9791 NK185 Wee1 9791 NK148-2 Snik 174 PN023 CREB1 383 PK855 CK	Pan-specific W Pan-specific Po	belson proto-oncogene-encoded protein-tyrosine kinase 0, 0 Vee1 protein-tyrosine kinase 0, 0 Vee1 protein-tyrosine kinase 0, 0 Volo-like protein kinase 2 (serum-inducible kinase (SNK)) 0, 0	0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0 0,0	0,0 0,0	20 10 14 6	45 23	256 1548 21 61 15 110	31 34	484 81 19 61 39 115 75 123	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0, 0 0,	0,0 7	10	15 12	10 29 10 32	14	8 54 10 79	-62 -54	.053	4 10	11 NP_003381 P30291 5 NP_00613 Q9NY/3
174 PN023 CREB1 383 PK655 ICK 839 NK178 TrkA 463 PK044 MAPKAPK2	S129/S133 C/ Y156+T157 In Pan-specific No	Tobio-like protein kinase 2 (serum -inducible kinase (SNK)) 0, 0  AMP response element binding protein 1 0, 0  AMP response element binding protein 1 0, 0  element growth factor (NKE) receptor-lyyrosine kinase 0, 0  elemen growth factor (NKE) receptor-lyyrosine kinase 0, 0  factor (NKE) receptor-lyyrosine kinase 1 1, 1  factor (NKE) receptor-lyyrosine kinase 2 1, 1  factor (NKE) receptor-lyyrosine kinase 1  factor (NKE) receptor-lyyrosine kina	0,0 0,0 0,0 0,0 1,1 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	25 15 55 10 45 158 565 231	19 30 42	35 209 50 151 40 152	61 59 88	75 123 49 82 55 63 848 73			13 9 12 17	13 13 15	22 56 17 33 20 58	23 17 24	83 29 8 54 10 79 17 72 9 53 17 72 285 97	-62 -72 -73		1 6 4 8 1 10	<ul> <li>NP_004370 P16220</li> <li>NP_055735.1 Q9UP29</li> <li>NP_002520 P04629</li> </ul>
463 PK044 MAPKAPK2 650 PK075-2 PKCb1/2 660 PK081-2 PKCe	T222 M T500 Pi S729 Pi	fitogen-activated protein kinase-activated protein kinase 2 1,1 frotein-serine kinase C beta 1/2 0,0 frotein-serine kinase C epsiton 0,0	0,0 0,0 0,0 0,0 0,0 0,0	0, 0 0, 0 0, 0 0, 0 0, 0 0, 0	565 231 27 10 171 6	2299 30 18	2053 627 377 180 19 170	1155 125 77	848 73 141 113 77 99	0, 0 0, 1 0, 0 0, 0 0, 0 0, 0 0, 0 1, 1 0, 0 0, 0	1,1 315 0,0 9 0,0 5	17 10 7	40 11 9	285 808 20 74 12 30	293 25 13	285 97 25 100 9 69	-75 -80 -84	.148 .210 .152	1 8 9 9 1 9	111 NP_001339 Q43293 3 NP_005148 P00514 111 NP_003381 P30291 5 NP_006813 P30291 5 NP_005370 P16220 3 NP_055735.1 Q54P20 5 NP_004750 P40137 5 NP_004750 P40137 7 NP_005391 Q02156
<u> </u>				Average Median	3991 399 1545 149	1 3991	3991 3991 1726 2278 60269 74340	39	91 54 492 25		Average 31	991 3991 597 1688	3991 1753	3991 3991 1745 1646	3991 1680	421	J			<u> </u>
				Maximun	49061 5808	0 47720	60269 74340	572	65	l	Maximum 42i	998 47565	59731	47453 80921	55395		1			

Full Analysis: 10 Individual Wounds

										Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median
										1545	1490	1864	1726	2278
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	1-	2-	Flag- Patient 3- Smaller	4-	5-	Globally Normalized - Patient 1- Smaller	Globally Normalized - Patient 2- Smaller	Globally Normalized - Patient 3- Smaller	Globally Normalized - Patient 4- Smaller	Globally Normalized - Patient 5- Smaller
									Minimum	13	5	16	- 11	28
									Total	3500000	3500000	3500000	3500000	3500000

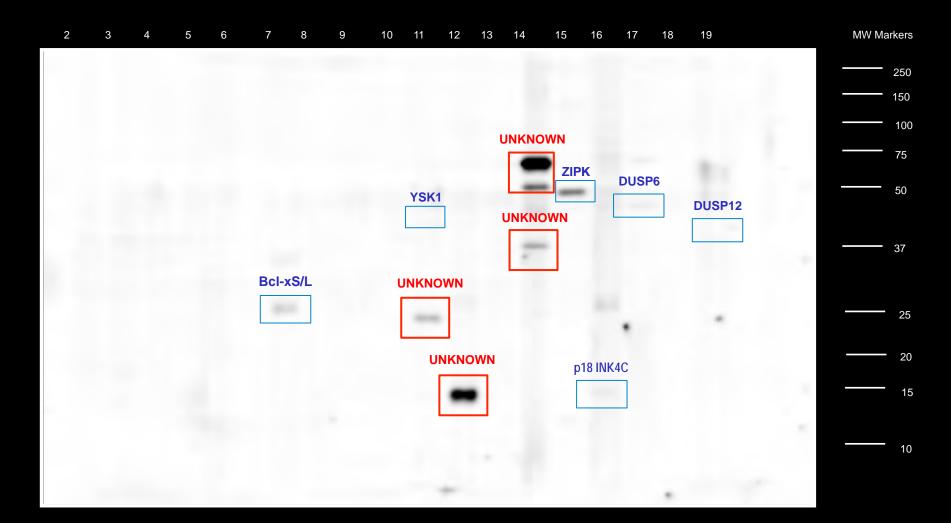
								Median	Median	
								1597	1688	
verage - Smaller	S. Dev Smaller	%S.Dev. Smaller	Flag- Patient 1- Bigger	Flag- Patient 2- Bigger	Flag- Patient 3- Bigger	Flag- Patient 4- Bigger	Flag- Patient 5- Bigger	Globally Normalized - Patient 1- Bigger	Globally Normalized - Patient 2- Bigger	No P
24							Minimum	5	5	
3500000							Total	3500000	3500000	

Average - Larger	S. Dev Larger	%S.Dev Larger	
13			
3500000			

%CFC - Average Larger from Average Smaller	Student T test p value	Block	Row	Column	Refseq	Uniprot Link

## Appendix H Pre-screen Results

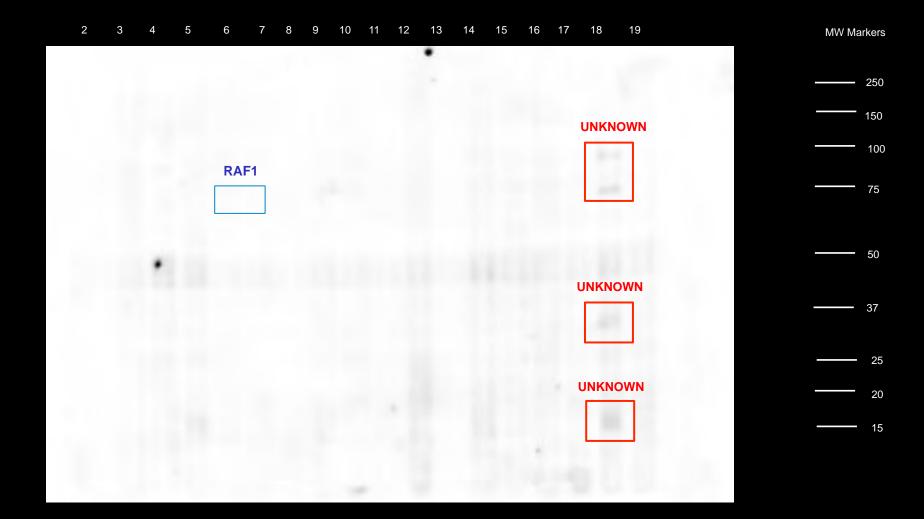
## Pre-Screen #1



No.	Lane	Ab Code	Target	Protein	Site	Strength
1	7	NN008	Bcl-xS/L	Bcl-xS/L	Pan-specific	Strong target
2	11	NK214	YSK1	YSK1	Pan-specific	Weak target
3	11	NK214	YSK1	Unknown	Pan-specific	Moderate x-reactive
4	12	NK002	ACK1	Unknown	Pan-specific	Strong x-reactive
5	14	NK001-2	Abl1	Unknown	Pan-Specific	Moderate x-reactive
6	14	NK001-2	Abl1	Unknown	Pan-Specific	Weak x-reactive
7	15	NK188-1	ZIPK	ZIPK	Pan-specific	Strong Target
8	16	NN077	p18 INK4c	p18 INK4c	Pan-specific	Weak target
9	17	NP040-2	DUSP6	DUSP6	Pan-specific	Weak target
10	19	NP046-3	DUSP12	DUSP12	Pan-specific	Weak target



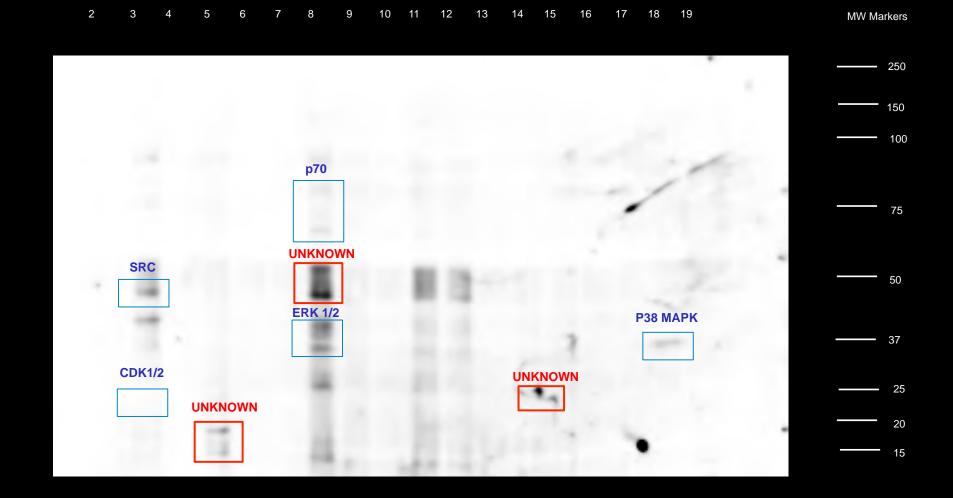
No.	Lane	Ab Code	Target	Protein	Site	Strength
1	4	NK253-3	WNK2	Unknown	Pan-specific	Strong x-reactive
2	9	NP030-3	DUSP3	DUSP3	Pan-specific	Weak target
3	9	NP030-3	DUSP3	Unknown	Pan-specific	Weak x-reactive
4	11	NN186	CD63	Unknown	Pan-specific	Moderate cross x-reactive
5	11	NN186	CD63	CD63	Pan-specific	Strong target (dirty)
6	18	NK105-5	MKK6	MKK6	Pan-specific	Weak target



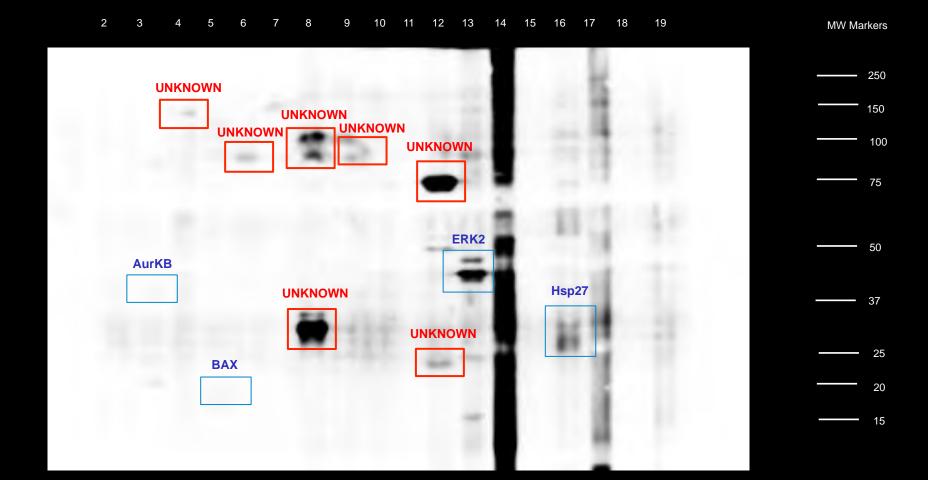
No.	Lane	Ab Code	Target	Proteir	n Site	Strength
1	6	NK155-6	RAF1	RAF1	Pan-specific	Weak target
2	18	PK800	Ron	Unknown	Y1238	Weak x-reactive
3	18	PK800	Ron	Unknown	Y1238	Weak x-reactive
4	18	PK800	Ron	Unknown	Y1238	Weak x-reactive



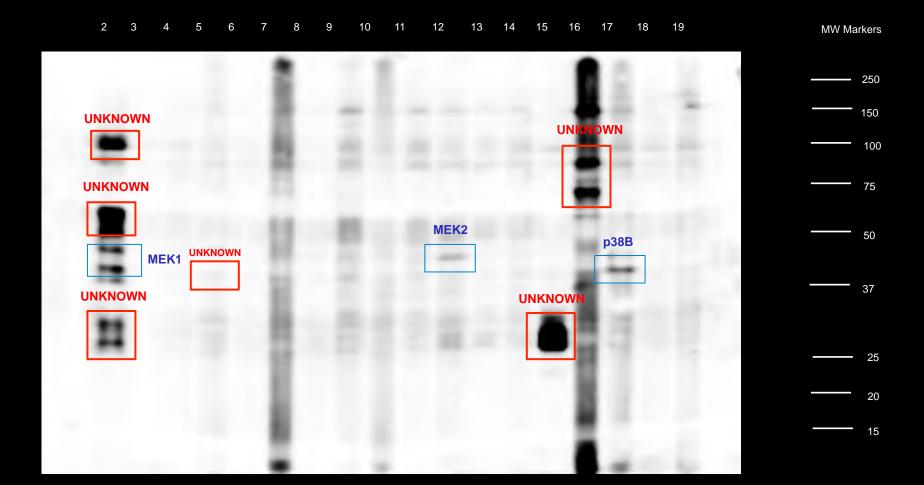
No.	Lane	Ab Code	Target	Protein	Site	Strength
1	3	NK120-3	р38а МАРК	p38a MAPK	Pan-specific	Strong Target
2	4	NK025-2	CDK1	CDK1 (CDC2)	Pan-specific	Weak target
3	4	NK055-NK056	Erk1/2	Erk1/2	Pan-specific	Weak target
4	6	NK0456	Erk2	Erk2	Pan-specific	Weak target
5	13	NK141	PKCz	PKCz	Pan-specific	Weak target
6	20	NK041	CK2a	CK2a	Pan-specific	Moderate target



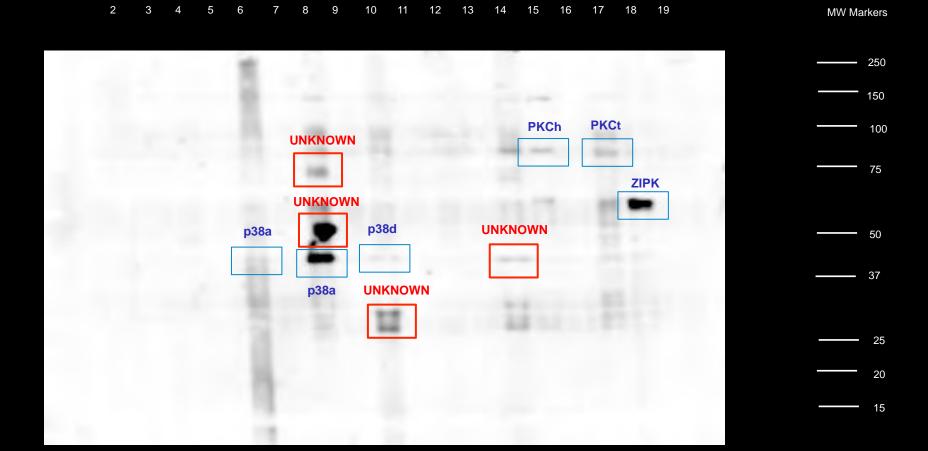
No.	Lane	Ab Code	Target	Protein	Site	Strength
1	3	PK108	Src	Src	Y530	Strong target
2	3	PK007-2	CDK1/2	CDK1/2	Y15	Weak target
3	5	PK073/PK107	PKCa or Src	Unknown	S657 / Y419	Moderate x-reactive
4	8	PK147	p70 S6 Kinase	p70 S6K	T412	Weak target
5	8	PK147/PK168/PK170	p70 or Erk1/2	Unknown	Phospho-site	Strong x-reactive
6	8	PK168-PK169	p44/42 MAPK	Erk1/2	Y204/Y187	Strong target
6	8	PK170-PK171	p44/42 MAPK	Erk1/2	T202/T185	Strong target
7	14	PK072	PKBa (Akt1)	Unknown	S473	Moderate x-reactive
8	18	PK060-3	p38a MAPK	p38a MAPK	T180/Y182	Moderate target



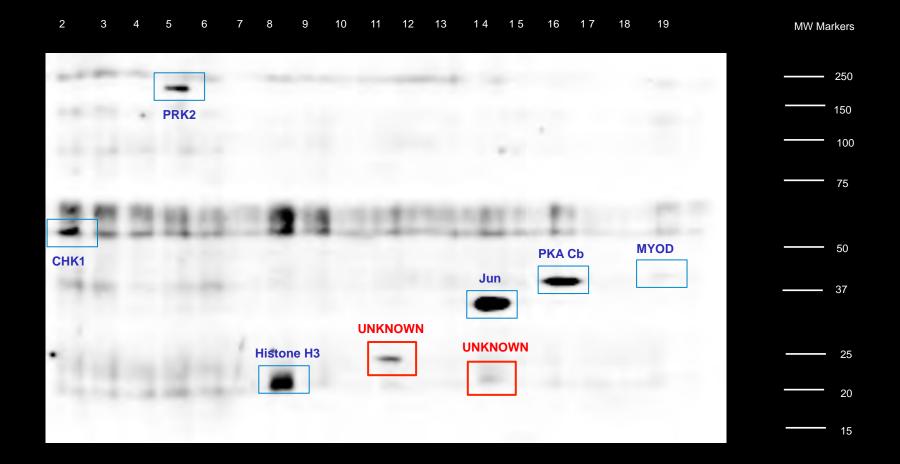
No.	Lane	Ab Code	e Target	Protein	Site	Strength
1	3	NK193-4	AurKB	AurKB	Pan-specific	Weak target
2	4	NK130-9	Akt2	Unknown	Pan-specific	Weak x-reactive
3	5	NN005	Bax	Bax	Pan-specific	Weak target
4	6	NN011	Caspase 1	Unknown	Pan-specific	Weal x-reactive
5	8	NK055-1	ERK1	Unknown	Pan-Specific	Strong x-reactive
6	8	NK055-1	ERK1	Unknown	Pan-Specific	Strong x-reactive
7	9	NK028-4	Cdk5	Unknown	Pan-specific	Moderate x-reactive
8	12	NK236-3	FGFR3	Unknown	Pan-specific	Strong x-reactive
9	12	NK236-3	FGFR3	Unknown	Pan-specific	Moderate x-reactive
10	13	NK056-4	ERK2	ERK2	Pan-Specific	Strong target
11	16	NN165-1	Hsp90 beta	Hsp90 beta	Pan-specific	Strong target



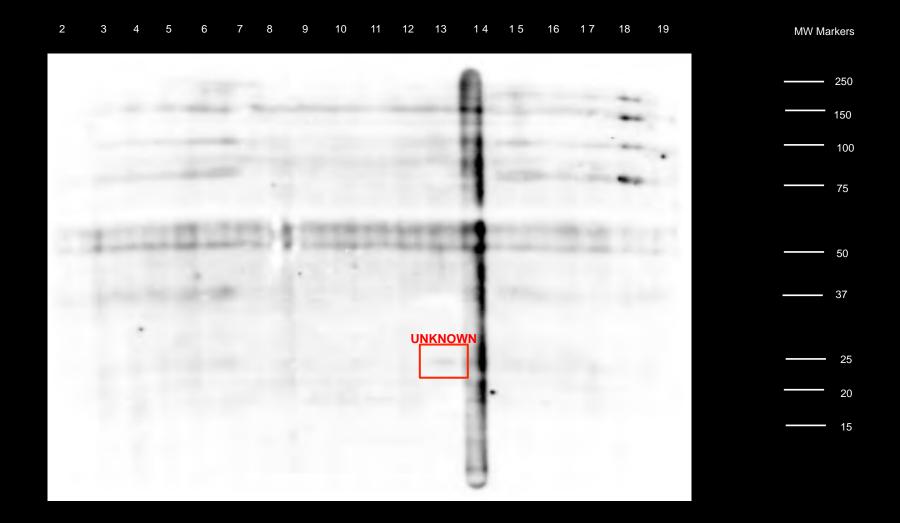
No.	Lane	Ab Code	e Target	Protein	Site	Strength
1	2	NK099-8	MEK1	Unknown	Pan-Specific	Strong x-reactive
2	2	NK099-8	MEK1	Unknown	Pan-Specific	Strong x-reactive
3	2	NK099-8	MEK1	MEK1 (MAP2K1)	Pan-Specific	Strong target
4	2	NK099-8	MEK1	Unknown	Pan-Specific	Strong x-reactive
5	5	NK155-5	Raf1	Unknown	Pan-specific	Weak x-reactive
6	12	NK100-6	MEK2	MEK2 (MAP2K2)	Pan-Specific	Strong Target
7	15	NK172-2	Src	Unknown	Pan-specific	Strong x-reactive
8	16	NK106-5	MKK7	Unknown	Pan-specific	Strong x-reactive (dirty)
9	17	NK248-1	p38b MAPK	p38b MAPK	Pan-specific	Strong target



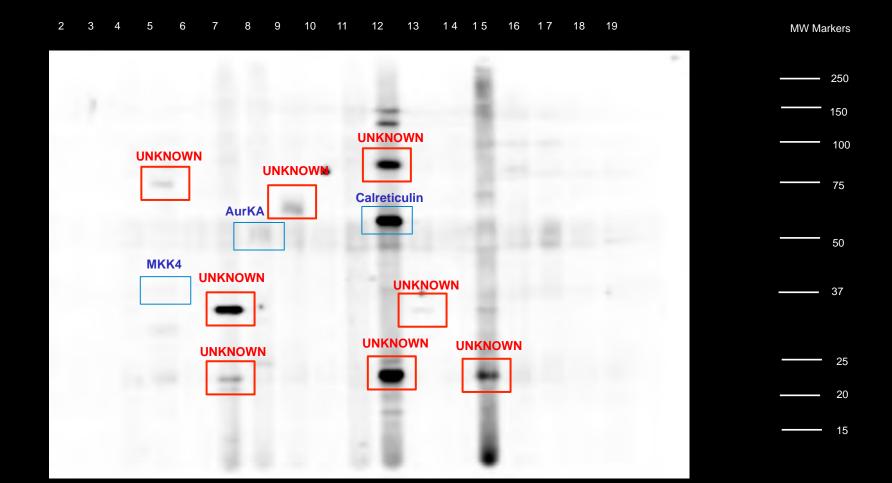
No.	Lane	Ab Code	e Target	Protein	Site	Strength
1	6	PK739	p38a MAPK	p38a MAPK	T180+Y182	Weak target (dirty)
2	8	NK120-3	p38a MAPK	Unknown	Pan-specific	Moderate x-reactive
3	8	NK120-3	p38a MAPK	Unknown	Pan-specific	Strong x-reactive
4	8	NK120-3	p38a MAPK	p38a MAPK	Pan-specific	Strong target
5	10	NK121-4	p38d MAPK	p38d MAPK	Pan-specific	Weak target
6	10	NK121-4	p38d MAPK	Unknown	Pan-specific	Moderate x-reactive
7	14	NN156	PLC R(PLCg2)	Unknown	Pan-specific	Moderate x-reactive
8	15	NK218	nPKC h	PKC h	Pan-specific	Moderate Target
9	17	PK089-1	PKCt	PKCq	S676	Moderate Target
10	18	NK188-1	ZIPK	ZIPK	Pan-specific	Strong target



No.	Lane	Ab Code	Target	Protein	Site	Strength
1	2	PK577	Chk1	Chk1	S280	Moderate target
2	5	NK149	PRK2	PRK2 (PKN2)	Pan-specific	Strong target
3	8	PN100	Histone H3	Unknown	T11	Strong target
4	11	NN093	Rb	Unknown	Pan-specific	Moderate x-reactive
5	14	PN163	Jun	Jun	T91	Strong target
6	15	NK187	ZAP70	Unknown	Pan-specific	Weak x-reactive
7	16	PK068	PKA Cb	PKA Cb	S338	Strong target
8	19	PN182	MyoD	MyoD	S200	Weak target



No.	Lane	Ab Code	Target	Protein	Site	Strength
1	13	NK157	RIP2/RICK	Unknown	Pan-specific	Weak x-reactive



No.	Lane	Ab Code	Target	Protein	Site	Strength
1	5	NK103-6	MKK4	MKK4	Pan-specific	Weak target
2	5	NK103-6	MKK4	Unknown	Pan-specific	Weak x-reactive
3	7	NK054-4	ErbB2	Unknown	Pan-Specific	Strong x-reactive
4	7	NK054-4	ErbB2	Unknown	Pan-Specific	Weak x-reactive
5	8	NK008-3	AurKA	AurKa	Pan-Specific	Weak target
6	9	NK244-2	Ret	Unknown	Pan-specific	Strong x-reactive
7	12	NN137-1	Calreticulin	Target	Pan-specific	Strong target (dirty)
8	12	NN137-1	Calreticulin	Unknown	Pan-specific	Strong x-reactive (dirty)
9	12	NN137-1	Calreticulin	Unknown	Pan-specific	Strong x-reactive (dirty)
10	13	PN071	Rb	Unknown	T826	Weak x-reactive
11	15	NK250-1	SIK3	Unknown	Pan-specific	Strong x-reactive (dirty)

# Appendix I Quantitative Microarray

2 ECPU-B 7 1 88 932.7 326.7 276.3 1579.1 351.7 816.1 3 52.7 816.1 3 52.7 816.1 84.2 119.1 840.1 75.7 848.8 87.8 77.7 848.8 87.8 77.7 84 ECPU-D 35 6 4.29 1191.1 840.1 75.7 7.7 848.8 87.8 77.7 848.8 87.8 77.7 848.8 87.8 87	AG ID	Code ECPU-A	Study Time 56	protein ug/ul 10.70	MIG, pg/ml 515.2	MMP-9, ng/ml 1546.4	<b>RBP-4, ng/ml</b> 1118.2	<b>S100A8, ng/ml</b> 2169.0	<b>S100A9, ng/ml</b> 77.6	TGFBR3, pg/ml 3459.2
4 ECPUC 35 2.73 2279 1528.3 382.7 4431.5 962.0 828.0 5 ECPUC 48 1.16 211.5 2472.1 257.1 478.8 1067.1 679.1 6 ECPUD 21 0.26 133.5 506.4 85.9 1993.2 1096.5 602.3 7 6 ECPUD 21 0.26 133.5 506.4 85.9 1993.2 1096.5 602.3 7 6 ECPUD 25 0.14 52.1 143.7 1.5 80.0 7 1125.6 502.3 8 6 ECPUD 25 0.14 52.1 143.7 1.5 80.0 7 1125.6 502.3 8 6 ECPUD 2 1 3.0 1.0 1125.1 143.7 1.5 8 200.7 1125.6 502.3 1 1125.1 112	2	ECPU-B	7	1.88	932.7	326.7	276.3	1579.1	351.7	816.1
6 ECPULC 48 1.16 211.5 2472.1 257.1 4795.8 1097.1 6791. 6 ECPULD 35 0.14 52.1 143.7 1.5 2400.7 1126.6 502.3 7 ECPULD 35 0.14 52.1 143.7 1.5 2400.7 1126.6 503.3 8 ECPULE 28 0.30 48.0 324.1 31.6 3570.9 1147.2 391.7 9 ECPULF 21 4.52 1140.7 1100.5 147.3 150.5 2400.7 1126.6 530.3 11 ECPULH 4.8 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	3	ECPU-B	56	4.29	1191.1	840.1	757.7	848.8	67.8	770.7
6	4	ECPU-C	35	2.73	227.9	1528.3	362.7	4431.5	962.0	828.0
7         ECPUD         35         0.14         52.1         1.43.7         1.5         249.7         1125.6         530.3           8         ECPUF         28         30         48.0         324.1         31.6         3570.9         1147.2         391.7           9         ECPUF         21         4.52         140.7         1100.5         147.3         1080.8         1026.2         1592.2           10         ECPUF         21         4.52         140.7         1100.5         147.3         1080.8         1026.2         1592.2           11         ECPUH         34         0.45         132.1         947.2         306.5         1079.9         1121.6         446.5           13         ECPUJ         44         1.70         550.0         301.6         30.85         107.8         1121.6         449.5           13         ECPUJ         21         1.46         78.1         50.0         301.6         30.6         30.6         100.0         30.7           14         ECPUJ         49         3.91         78.1         222.1         34.0         110.9         30.8         100.8         20.7         456.5         366.2         200.7	5	ECPU-C	48	1.16	211.5	2472.1	257.1	4795.8	1067.1	679.1
B	6	ECPU-D	21	0.26	133.5	506.4	85.9	1993.2	1069.5	802.3
Per	7	ECPU-D	35	0.14	52.1	143.7	1.5	2460.7	1125.6	530.3
10	8	ECPU-E	28	0.30	48.0	324.1	31.6	3570.9	1147.2	391.7
11	9	ECPU-F	21	4.52	140.7	1100.5	147.3	1050.8	1026.2	1592.2
12	10	ECPU-G	21	3.93	113.4	1043.4	233.2	1314.6	1081.5	1938.1
13	11	ECPU-H	34	0.45	132.1	947.2	306.5	1076.9	1121.6	446.5
14	12	ECPU-H	48	1.70	155.3	1016.5	483.1	1188.8	1136.0	879.7
16   ECPU-J   28   1.97   68.4   75.26   167.9   1428.0   1043.8   1028.9     16   ECPU-J   49   3.91   78.1   2228.1   3494.   1161.1   991.6   928.8     17   ECPU-L   20   8.77   456.5   3963.6   2203.7   465.6   299.7   3133.4     18   ECPU-M   21   0.82   133.5   260.1   4118.   1052.0   1133.6   222.8     19   ECPU-M   42   0.99   130.6   721.4   260.6   1315.5   1119.2   97.5     20   ECPU-N   14   0.63   1595.0   554316.3   5462.6   1342.7   74.5   2548.1     21   ECPU-N   21   18.83   1638.3   2341.9   8814.1   1092.9   41.7   10037.7     22   ECPU-N   42   70.7   1481.2   394980.0   1640.3   1678.4   78.5   571.8     23   ECPU-N   42   70.7   1481.2   394980.0   1640.3   1678.4   78.5   571.8     24   ECPU-O   7   163   178.8   1652.1   2699.1   1520.1   1124.8   1199.5     25   ECPU-O   21   1.20   87.9   719.9   819.8   1543.2   1167.3   341.3     26   ECPU-O   28   1.92   117.7   2710.1   1049.6   1519.5   1079.9   625.2     27   ECPU-O   36   0.33   58.9   470.3   274.1   1265.4   1132.8   314.7     28   ECPU-O   43   2.32   153.8   4351.8   1543.7   1617.8   1107.2   684.9     29   ECPU-P   20   1.04   80.9   383.8   258.0   1220.2   1101.5   362.8     30   ECPU-P   34   0.39   67.1   210.3   293.3   1630.0   1156.5   606.0     31   ECPU-P   34   0.39   67.1   210.3   293.3   1630.0   1156.5   606.0     32   ECPU-P   57   4.07   211.5   140.3   2422.5   1224.6   427.4   3876.0     33   ECPU-P   57   4.07   211.5   140.3   2422.5   1224.6   427.4   3876.0     34   ECPU-Q   41   0.21   9.5   11.7   70.0   76.3   109.6   100.6     35   ECPU-Q   50   0.77   19.3   77.2   119.6   945.3   1019.0   265.7     36   ECPU-P   57   4.07   211.5   140.3   2422.5   1224.6   427.4   3876.0     37   ECPU-Q   51   4.06   63.0   222.8   2354.1   361.3   1277.5   116.0   362.8     41   ECPU-R   57   1.66   73.3   139.3   324.1   361.3   1277.5   116.6   690.7     41   ECPU-R   57   1.66   73.3   139.3   324.1   361.3   1277.5   116.0   690.7     44   ECPU-R   57   1.66   63.0   222.3   231.8   1407.4   1096.1   10	13	ECPU-J	14	1.66	204.0	3548.9	319.6	1390.0	1121.6	382.7
16	14	ECPU-J	21	1.46	78.1	507.1	381.6	1608.5	1010.2	1073.8
17	15	ECPU-J	28	1.97	68.4	752.6	167.9	1428.0	1043.8	1028.9
18	16	ECPU-J	49	3.91	78.1	2228.1	349.4	1161.1	931.6	929.8
19	17	ECPU-L	20	8.77	456.5	3963.6	2203.7	4655.6	269.7	3133.4
ECPUN	18	ECPU-M	21	0.82	133.5	260.1	411.8	1052.0	1133.6	222.8
CPU-N			42							
ECPU-N   21										
22         ECPLN         42         7.07         1481 2         394980.0         1640.3         1678.4         78.5         571.8           23         ECPLIO         7         1.63         178.8         1652.1         2699.1         1520.1         1124.8         1139.5           26         ECPLIO         21         1.20         87.9         719.9         819.8         1543.2         1167.3         341.3           26         ECPLIO         28         1.92         117.7         2710.1         1049.6         1519.5         1079.9         625.2           27         ECPLIO         36         0.33         58.9         470.3         274.1         1265.4         1132.8         314.7           28         ECPLIP         43         2.32         153.8         4351.8         1543.7         1617.8         1107.5         362.8           30         ECPLIP         20         1.04         80.9         383.8         258.0         1220.2         1101.5         362.8           31         ECPLIP         27         4.21         218.9         222.6         2354.4         959.3         961.2         4242.9           31         ECPLIP         34	21	ECPU-N	21	18.83	1638.3	2341.9	8814.1			10037.7
ECPU-N   66   5.23   1313.4   327487.5   1113.2   2873.0   1033.4   492.8	22		42	7.07						
25         ECPU-O         21         1 20         87.9         719.9         819.8         1543.2         1167.3         341.3           26         ECPU-O         28         1 92         117.7         2710.1         1049.6         1519.5         1079.9         625.2           27         ECPU-O         43         2.32         153.8         4351.8         1543.7         1617.8         1107.2         684.9           29         ECPU-P         20         1.04         80.9         383.8         258.0         1220.2         1101.5         362.8           30         ECPU-P         27         4.21         218.9         222.6         2354.4         959.3         961.2         4242.9           31         ECPU-P         34         0.39         67.1         210.3         293.3         1630.0         1158.5         606.0           32         ECPU-P         41         1.08         102.0         395.6         309.4         2341.4         1134.4         472.4           43         ECPU-P         41         1.08         102.0         395.6         309.4         2341.4         1134.4         472.4           43         ECPU-D         6 <td< td=""><td>23</td><td>ECPU-N</td><td>56</td><td>5.23</td><td></td><td></td><td></td><td></td><td>1033.4</td><td></td></td<>	23	ECPU-N	56	5.23					1033.4	
25         ECPU-O         21         1 20         87.9         719.9         819.8         1543.2         1167.3         341.3           26         ECPU-O         28         1 92         117.7         2710.1         1049.6         1519.5         1079.9         625.2           27         ECPU-O         36         0.33         58.9         470.3         274.1         1265.4         1132.8         314.7           28         ECPU-D         43         2.32         153.8         4351.8         1543.7         1617.8         1107.2         684.9           29         ECPU-P         20         1.04         80.9         383.8         258.0         1220.2         1101.5         362.8           30         ECPU-P         27         4.21         218.9         222.6         2354.4         959.3         961.2         4242.9           31         ECPU-P         34         0.39         67.1         210.3         293.3         1630.0         1158.5         606.0           32         ECPU-P         41         1.08         102.0         395.6         309.4         2341.4         1134.4         472.4         3472.4           33         ECPU-D			7							
26         ECPU-O         28         192         117.7         2710.1         1049.6         1519.5         1079.9         625.2           27         ECPU-O         36         0.33         58.9         470.3         274.1         1265.4         1132.8         314.7           28         ECPU-D         20         1.04         80.9         383.8         258.0         1220.2         1101.5         302.8           30         ECPU-P         27         4.21         218.9         222.6         2354.4         959.3         961.2         4242.9           31         ECPU-P         34         0.39         67.1         210.3         293.3         1630.0         1158.5         606.0           32         ECPU-P         41         1.08         102.0         395.6         309.4         2341.4         1134.4         472.4           33         ECPU-P         57         4.07         211.5         140.3         2422.5         122.6         427.4         3376.0           34         ECPU-Q         6         0.77         177.3         500.4         125.0         1179.3         1097.5         241.6           35         ECPU-Q         20         0.	25		21	1.20						341.3
27										
28         ECPU-O         43         2.32         153.8         4351.8         1543.7         1617.8         1107.2         684.9           29         ECPU-P         20         1.04         80.9         383.8         258.0         1220.2         1101.5         362.8           30         ECPU-P         27         4.21         218.9         222.6         2354.4         959.3         961.2         4242.9           31         ECPU-P         34         0.39         67.1         210.3         293.3         1630.0         1155.5         606.0           32         ECPU-P         41         1.08         102.0         395.6         309.4         2341.4         1134.4         472.4           33         ECPU-P         57         4.07         211.5         140.3         2422.5         1224.6         427.4         3876.0           34         ECPU-Q         6         0.77         177.3         500.4         125.0         1179.3         1097.5         241.6           35         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1109.0         265.7           36         ECPU-Q         41         0.										
29         ECPUP         20         1.04         80.9         383.8         258.0         1220.2         110.15         362.8           30         ECPU-P         27         4.21         218.9         222.6         2354.4         959.3         961.2         4242.9           31         ECPU-P         34         0.39         67.1         210.3         293.3         1630.0         1158.5         606.0           32         ECPU-P         47         1.10.8         102.0         395.6         309.4         2341.4         1134.4         472.4         3876.0           34         ECPU-Q         6         0.77         177.3         500.4         125.0         1179.3         1097.5         2416.           35         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1019.0         265.7           36         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1019.0         265.7           36         ECPU-Q         34         0.25         9.5         78.2         59.5         978.3         1094.3         100.6           37         ECPU-Q         41										
Secour										
32         ECPU-P         41         1.08         102.0         395.6         309.4         2341.4         1134.4         472.4           33         ECPU-P         57         4.07         211.5         140.3         2422.5         1224.6         427.4         3876.0           34         ECPU-Q         6         0.77         177.3         500.4         125.0         1179.3         1094.3         109.0         265.7           35         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1019.0         265.7           36         ECPU-Q         41         0.21         9.5         78.2         59.5         979.3         1094.3         100.6           37         ECPU-Q         41         0.21         9.5         11.7         70.0         76.3         109.6         124.1           38         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34			27							
33         ECPU-P         57         4.07         211.5         140.3         2422.5         1224.6         427.4         3876.0           34         ECPU-Q         6         0.77         177.3         500.4         125.0         1179.3         1097.5         241.6           35         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1019.0         265.7           36         ECPU-Q         34         0.25         9.5         78.2         59.5         979.3         1094.3         100.6           37         ECPU-Q         41         0.21         9.5         11.7         70.0         76.3         109.6         124.1           38         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34         3.77										
33         ECPU-P         57         4.07         211.5         140.3         2422.5         1224.6         427.4         3876.0           34         ECPU-Q         6         0.77         177.3         500.4         125.0         1179.3         1097.5         241.6           35         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1019.0         265.7           36         ECPU-Q         34         0.25         9.5         78.2         59.5         979.3         1094.3         100.6           37         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           38         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           40         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           41         ECPU-R         57         1.64 <td>32</td> <td>ECPU-P</td> <td>41</td> <td>1.08</td> <td>102.0</td> <td>395.6</td> <td>309.4</td> <td>2341.4</td> <td>1134.4</td> <td>472.4</td>	32	ECPU-P	41	1.08	102.0	395.6	309.4	2341.4	1134.4	472.4
35         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1019.0         265.7           36         ECPU-Q         34         0.25         9.5         78.2         59.5         979.3         1094.3         100.6           37         ECPU-Q         41         0.21         9.5         11.7         70.0         76.3         109.6         124.1           38         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34         3.77         277.9         935.3         1735.7         1609.8         1006.1         3638.1           41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         15         1.06         201.0         377.9         333.0         1017.9         1129.6         690.7           43         ECPU-S         27         0.97	33	ECPU-P	57	4.07	211.5	140.3	2422.5	1224.6	427.4	3876.0
35         ECPU-Q         20         0.27         19.3         77.2         119.6         945.3         1019.0         265.7           36         ECPU-Q         34         0.25         9.5         78.2         59.5         979.3         1094.3         100.6           37         ECPU-Q         41         0.21         9.5         11.7         70.0         76.3         109.6         124.1           38         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         20         0.73         199.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34         3.77         277.9         935.3         1735.7         1609.8         1006.1         3638.1           41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         57         1.66         201.0         377.9         333.0         1017.9         1129.6         690.7           43         ECPU-S         27         0.97	34	ECPU-Q	6	0.77	177.3	500.4	125.0	1179.3	1097.5	241.6
36         ECPU-Q         34         0.25         9.5         78.2         59.5         979.3         1094.3         100.6           37         ECPU-Q         41         0.21         9.5         11.7         70.0         76.3         109.6         124.1           38         ECPU-R         15         0.98         152.4         33.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34         3.77         277.9         935.3         1735.7         1609.8         1006.1         3638.1           41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         57         1.06         201.0         336.4         630.5         1082.7         1136.8         1172.5           43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02										
37         ECPU-Q         41         0.21         9.5         11.7         70.0         76.3         109.6         124.1           38         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34         3.77         277.9         935.3         1735.7         1609.8         1006.1         3638.1           41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         15         1.06         201.0         336.4         630.5         1082.7         1136.8         1172.5           43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           45         ECPU-T         9         1.82<			34		9.5					
38         ECPU-R         15         0.98         152.4         333.7         549.7         1164.8         1111.2         712.1           39         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34         3.77         277.9         935.3         1735.7         1609.8         1006.1         3638.1           41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         15         1.06         201.0         336.4         630.5         1082.7         1136.8         1172.5           43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           46         ECPU-T         21         <			41							
39         ECPU-R         20         0.73         139.3         324.1         351.3         1277.5         1116.0         222.8           40         ECPU-R         34         3.77         277.9         935.3         1735.7         1609.8         1006.1         3638.1           41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         15         1.06         201.0         336.4         630.5         1082.7         1136.8         1172.5           43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           46         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           47         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42										
40         ECPU-R         34         3.77         277.9         935.3         1735.7         1609.8         1006.1         3638.1           41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         15         1.06         201.0         336.4         630.5         1082.7         1136.8         1172.5           43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           45         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42			20							
41         ECPU-R         57         1.64         78.1         983.9         382.7         1173.3         1122.4         446.5           42         ECPU-S         15         1.06         201.0         336.4         630.5         1082.7         1136.8         1172.5           43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           46         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-B         55         5.38         2440.2         843.3         1688.8         2666.9         303.7         4206.2           49         ECPU-A         7         6.										
42         ECPU-S         15         1.06         201.0         336.4         630.5         1082.7         1136.8         1172.5           43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           46         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         7         6.										
43         ECPU-S         27         0.97         201.0         377.9         333.0         1017.9         1129.6         690.7           44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           46         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-B         55         5.38         2440.2         843.3         1688.8         2666.9         303.7         4206.2           49         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21										
44         ECPU-S         57         1.02         150.9         333.5         342.4         1649.3         1135.2         571.8           45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           46         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-U         55         5.38         2440.2         843.3         1688.8         2666.9         303.7         4206.2           49         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         446.4           52         ECPU-B         49										
45         ECPU-T         9         1.82         181.7         308.7         1005.4         879.5         1104.8         1760.8           46         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-U         55         5.38         2440.2         843.3         1688.8         2666.9         303.7         4206.2           49         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         4446.4           52         ECPU-B         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         35										
46         ECPU-T         21         0.37         32.2         87.9         232.1         726.0         1080.7         274.4           47         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-U         55         5.38         2440.2         843.3         1688.8         2666.9         303.7         4206.2           49         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         4446.4           52         ECPU-A         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35										
47         ECPU-T         42         0.49         63.0         228.3         231.8         1407.4         1095.1         182.5           48         ECPU-U         55         5.38         2440.2         843.3         1688.8         2666.9         303.7         4206.2           49         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         4446.4           52         ECPU-A         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42			21							
48         ECPU-U         55         5.38         2440.2         843.3         1688.8         2666.9         303.7         4206.2           49         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         4446.4           52         ECPU-A         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49										
49         ECPU-A         7         6.88         2274.9         3537.4         1553.3         1542.6         1048.6         650.1           50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         4446.4           52         ECPU-A         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28										
50         ECPU-A         14         12.63         3325.8         166280.1         2514.1         1104.9         144.0         1447.0           51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         4446.4           52         ECPU-A         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42										
51         ECPU-A         21         33.54         803.7         3152.1         2430.1         1103.2         85.5         4446.4           52         ECPU-A         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42         3.95         244.5         4003.9         760.7         997.9         119.2         943.9										
52         ECPU-A         49         5.55         524.8         9186.8         943.9         1071.5         68.1         1301.5           53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42         3.95         244.5         4003.9         760.7         997.9         119.2         943.9										
53         ECPU-B         14         2.22         1445.1         421.0         499.2         1566.3         193.5         498.4           54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42         3.95         244.5         4003.9         760.7         997.9         119.2         943.9										
54         ECPU-B         35         2.76         398.3         356.8         526.2         884.1         1039.8         1330.9           55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42         3.95         244.5         4003.9         760.7         997.9         119.2         943.9										
55         ECPU-B         42         26.49         2490.2         534.9         7246.5         143.8         7.8         7947.9           56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42         3.95         244.5         4003.9         760.7         997.9         119.2         943.9										
56         ECPU-B         49         26.32         1971.4         157.6         6406.8         44.0         2.8         7273.2           57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42         3.95         244.5         4003.9         760.7         997.9         119.2         943.9										
57         ECPU-C         28         5.41         293.1         1499.4         296.2         519.4         351.2         790.4           58         ECPU-C         42         3.95         244.5         4003.9         760.7         997.9         119.2         943.9										
58 ECPU-C 42 3.95 244.5 4003.9 760.7 997.9 119.2 943.9										
59 FCPLC 55 2.04 210.0 2128.4 429.5 904.8 1033.4 562.3	59	ECPU-C	55	2.04	210.0	2128.4	429.5	904.8	1033.4	562.3

Average Concentration

Average Concentration	AG ID	Code ECPU-D	Study Tim	e r protein ug/ul 4.62	MIG, pg/ml 648.6	<b>MMP-9, ng/ml</b> 11896.6	RBP-4, ng/ml 256.4	<b>S100A8, ng/ml</b> 981.0	<b>S100A9, ng/ml</b> 152.5	TGFBR3, pg/ml 71.7
	61	ECPU-D	28	0.32	183.2	174.3	20.7	1374.4	1117.6	154.6
	62	ECPU-D	41	0.49	49.4	290.2	1.9	1188.1	985.3	321.8
	63	ECPU-D	50	0.12	44.0	54.6	34.6	1231.5	1079.9	496.6
	64	ECPU-E	21	11.78	270.3	743.8	488.1	1079.8	62.5	3583.1
	65	ECPU-E	35	0.31	53.4	207.9	15.7	1393.5	1051.0	162.8
	66	ECPU-E	56	4.93	96.3	161.9	318.8	337.6	73.6	2316.8
	67	ECPU-F	14	4.14	82.3	428.7	324.1	1112.6	1051.8	1949.1
	68	ECPU-F	28	3.47	78.1	595.4	197.4	984.2	1059.1	1607.2
	69	ECPU-G	14	2.50	74.0	1547.1	262.8	1343.2	1025.4	1502.3
	70	ECPU-G	34	3.05	36.1	390.7	217.4	893.8	1052.6	1802.2
	71	ECPU-H	13	2.67	462.8	5558.8	589.1	1171.4	1055.8	774.7
	72	ECPU-I	34	1.13	72.6	433.5	259.0	951.7	1083.9	426.3
	73	ECPU-I	48	9.07	392.1	447843.2	2618.3	1306.4	101.0	657.8
		ECPU-J	40 7		109.1		379.8		990.9	195.9
	74 75			2.36		10315.1		1452.4		
	75 70	ECPU-J	35	0.30	129.2	425.8	73.2	943.7	1107.2	130.4
	76 	ECPU-J	42	0.89	24.4	1154.3	83.0	988.1	1133.6	149.7
	77	ECPU-J	56	8.53	68.4	1444.3	707.2	941.9	98.4	1568.6
	78	ECPU-K	13	0.90	381.2	1039.7	232.1	1281.4	988.5	444.7
	79	ECPU-L	7	3.15	532.7	1636.6	254.2	1751.8	1011.0	828.0
	80	ECPU-L	28	5.47	407.7	4507.4	703.8	1594.0	431.5	1902.9
	81	ECPU-N	7	12.14	8225.1	343037.1	3509.1	1165.9	95.9	4705.9
	82	ECPU-N	29	5.32	790.5	12075.9	1500.6	1386.4	219.1	1440.6
	83	ECPU-N	49	5.95	1083.2	345957.6	1433.1	1078.9	165.3	85.2
	84	ECPU-O	15	0.30	50.7	412.0	431.9	1125.7	1026.2	337.8
	85	ECPU-O	51	2.34	241.5	7535.7	1744.6	1140.1	1051.8	1145.6
	86	ECPU-O	58	2.07	205.2	2023.5	2087.4	302.4	8472.2	476.3
	87	ECPU-Q	15	0.82	77.7	138.7	406.1	296.1	2555.9	167.2
	88	ECPU-Q	27	3.38	115.9	443.7	772.1	295.6	8051.5	2292.4
	89	ECPU-R	6	0.24	31.7	102.7	1.9	274.3	8635.8	50.3
	90	ECPU-R	27	2.34	117.1	422.2	534.9	304.0	3329.8	1661.9
	91	ECPU-S	6	0.20	205.2	336.9	82.2	309.7	8472.2	57.0
	92	ECPU-S	20	0.45	254.0	262.0	233.9	312.5	8834.4	160.1
	93	ECPU-S	34	1.35	1339.6	945.6	284.6	297.3	8986.3	494.4
	94	ECPU-T	28	2.07	550.2	175.0	1019.0	280.5	1671.5	1694.1
	95	ECPU-U	7	4.46	750.6	887.6	877.5	285.2	672.5	1092.3
	96	ECPU-U	14	21.07	2487.7	1451.0	8940.3	239.0	12.8	15495.3
	90	ECFU-U	14	21.07	2407.7	1431.0	0940.3	239.0	12.0	15495.5
Replicate 1	AG ID	Code	Study Tim	e r protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
·	1	ECPU-A	56	10.70	562.1	1541.8	1250.1	2012.8	75.3	3531.9
	2	ECPU-B	7	1.88	996.2	365.4	302.4	1434.6	334.3	815.7
	3	ECPU-B	56	4.29	1259.2	930.0	820.8	763.2	63.8	762.5
	4	ECPU-C	35	2.73	240.5	1657.7	366.7	3977.0	903.4	817.5
	5	ECPU-C	48	1.16	222.7	2627.2	259.4	5116.4	1191.2	669.2
	6	ECPU-D	21	0.26	136.1	527.3	83.9	2058.3	1155.6	765.2
	7	ECPU-D	35	0.14	49.8	146.6	1.4	2536.1	1213.8	504.8
	8	ECPU-E	28	0.30	51.0	324.0	29.4	3673.0	1234.7	384.8
	9	ECPU-F	21	4.52	148.0	1069.5	135.7	1069.8	1093.2	1548.2
	10	ECPU-G	21	3.93	113.2	993.5	214.4	1335.7	1149.8	1880.7
	11	ECPU-H	34	0.45	131.6	821.8	335.0	1045.0	1138.7	432.5
	12	ECPU-H	48	1.70	150.1	864.1	512.2	1118.7	1118.6	826.2
	13	ECPU-J	14	1.66	203.7	2955.9	350.2	1351.6	1141.1	371.4
	14	ECPU-J	21	1.46	77.9	474.5	417.3	1560.9	1025.7	1040.0
	15	ECPU-J	28	1.97	68.1	690.0	173.5	1383.0	1057.8	934.8
	16	ECPU-J	49	3.91	91.6	2067.9	360.3	1099.8	876.1	843.0
	17	ECPU-L	20	8.77	518.8	4454.7	2195.1	4400.9	253.1	2721.8
	18	ECPU-M	21	0.82	151.4	286.4	409.3	922.9	1044.8	193.2
	19	ECPU-M	42	0.59	147.8	741.4	250.5	1151.7	1029.4	82.6
	20	ECPU-N	14	0.63	1729.6	558190.9	5240.5	1173.1	64.3	2156.0

<b>AG ID</b> 21	Code ECPU-N	Study Time	e r protein ug/ul 18.83	MIG, pg/ml 1772.9	MMP-9, ng/ml 2310.6	<b>RBP-4, ng/ml</b> 8438.8	<b>S100A8</b> , <b>ng/ml</b> 1048.4	<b>S100A9, ng/ml</b> 35.9	<b>TGFBR3, pg/ml</b> 8476.1
22	ECPU-N	42	7.07	1599.8	358140.3	1441.7	1606.9	75.1	525.7
23	ECPU-N	56	5.23	1415.7	290944.6	976.5	2745.2	922.7	452.2
24	ECPU-O	7	1.63	202.8	1438.1	2814.5	1355.2	1002.3	1168.9
25	ECPU-O	21	1.20	91.5	745.0	853.1	1373.0	1010.0	349.5
26	ECPU-O	28	1.92	132.7	2747.8	1020.2	1276.2	932.5	597.2
27	ECPU-O	36	0.33	62.4	423.8	265.9	1060.7	976.3	287.1
28	ECPU-O	43	2.32	165.1	4313.4	1431.6	1536.9	1081.3	638.6
29	ECPU-P	20	1.04	79.2	372.7	238.8	1119.7	1073.7	337.7
30	ECPU-P	27	4.21	213.7	215.7	2372.5	1040.5	935.1	3861.6
31	ECPU-P	34	0.39	60.8	189.5	277.7	1820.8	1081.6	529.4
32	ECPU-P	41	1.08	85.3	355.8	292.4	2610.1	1057.1	411.8
33	ECPU-P	57	4.07	197.7	140.3	2569.4	1362.4	430.9	3658.9
34	ECPU-Q	6	0.77	158.3	499.3	123.7	1309.4	1056.8	227.6
3 <del>4</del> 35	ECPU-Q ECPU-Q	20	0.77	19.1	87.0	118.1	981.3	1061.6	249.8
36	ECPU-Q	34	0.25	8.7	87.9	68.7	981.1	1137.8	87.2
37	ECPU-Q ECPU-Q	34 41	0.25	9.9	13.2	80.6	76.3	1137.6	107.3
38	ECPU-R		0.21	9.9 154.6	366.8	619.7	1303.1	1128.7	603.1
	ECPU-R ECPU-R	15	0.98						
39		20		159.7	352.7	392.0	1414.6	1122.1	186.8
40	ECPU-R	34	3.77	304.5	997.2	1933.0	1779.1	1009.6	3043.8
41	ECPU-R	57	1.64	85.5	1027.8	425.3	1294.1	1124.0	372.8
42	ECPU-S	15	1.06	212.8	344.3	678.4	1155.9	1102.0	1099.8
43	ECPU-S	27	0.97	212.4	379.0	357.6	1084.5	1092.8	646.6
44	ECPU-S	57	1.02	149.6	327.7	366.8	1753.8	1096.1	534.2
45	ECPU-T	9	1.82	178.3	297.2	1066.3	925.7	1055.8	1628.3
46	ECPU-T	21	0.37	31.5	83.0	245.7	762.6	1030.7	253.2
47	ECPU-T	42	0.49	61.5	242.1	244.8	1475.4	1042.4	168.1
48	ECPU-U	55	5.38	2312.3	876.5	1730.1	2566.5	280.3	3757.1
49	ECPU-A	7	6.88	2227.5	3602.5	1644.3	1534.0	1000.2	600.1
50	ECPU-A	14	12.63	3250.0	165916.8	2656.1	1096.5	137.1	1332.9
51	ECPU-A	21	33.54	783.8	3081.6	2562.3	1092.6	81.2	4087.6
52	ECPU-A	49	5.55	485.2	9092.1	993.2	1018.6	64.6	1194.1
53	ECPU-B	14	2.22	1333.4	370.4	524.2	1486.0	183.1	456.4
54	ECPU-B	35	2.76	355.8	307.5	551.5	837.1	981.9	1216.1
55	ECPU-B	42	26.49	2219.7	451.7	7579.5	135.9	7.4	7248.2
56	ECPU-B	49	26.32	1982.1	136.8	6687.8	41.5	2.6	6619.6
57	ECPU-C	28	5.41	294.1	1275.3	308.6	488.8	329.6	718.0
58	ECPU-C	42	3.95	232.6	3336.8	790.9	937.3	111.6	855.6
59	ECPU-C	55	2.04	199.3	1947.9	445.7	848.2	966.2	508.7
60	ECPU-D	8	4.62	614.5	10667.8	265.5	917.7	142.3	64.7
61	ECPU-D	28	0.32	173.3	153.2	21.4	1283.2	1040.7	139.3
62	ECPU-D	41	0.49	51.3	249.8	1.9	1040.4	915.7	289.4
63	ECPU-D	50	0.12	43.8	46.0	35.7	1076.4	1001.6	445.7
64	ECPU-E	21	11.78	268.3	690.0	501.4	941.9	57.9	3312.1
65	ECPU-E	35	0.31	52.9	189.0	16.1	1213.1	970.9	150.2
66	ECPU-E	56	4.93	95.3	146.8	326.2	293.3	67.9	2133.0
67	ECPU-F	14	4.14	78.8	377.1	308.4	1061.4	967.8	1790.9
68	ECPU-F	28	3.47	74.6	522.7	187.4	937.0	972.5	1473.8
69	ECPU-G	14	2.50	70.5	1355.7	249.1	1276.1	939.7	1374.9
70	ECPU-G	34	3.05	37.9	341.7	205.6	847.5	962.7	1813.2
71	ECPU-H	13	2.67	485.5	5459.1	556.0	1108.5	963.7	777.9
72	ECPU-I	34	1.13	76.0	424.9	244.0	898.8	987.4	427.2
73	ECPU-I	48	9.07	393.3	438052.1	2461.2	1231.3	91.8	657.9
74	ECPU-J	7	2.36	109.2	10069.4	356.3	1366.1	899.0	184.1
75	ECPU-J	35	0.30	129.0	414.8	68.6	885.9	1002.5	118.9
76	ECPU-J	42	0.89	23.6	1122.3	77.6	925.7	1024.4	144.7
77	ECPU-J	56	8.53	66.2	1401.5	659.4	880.7	88.8	1512.5
78	ECPU-K	13	0.90	356.8	1006.8	216.0	1195.7	889.7	427.9
79	ECPU-L	7	3.15	468.6	1581.7	236.1	1631.4	908.1	795.2

Average Concentration

Average Concentration	AG ID	Code	Study T	ime r protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
Average Concentration	80 80	ECPU-L	28	5.47	391.9	4648.0	758.2	1736.2	451.0	2133.1
	81	ECPU-N	7	12.14	8403.2	377192.8	3864.2	1225.4	98.1	5164.4
	82	ECPU-N	29	5.32	831.9	13676.6	1702.1	1500.9	221.9	1564.9
	83	ECPU-N	49	5.95	1174.0	374576.3	1645.2	1203.0	167.1	92.4
	84	ECPU-O	15	0.30	56.6	459.5	490.9	1211.3	1129.3	365.4
	85	ECPU-O	51	2.34	277.7	8034.1	1962.9	1183.9	1120.5	1199.8
	86	ECPU-O	58	2.07	233.6	2135.8	2325.1	303.0	9007.2	497.8
	87	ECPU-Q	15	0.82	87.6	144.9	447.8	286.3	2711.8	180.4
	88	ECPU-Q	27	3.38		458.9			8455.7	2447.4
					129.3		842.9	275.8		
	89	ECPU-R	6	0.24	35.0	105.2	2.1	247.0	9051.2	53.6
	90	ECPU-R	27	2.34	128.1	428.0	572.4	272.8	3332.9	1767.1
	91	ECPU-S	6	0.20	222.2	338.2	87.1	268.2	8224.0	58.7
	92	ECPU-S	20	0.45	272.2	260.4	245.3	282.3	8861.4	170.6
	93	ECPU-S	34	1.35	1374.0	930.2	295.5	259.1	8995.8	525.7
	94	ECPU-T	28	2.07	558.7	170.4	1047.4	242.1	1669.9	1689.9
	95	ECPU-U	7	4.46	754.5	855.8	892.9	271.2	623.5	1087.4
	96	ECPU-U	14	21.07	2475.7	1385.0	9006.3	225.0	11.9	14777.9
Replicate 2	AG ID	Code	Study T	ime r protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
· p =	1	ECPU-A	56	10.70	468.3	1551.1	986.2	2325.2	79.8	3386.6
	2	ECPU-B	7	1.88	869.2	288.0	250.2	1723.6	369.1	816.5
	3	ECPU-B	, 56	4.29	1123.0	750.2	694.5	934.3	71.9	779.0
	4	ECPU-C	35	2.73	215.4	1398.9	358.7	4886.1	1020.7	838.4
	5	ECPU-C	48	1.16	200.3	2317.0	254.8	4475.1	943.0	689.0
	6	ECPU-D	21	0.26	130.9	485.5	87.9	1928.0	983.3	839.3
	7	ECPU-D	35	0.14	54.4	140.8	1.6	2385.3	1037.4	555.7
	8	ECPU-E	28	0.30	45.1	324.2	33.8	3468.9	1059.8	398.6
	9	ECPU-F	21	4.52	133.5	1131.4	158.9	1031.8	959.2	1636.2
	10	ECPU-G	21	3.93	113.5	1093.2	251.9	1293.5	1013.2	1995.4
	11	ECPU-H	34	0.45	132.5	1072.6	277.9	1108.9	1104.4	460.6
	12	ECPU-H	48	1.70	160.5	1168.9	454.0	1258.9	1153.5	933.2
	13	ECPU-J	14	1.66	204.3	4142.0	289.1	1428.3	1102.0	393.9
	14	ECPU-J	21	1.46	78.4	539.7	346.0	1656.0	994.6	1107.5
	15	ECPU-J	28	1.97	68.8	815.2	162.3	1473.0	1029.9	1123.0
	16	ECPU-J	49	3.91	64.7	2388.4	338.5	1222.4	987.1	1016.5
	17	ECPU-L	20	8.77	394.2	3472.5	2212.4	4910.4	286.3	3545.1
	18	ECPU-M	21	0.82	115.6	233.7	414.2	1181.2	1222.5	252.5
	19	ECPU-M	42	0.59	113.4	701.4	270.7	1479.3	1209.0	112.3
	20	ECPU-N	14	0.63	1460.5	550441.7	5684.6	1512.2	84.7	2940.2
	21	ECPU-N	21	18.83	1503.6	2373.1	9189.3	1137.3	47.5	11599.2
	22	ECPU-N	42	7.07	1362.7	431819.8	1838.9	1749.8	81.9	617.9
	23	ECPU-N	56	5.23	1211.2	364030.4	1250.0	3000.8	1144.1	533.5
	24	ECPU-O	7	1.63	154.8	1866.1	2583.7	1685.1	1247.3	1110.0
	25	ECPU-O	21	1.20	84.3	694.8	786.4	1713.4	1324.6	333.2
	26	ECPU-O	28	1.92	102.7	2672.4	1078.9	1762.8	1227.3	653.2
	27	ECPU-O	36	0.33	55.4	516.8	282.4	1470.1	1289.4	342.3
	28	ECPU-O	43	2.32	142.5	4390.1	1655.8	1698.8	1133.0	731.1
	29	ECPU-P	20	1.04	82.7	394.9	277.3	1320.7	1129.4	388.0
	30	ECPU-P	27	4.21	224.1	229.4	2336.2	878.0	987.4	4624.1
	31	ECPU-P	34	0.39	73.4	231.1	308.8	1439.3	1235.3	682.7
	32	ECPU-P		1.08	73. <del>4</del> 118.7	435.4	326.3	2072.7	1211.8	533.0
			41							
	33	ECPU-P	57	4.07	225.2	140.3	2275.5	1086.8	423.9	4093.1
	34	ECPU-Q	6	0.77	196.3	501.4	126.2	1049.2	1138.3	255.6
	35	ECPU-Q	20	0.27	19.5	67.3	121.0	909.2	976.4	281.6
	36	ECPU-Q	34	0.25	10.3	68.4	50.3	977.5	1050.9	114.0
	37	ECPU-Q	41	0.21	9.2	10.3	59.4	76.3	105.5	140.8
	38	ECPU-R	15	0.98	150.1	300.5	479.6	1026.4	1093.6	821.1
	39	ECPU-R	20	0.73	118.9	295.5	310.6	1140.3	1109.9	258.8
	40	ECPU-R	34	3.77	251.2	873.4	1538.5	1440.6	1002.7	4232.4

<b>AG ID</b> 41	Code ECPU-R	Study T 57	ime r protein ug/ul 1.64	MIG, pg/ml 70.8	MMP-9, ng/ml 940.0	<b>RBP-4, ng/ml</b> 340.0	<b>S100A8, ng/ml</b> 1052.5	<b>S100A9, ng/ml</b> 1120.8	TGFBR3, pg/ml 520.2
42	ECPU-S	15	1.06	189.2	328.4	582.7	1009.5	1171.6	1245.2
43	ECPU-S	27	0.97	189.6	376.9	308.5	951.2	1166.4	734.8
44	ECPU-S	57	1.02	152.3	339.3	317.9	1544.8	1174.4	609.4
	ECPU-S ECPU-T		1.02		339.3		833.4		1893.3
45		9		185.2		944.5		1153.7	
46	ECPU-T	21	0.37	32.8	92.9	218.6	689.4	1130.7	295.5
47	ECPU-T	42	0.49	64.4	214.4	218.7	1339.5	1147.9	197.0
48	ECPU-U	55	5.38	2568.1	810.1	1647.5	2767.4	327.0	4655.4
49	ECPU-A	7	6.88	2322.3	3472.4	1462.3	1551.2	1097.0	700.2
50	ECPU-A	14	12.63	3401.6	166643.3	2372.1	1113.2	151.0	1561.1
51	ECPU-A	21	33.54	823.6	3222.5	2298.0	1113.7	89.7	4805.3
52	ECPU-A	49	5.55	564.4	9281.6	894.6	1124.4	71.6	1409.0
53	ECPU-B	14	2.22	1556.9	471.7	474.1	1646.6	203.9	540.5
54	ECPU-B	35	2.76	440.9	406.1	500.9	931.1	1097.7	1445.6
55	ECPU-B	42	26.49	2760.6	618.1	6913.4	151.7	8.3	8647.7
56	ECPU-B	49	26.32	1960.6	178.4	6125.7	46.5	3.0	7926.9
57	ECPU-C	28	5.41	292.1	1723.5	283.8	549.9	372.7	862.9
58	ECPU-C	42	3.95	256.4	4671.1	730.5	1058.5	126.7	1032.1
59	ECPU-C	55	2.04	220.6	2308.9	413.4	961.5	1100.6	615.9
60	ECPU-D	8	4.62	682.6	13125.5	247.3	1044.2	162.7	78.7
61	ECPU-D	28	0.32	193.2	195.5	20.0	1465.6	1194.5	169.9
62	ECPU-D	41	0.49	47.5	330.6	1.8	1335.7	1054.9	354.2
63	ECPU-D	50	0.12	44.3	63.1	33.6	1386.7	1158.2	547.5
64	ECPU-E	21	11.78	272.2	797.5	474.8	1217.8	67.2	3854.1
65	ECPU-E	35	0.31	53.9	226.8	15.3	1574.0	1131.2	175.4
66	ECPU-E	56	4.93	97.4	176.9	311.4	381.9	79.3	2500.6
67	ECPU-F	14	4.14	85.8	480.2	339.9	1163.9	1135.9	2107.3
68	ECPU-F	28	3.47	81.6	668.0	207.3	1031.5	1145.6	1740.6
69	ECPU-G	14	2.50	77.4	1738.6	276.6	1410.2	1111.1	1629.8
70	ECPU-G	34	3.05	34.2	439.7	229.2	940.1	1142.6	1791.1
71	ECPU-H	13	2.67	440.1	5658.5	622.2	1234.4	1148.0	771.5
72	ECPU-I	34	1.13	69.2	442.1	274.1	1004.6	1180.5	425.4
73	ECPU-I	48	9.07	390.9	457634.3	2775.4	1381.5	110.2	657.8
74	ECPU-J	7	2.36	109.0	10560.8	403.4	1538.6	1082.8	207.6
75	ECPU-J	35	0.30	129.3	436.8	77.9	1001.5	1211.8	142.0
76	ECPU-J	42	0.89	25.2	1186.3	88.5	1050.5	1242.8	154.8
77	ECPU-J	56	8.53	70.7	1487.2	754.9	1003.2	108.1	1624.6
78	ECPU-K	13	0.90	405.6	1072.6	248.2	1367.1	1087.3	461.4
79	ECPU-L	7	3.15	596.9	1691.5	272.3	1872.2	1113.8	860.8
79 80	ECPU-L	7 28	5.47	423.6	4366.7	649.5	1451.8	412.0	1672.6
81	ECPU-L ECPU-N	20 7	12.14	8047.1	308881.4	3153.9	1106.3	93.6	4247.4
82	ECPU-N	7 29	5.32	749.2	10475.1	1299.1	1271.9	216.3	1316.4
83	ECPU-N ECPU-O	49	5.95	992.3	317338.9	1221.0	954.7	163.5	78.1
84		15	0.30	44.8	364.5	373.0	1040.1	923.0	310.1
85	ECPU-O	51	2.34	205.3	7037.3	1526.3	1096.3	983.2	1091.5
86	ECPU-O	58	2.07	176.8	1911.3	1849.7	301.7	7937.1	454.8
87	ECPU-Q	15	0.82	67.8	132.5	364.4	305.8	2399.9	154.1
88	ECPU-Q	27	3.38	102.5	428.4	701.3	315.4	7647.3	2137.5
89	ECPU-R	6	0.24	28.4	100.2	1.8	301.6	8220.4	47.0
90	ECPU-R	27	2.34	106.2	416.3	497.5	335.2	3326.7	1556.6
91	ECPU-S	6	0.20	188.3	335.7	77.3	351.3	8720.3	55.2
92	ECPU-S	20	0.45	235.8	263.7	222.5	342.8	8807.4	149.6
93	ECPU-S	34	1.35	1305.2	960.9	273.8	335.4	8976.9	463.0
94	ECPU-T	28	2.07	541.7	179.5	990.6	318.9	1673.1	1698.3
		_			0.40	000 /	0000	=0.4 =	400=0
95 96	ECPU-U ECPU-U	7 14	4.46 21.07	746.6 2499.6	919.4 1516.9	862.1 8874.4	299.2 252.9	721.5 13.8	1097.2 16212.6

Average Concentration

# Appendix J SRM Transition Parameters

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re	Product Ion	MS2 Re	Dwell Fragmento	r Collision Energy	Cell Accelerat	or \ Ion Name
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	321.700306	Unit	5 3	80	24.1	6 y6
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	345.22448	Unit	5 3	80	24.1	4 y3
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	' Unit	356.697429	Unit	5 3	80	24.1	4 b7
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	371.192511	Unit	5 3	80	24.1	4 b4
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	390.229762	Unit	5 3	80	24.1	4 y7
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	413.239461	Unit	5 3	80	24.1	4 b8
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	442.277243	Unit	5 3	80	24.1	4 y4
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	446.771794	Unit	5 3	80	24.1	4 y8
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	481.768917	Unit	5 3	80	24.1	4 b9
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	484.276575	Unit	5 3	80	24.1	4 b5
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	496.306001	Unit	5 3	80	24.1	4 y9
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	525.284931	Unit	5 3	80	24.1	4 b10
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	555.361307	Unit	5 3	80	24.1	4 y5
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	560.827297	Unit	5 3	80	24.1	4 y10
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	581.826963	Unit	5 3	80	24.1	4 b11
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	613.319168	Unit	5 3	80	24.1	4 b6
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	' Unit	617.369329	Unit	5 3	80	24.1	4 y11
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	630.353345	Unit	5 3	80	24.1	4 b12
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947		642.393336		5 3	80	24.1	4 y6
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947	7 Unit	665.871902	Unit	5 3	80	24.1	4 b13
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		204.134267			80	15	4 y2
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		227.175404			80	15	4 b2
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		231.121357			80	15	4 y5
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		236.153614			80	15	4 b4
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		264.664346			80	15	4 b5
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		275.171381		5 3	880	15	4 y3
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		287.663389		5 3	880	15	4 y6
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		316.174121		5 3	80	15	4 y7
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459	Unit	321.206378	Unit	5 3	80	15	4 b6
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		346.208495	Unit	5 3	80	15	4 y4
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		358.215889			80	15	4 b3
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459	Unit	372.716153	Unit	5 3	80	15	4 y8
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		378.71985	Unit	5 3	80	15	4 b7
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		414.238407	Unit	5 3	80	15	4 b8
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459	Unit	438.236395	Unit	5 3	880	15	4 y9
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		449.756964		5 3	880	15	4 b9
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459		461.235438	Unit	5 3	80	15	4 y5
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459	Unit	471.299953	Unit	5 3	80	15	4 b4
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459	Unit	478.267695	Unit	5 3	80	15	4 b10
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459	Unit	494.778427	Unit	5 3	80	15	4 y10
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	490.748378	Unit	5 3	880	41.1	4 y10
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	491.738771	Unit	5 3	880	41.1	4 b8
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	526.266935	Unit	5 3	880	41.1	4 y11
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	536.253731	Unit	5 3	880	41.1	4 b4
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	556.260068	Unit	5 3	880	41.1	4 b9
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	563.303518	Unit	5 3	880	41.1	4 y5
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	591.787178	Unit	5 3	880	41.1	4 y12
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	607.290845	Unit	5 3	880	41.1	4 b5
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	620.289356	Unit	5 3	880	41.1	4 b10
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554		650.335546			880	41.1	4 y6
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554		656.308474			880	41.1	4 y13
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554		684.810653		5 3	880	41.1	4 b11
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554		720.337763	Unit	5 3	880	41.1	4 y14
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554		720.374909		5 3	880	41.1	4 b6
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit	737.367575	Unit	5 3	880	41.1	4 y7

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ior	MS2 Re	Dwell Fragmento	r Collision Energy	Cell Accelerato	r \ Ion Name
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554			-	380	41.1	4 b12
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554		06 Unit	5	380	41.1	4 y15
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit 785.8494	52 Unit	5	380	41.1	4 b13
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit 808.4046	88 Unit	5	380	41.1	4 y8
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554	Unit 835.4018	52 Unit	5	380	41.1	4 b7
CDC34	GLQEEPVEGFR	630.814584	Unit 279.1319	22 Unit	5	380	17.9	4 b5
CDC34	GLQEEPVEGFR	630.814584	Unit 299.1713	81 Unit	5	380	17.9	4 b3
CDC34	GLQEEPVEGFR	630.814584	Unit 304.1635	56 Unit	5	380	17.9	4 y5
CDC34	GLQEEPVEGFR	630.814584	Unit 322.1873	66 Unit	5	380	17.9	4 y2
CDC34	GLQEEPVEGFR	630.814584	Unit 327.6583	04 Unit	5	380	17.9	4 b6
CDC34	GLQEEPVEGFR	630.814584	Unit 352.6899	38 Unit	5	380	17.9	4 y6
CDC34	GLQEEPVEGFR	630.814584	Unit 377.1925	11 Unit		380	17.9	4 b7
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 y3
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 y7
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 b4
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 b8
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 b9
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 y8
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 y4
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 b10
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 y9
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 b5
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 y10
CDC34	GLQEEPVEGFR	630.814584				380	17.9	4 y5
CDC34 Cdk3	GLQEEPVEGFR IGEGTYGVVYK	630.814584				380 380	17.9 16.6	4 b6 4 b5
Cdk3	IGEGTYGVVYK	593.311146 593.311146				380	16.6	
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 y4 4 y5
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 b3
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 y2
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 b6
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 b7
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 b4
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 y6
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 b8
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 y3
Cdk3	IGEGTYGVVYK	593.311146				380	16.6	4 y7
Cdk3	IGEGTYGVVYK	593.311146	Unit 438.7267	'18 Unit	5 3	380	16.6	4 b9
Cdk3	IGEGTYGVVYK	593.311146	Unit 443.7370	85 Unit	5	380	16.6	4 y8
Cdk3	IGEGTYGVVYK	593.311146	Unit 458.2245	39 Unit	5 3	380	16.6	4 b5
Cdk3	IGEGTYGVVYK	593.311146	Unit 508.2583	82 Unit	5 3	380	16.6	4 y9
Cdk3	IGEGTYGVVYK	593.311146	Unit 508.312	96 Unit	5 3	380	16.6	4 y4
Cdk3	IGEGTYGVVYK	593.311146	Unit 520.2583	82 Unit	5	380	16.6	4 b10
Cdk3	IGEGTYGVVYK	593.311146	Unit 536.7691	.14 Unit	5	380	16.6	4 y10
Cdk3	IGEGTYGVVYK	593.311146	Unit 565.3344	24 Unit	5	380	16.6	4 y5
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit 363.1874	25 Unit	5	380	24.9	4 y3
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit 372.6841	.33 Unit		380	24.9	4 b6
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342				380	24.9	4 y7
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342				380	24.9	4 b3
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342				380	24.9	4 b7
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342				380	24.9	4 y8
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342				380	24.9	4 y4
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342				380	24.9	4 b8
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342				380	24.9	4 b4
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit 517.2527	7/4 Unit	5	380	24.9	4 y9

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re	Product Ion	MS2 Re Dwe	ell Fragmentor	Collision Energy	Cell Accelera	tor Vion Name
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342		549.251482 U		5 38		24.9	4 y5
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	550.778239 เ	Jnit	5 38	0	24.9	4 b9
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	573.794806 L	Jnit	5 38	0	24.9	4 y10
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	586.296796 เ	Jnit	5 38	0	24.9	4 b10
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	616.302412 U	Jnit	5 38	0	24.9	4 b5
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	622.321188 U	Jnit	5 38	0	24.9	4 y11
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	643.810267 L	Jnit	5 38	0	24.9	4 b11
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	646.304246 L	Jnit	5 38	0	24.9	4 y6
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	687.326281 U	Jnit	5 38	0	24.9	4 b12
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342	Unit	690.850644 L	Jnit	5 38	0	24.9	4 y12
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	147.594247 U	Jnit	5 38	0	14.2	4 y2
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	151.589161 U	Jnit	5 38	0	14.2	4 b3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	197.128454 U	Jnit	5 38	0	14.2	4 y3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	215.139019 \	Jnit	5 38	0	14.2	4 b2
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	225.123368 U	Jnit	5 38	0	14.2	4 b4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	247.652293 L	Jnit	5 38	0	14.2	4 y4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	281.6654 L	Jnit	5 38	0	14.2	4 b5
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	294.181218 U	Jnit	5 38	0	14.2	4 y2
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	302.171047 U	Jnit	5 38	0	14.2	4 b3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	304.194325 U	Jnit	5 38	0	14.2	4 y5
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	332.18924 U	Jnit	5 38	0	14.2	4 b6
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	377.728532 U	Jnit	5 38	0	14.2	4 y6
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	381.723447 U	Jnit	5 38	0	14.2	4 b7
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	393.249632 U	Jnit	5 38	0	14.2	4 y3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	421.244546 U	Jnit	5 38	0	14.2	4 y7
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	449.239461 U	Jnit	5 38	0	14.2	4 b4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	455.257654 L	Jnit	5 38	0	14.2	4 b8
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	471.768386 U	Jnit	5 38	0	14.2	4 y8
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	494.29731 U	Jnit	5 38	0	14.2	4 y4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418	Unit	562.323525 U	Jnit	5 38	0	14.2	4 b5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	175.071333 U	Jnit	5 38	0	12.5	4 b2
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	182.097351 U	Jnit	5 38	0	12.5	4 y3
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	201.123368 U		5 38	0	12.5	4 b4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	217.615908 U	Jnit	5 38	0	12.5	4 y4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	234.144832 U	Jnit	5 38	0	12.5	4 y2
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	265.152657 L		5 38		12.5	4 b5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	281.645196 U	Jnit	5 38	0	12.5	4 y5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	288.155397 U		5 38	0	12.5	4 b3
DCC-interacting protein 13-alpha	SSILQAESK	481.761289		300.671214 U		5 38		12.5	4 b6
DCC-interacting protein 13-alpha	SSILQAESK	481.761289		338.187228 L		5 38		12.5	4 y6
DCC-interacting protein 13-alpha	SSILQAESK	481.761289		363.187425 L		5 38		12.5	4 y3
DCC-interacting protein 13-alpha	SSILQAESK	481.761289		365.192511 U		5 38		12.5	4 b7
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	394.72926 L		5 38		12.5	4 y7
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	401.239461 U	Jnit	5 38	0	12.5	4 b4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289		408.708525 L		5 38		12.5	4 b8
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	434.224539 L		5 38		12.5	4 y4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	438.245275 L	Jnit	5 38	0	12.5	4 y8
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	529.298038 L		5 38	0	12.5	4 b5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	562.283117 U		5 38	0	12.5	4 y5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289	Unit	600.335152 U		5 38	0	12.5	4 b6
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	347.167359 U		5 38	0	23.3	4 y3
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	356.217997 U	Jnit	5 38	0	23.3	4 b3
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	357.687061 U		5 38	0	23.3	4 b6
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	359.671942 U	Jnit	5 38	0	23.3	4 y6
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	421.71635 U	Jnit	5 38	0	23.3	4 b7

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Res	Product Ion	MS2 Re	Dwell Fragmento	r Collision Energy	Cell Accelerat	or Vion Name
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		423.701231		•	380	23.3	4 y7
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	457.265676		5	380	23.3	4 b4
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		476.209952			380	23.3	4 y4
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		486.237647			380	23.3	4 b8
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		488.222528			380	23.3	4 y8
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		542.779679			380	23.3	4 b9
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		552.251817			380	23.3	4 y9
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		585.324253			380	23.3	4 b5
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	589.294016	Unit	5	380	23.3	4 y5
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		602.775656		5	380	23.3	4 y10
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		607.300975		5	380	23.3	4 b10
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		664.814447			380	23.3	4 b11
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		667.296952		5	380	23.3	4 y11
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016		693.325178		5	380	23.3	4 b12
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016	Unit	714.366846	Unit	5	380	23.3	4 b6
L-selectin	AEIEYLEK	497.758215	Unit	138.581336	Unit	5	380	13.1	4 y2
L-selectin	AEIEYLEK	497.758215	Unit	147.112804	Unit	5	380	13.1	4 y1
L-selectin	AEIEYLEK	497.758215	Unit	157.589161	Unit	5	380	13.1	4 b3
L-selectin	AEIEYLEK	497.758215	Unit	195.123368	Unit	5	380	13.1	4 y3
L-selectin	AEIEYLEK	497.758215	Unit	201.086983	Unit	5	380	13.1	4 b2
L-selectin	AEIEYLEK	497.758215	Unit	222.110458	Unit	5	380	13.1	4 b4
L-selectin	AEIEYLEK	497.758215	Unit	276.155397	Unit	5	380	13.1	4 y2
L-selectin	AEIEYLEK	497.758215	Unit	276.655033	Unit	5	380	13.1	4 y4
L-selectin	AEIEYLEK	497.758215	Unit	303.642122	Unit	5	380	13.1	4 b5
L-selectin	AEIEYLEK	497.758215	Unit	314.171047	Unit	5	380	13.1	4 b3
L-selectin	AEIEYLEK	497.758215	Unit	341.176329	Unit	5	380	13.1	4 y5
L-selectin	AEIEYLEK	497.758215	Unit	360.184154	Unit	5	380	13.1	4 b6
L-selectin	AEIEYLEK	497.758215	Unit	389.239461	Unit	5	380	13.1	4 y3
L-selectin	AEIEYLEK	497.758215	Unit	397.718361	Unit	5	380	13.1	4 y6
L-selectin	AEIEYLEK	497.758215	Unit	424.705451	Unit		380	13.1	4 b7
L-selectin	AEIEYLEK	497.758215	Unit	443.21364	Unit		380	13.1	4 b4
L-selectin	AEIEYLEK	497.758215	Unit	462.239658	Unit		380	13.1	4 y7
L-selectin	AEIEYLEK	497.758215		552.302789			380	13.1	4 y4
L-selectin	AEIEYLEK	497.758215		606.276969			380	13.1	4 b5
L-selectin	AEIEYLEK	497.758215		681.345383			380	13.1	4 y5
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		449.680496			380	32.5	4 y7
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		452.186903			380	32.5	4 b8
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		470.224539			380	32.5	4 b5
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		485.199053			380	32.5	4 y8
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		502.710742			380	32.5	4 b9
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		506.220516			380	32.5	4 y4
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		535.722892			380	32.5	4 y9
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		553.234581			380	32.5	4 b10
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		586.246731			380	32.5	4 y10
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		588.753138			380	32.5	4 b11
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		621.247459			380	32.5	4 y5
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		629.762745			380	32.5	4 y11
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		645.774602			380	32.5	4 b12
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		656.303852			380	32.5 32.5	4 b6
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		709.77807			380	32.5 32.5	4 y12 4 b13
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 1037.426358		727.306266 784.310788			380 380	32.5 32.5	4 b13 4 y6
matrix metalloproteinase-9 matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		784.310788 784.819737			380 380	32.5 32.5	4 y6 4 b14
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR  SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		802.817726			380	32.5	4 y13
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358		816.334501		-	380	32.5	4 y15 4 b7
many metallopi otelilase s	5552. Teliviralishing Halling Indian	1007.420000		010.334301	J	3		32.3	7 57

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion MS1 Re	e: Product Ion MS	32 Re Dwell Fragmento	r Collision Energy	Cell Accelerator	\ Ion Name
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	373.25578 Uni	•	0,	24.3 4	4 y3
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	380.710348 Uni				4 y6
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	384.705588 Uni				4 b7
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	387.202681 Uni				4 b3
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	424.226362 Uni				4 y7
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	428.221602 Uni				4 b8
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	459.744919 Uni				4 y8
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	486.271095 Uni				4 b4
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	501.314357 Uni				4 y4
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	508.236927 Uni				4 b9
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	516.766383 Uni				4 y9
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	557.771134 Uni				4 b10
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	565.292765 Uni				4 y10
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR						4 y10 4 b5
· · · · · ·	The state of the s	807.924674 Unit 807.924674 Unit	583.323859 Uni				
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	600.382771 Uni				4 y5
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR		614.826972 Uni				4 y11
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	621.800422 Uni				4 b11
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	658.342986 Uni				4 y12
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	671.334629 Uni				4 b12
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVR	807.924674 Unit	697.366787 Uni				4 b6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	336.663586 Uni				4 b6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	365.174318 Uni				4 b7
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	384.689081 Uni				4 y6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	403.229959 Uni				4 y3
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	429.234376 Uni				4 b4
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	429.695615 Uni				4 b8
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	449.210377 Uni				4 y7
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	477.721109 Uni				4 y8
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	503.229821 Uni				4 b9
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	534.270443 Uni				4 y4
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	535.234581 Uni				4 y9
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	546.745836 Uni				4 b10
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	557.292953 Uni				4 b5
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	599.26387 Uni				4 y10
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	612.266078 Uni	it 5	880	24.5	4 b11
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	621.302472 Uni				4 y5
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	655.805902 Uni				4 y11
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	669.77955 Uni	it 5	880	24.5	4 b12
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	672.319896 Uni	it 5	880	24.5	4 b6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	712.347934 Uni	it 5	880	24.5	4 y12
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	447.235044 Uni	it 5	880	34 4	4 y3
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	463.218725 Uni	it 5	880	34 4	4 b4
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	466.727249 Uni	it 5	880	34 4	4 y8
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	470.22655 Uni	it 5	880	34 4	4 b8
protein \$100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	495.237981 Uni	it 5	80	34 4	4 y9
protein \$100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	526.768583 Uni	it 5	80	34 4	4 b9
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	551.780013 Uni	it 5	80	34 4	4 y10
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	562.261987 Uni	it 5	80	34 4	4 y4
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	583.310615 Uni	it 5	80		4 b10
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	592.261319 Uni	it 5	80	34 4	4 b5
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	608.322045 Uni	it 5	80	34 4	4 y11
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	611.821346 Uni		880		, 4 b11
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	633.299101 Uni		880		4 y5
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	651.838059 Uni	it 5	880		, 4 y12
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	669.334818 Uni	it 5	880		, 4 b12

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion MS1	L Re: Product Ion	MS2 Re Dwell Fragme	ntor Collision Energy	Cell Accelerat	or Vion Name
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	704.336215	Unit 5	380	34	4 y6
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	708.380091	Unit 5	380	34	4 y13
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	725.87685	Unit 5	380	34	4 b13
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	739.329733	Unit 5	380	34	4 b6
protein S100-A7	IDFSEFLSLLGDIAADYHK	1077.541319 Unit	761.395407	Unit 5	380	34	4 b14
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit	311.153189	Unit 5	380	21.4	4 b6
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y6
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit	367.695221	Unit 5	380	21.4	4 b7
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b4
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y7
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	, 4 y3
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b8
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y8
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y4
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b9
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b10
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b5
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y9
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y10
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b11
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y5
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b6
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 y11
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 b12
protein S100-A9	LGHPDTLNQGEFK	728.364972 Unit			380	21.4	4 v12
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 b7
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 b7 4 y8
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y8 4 y4
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 b8
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 b8
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y9
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y9 4 b9
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 b9 4 y5
pterin-4-alpha-carbinolamine denydratase isoform 1 pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y5 4 b5
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y10
· · · · · · · · · · · · · · · · · · ·	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y10 4 b10
pterin-4-alpha-carbinolamine dehydratase isoform 1 pterin-4-alpha-carbinolamine dehydratase isoform 1	·	869.44002 Unit			380	26.5	4 p10 4 y11
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y11 4 y6
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y6 4 b6
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 b0 4 b11
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 v12
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y12 4 b12
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y13
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 y13 4 b13
pterin-4-alpha-carbinolamine denydratase isoform 1  pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit			380	26.5	4 013 4 y7
retinol-binding protein 4	·	1306.585803 Unit			380	42.2	4 y7 4 b8
3.	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit			380	42.2	
retinol-binding protein 4					380	42.2	4 y9
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit			380	42.2 42.2	4 b9
retinol-binding protein 4		1306.585803 Unit			380	42.2 42.2	4 y5
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit					4 y10
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit			380 380	42.2 42.2	4 y11
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit					4 b10
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit			380	42.2	4 y12
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit			380	42.2	4 b5
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803 Unit	660.319896	Unit 5	380	42.2	4 y6

riend binding potters 4	Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Id	n MS	2 Re Dwell Fragmento	Collision Energy	Cell Accelerate	or V Ion Name
INTENDIT PRINTED PRINT	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 666.789	197 Uni	t 5 3	80	42.2	4 b11
INTROLEMENT PROTECTION AND STATE OF THE PROTECTION AND STA	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 706.324	124 Uni	t 5 3	80	42.2	4 y13
Profite   Prof	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 716.323	3404 Uni	t 5 3	80	42.2	4 b12
Performing processes   LINNOVE (CAN alsystation) ADMONTED TEDPEAN   1306.558503 Unit   75.87596 Unit   5   30   42.2   4.74	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 744.834	136 Uni	t 5 3	80	42.2	4 b13
INTENDICATION   INTENDICATION   1906   1905   1906   142   14   14   14   14   14   14   1	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 756.367	'515 Uni	t 5 3	80	42.2	4 b6
INTENDMENTING   CONTROL	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 763.837	'596 Uni	t 5 3	80	42.2	4 y14
MINONE   M	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 775.346	839 Uni	t 5 3	80	42.2	4 y7
	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 795.357	'976 Uni	t 5 3	80	42.2	4 b14
SIN-1	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 799.356	153 Uni	t 5 3	80	42.2	4 y15
SEP-1   LICPMASPOCLIPWTR   \$33.96845 Unit   \$42.79778 Unit   \$5   \$80   \$2.9   \$4.79	retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFTDTEDPAK	1306.585803	Unit 855.435	929 Uni	t 5 3	80	42.2	4 b7
Set 1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 393.237	'056 Uni	t 5 3	80	25.9	4 y6
Set	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 421.747	787 Uni	t 5 3	80	25.9	4 y7
Sept   LIGHMASPOGLIPVTR	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 433.224	1342 Uni	t 5 3	80	25.9	4 b9
Sept   LIGHMASPROGIPMTR	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 461.735	074 Uni	t 5 3	80	25.9	4 b10
Set 1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 462.245	943 Uni	t 5 3	80	25.9	4 y3
Selicia   LEPMASPPOLIPWTR   \$35,94854 Unit   \$15,82770 Unit   \$ 0	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 479.261	.259 Uni	t 5 3	80	25.9	4 y8
Sale-1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 495.292	.559 Uni	t 5 3	80	25.9	4 b5
Soli-1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 518.277	'106 Uni	t 5 3	80	25.9	4 b11
Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         55.3050 Unit         50.300         25.9         4 ylo           Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         57.4319138 Unit         5         380         25.9         4 yl1           Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         60.52227 Unit         5         380         25.9         4 yl1           Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         62.3 45827 Unit         5         380         25.9         4 yl3           Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         63.34876 Unit         53         380         25.9         4 yl7           Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         67.34877 Unit         5         380         25.9         4 yl2           Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         67.32877 Unit         5         380         25.9         4 yl2           Sa1-1         LLGPNASPDGLIPWTR         88.3 964854 Unit         71.62878 Unit         71.2270058 Unit         5         380         25.9         4 yl3           Sa1-1         LLGPNASPDGLIPWTR         89.3523930 Unit         71.62870 Unit         75.23800 Unit         75.2370 Unit         75.2380 Uni	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 527.787	'641 Uni	t 5 3	80	25.9	4 y9
Sa-1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 559.298	3707 Uni	t 5 3	80	25.9	4 y4
Sat-1   LICPMASPOGLIWTR   83,364854 unt   574,819.18 unt   5   380   25,9   4 11	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 566.329	673 Uni	t 5 3	80	25.9	4 b6
Sale	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 571.303	655 Uni	t 5 3	80	25.9	4 y10
Sale   LIGPNASPOCIPWTR	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 574.819	138 Uni	t 5 3	80	25.9	4 b12
Sal-1   LIGPNASPOGLIPWTR	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 606.822	212 Uni	t 5 3	80	25.9	4 y11
Sal-1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 623.34	1552 Uni	t 5 3	80	25.9	4 b13
Sal-1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 653.361	.701 Uni	t 5 3	80	25.9	4 b7
Stat-1         LLGPNASPDGLIPWTR         85.9 64854 Unit         712.3700S Unit         5         380         25.9         4 yi3           Stat.1         LLGPNASPDGLIPWTR         853.964854 Unit         716.385176 Unit         5         380         25.9         4 b7           TGFRR3         LLDPGALPALCNPPIR         899.532903 Unit         367.078662 Unit         5         380         27.6         4 y6           TGFRR3         LLDPGALPALCNPPIR         899.532903 Unit         392.24456 Unit         5         380         27.6         4 y8           TGFRR3         LLDPGALPALCNPPIR         899.532903 Unit         392.4456 Unit         5         380         27.6         4 y8           TGFRR3         LLDPGALPALCNPPIR         899.532903 Unit         492.74456 Unit         5         380         27.6         4 y8           TGFRR3         LLDPGALPALCNPPIR         899.532903 Unit         492.706984 Unit         5         380         27.6         4 y8           TGFRR3         LLDPGALPALCNPPIR         899.532903 Unit         452.706928 Unit         5         380         27.6         4 y8           TGFRR3         LLDPGALPALCNPPIR         899.532903 Unit         452.76625 Unit         5         380         27.6         4 y6 <t< td=""><td>Stat-1</td><td>LLGPNASPDGLIPWTR</td><td>853.964854</td><td>Unit 663.843</td><td>8676 Uni</td><td>t 5 3</td><td>80</td><td>25.9</td><td>4 y12</td></t<>	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 663.843	8676 Uni	t 5 3	80	25.9	4 y12
Stat-1	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 672.382	.771 Uni	t 5 3	80	25.9	4 y5
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         340.702514 Unit         5         380         27.6         4 b7           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         362.708662 Unit         5         380         27.6         4 y6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         385.25578 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         419.250694 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         445.770928 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         445.770928 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         455.286411 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         455.286411 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         452.308544 Unit         5         380         27.6         4 y4	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 712.370	058 Uni	t 5 3	80	25.9	4 y13
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         38.2,78662 Unit         5         380         27.6         4 y6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         387.245456 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         419.256694 Unit         5         380         27.6         4 y7           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         445.70928 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         445.769251 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         445.769251 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         481.29854 Unit         5         380         27.6         4 y4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         481.29854 Unit         5         380         27.6         4 y4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.2933 Unit         503.2933 Unit         503.2933 Unit         503.80	Stat-1	LLGPNASPDGLIPWTR	853.964854	Unit 716.385	176 Uni	t 5 3	80		4 b14
TGFBR3 IILDPGALPALQNPPIR 899.532903 Unit 385.25578 Unit 5 380 27.6 4 y3 1 GFBR3 IILDPGALPALQNPPIR 899.532903 Unit 397.244546 Unit 5 380 27.6 4 b8 1 UDPGALPALQNPPIR 899.532903 Unit 419.250694 Unit 5 380 27.6 4 b8 1 UDPGALPALQNPPIR 899.532903 Unit 45.50694 Unit 5 380 27.6 4 y7 1 GFBR3 IILDPGALPALQNPPIR 899.532903 Unit 45.77028 Unit 5 380 27.6 4 b9 1 UDPGALPALQNPPIR 899.532903 Unit 45.77028 Unit 5 380 27.6 4 b9 1 UDPGALPALQNPPIR 899.532903 Unit 45.78261 Unit 5 380 27.6 4 b4 10 10 10 10 10 10 10 10 10 10 10 10 10	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 340.702	2514 Uni	t 5 3	80	27.6	4 b7
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         397.244546 Unit         5         380         27.6         4 b8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         449.70928 Unit         5         380         27.6         4 b9           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         454.769251 Unit         5         380         27.6         4 b9           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         454.769251 Unit         5         380         27.6         4 b4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         451.2586411 Unit         5         380         27.6         4 b4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         481.289485 Unit         5         380         27.6         4 b1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         482.308544 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         537.831517 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         557.83157 Unit         5         380         27.6         4 y1	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 362.708	8662 Uni	t 5 3	80	27.6	4 y6
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         419.250694 Unit         5         380         27.6         4 y7           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         445.770928 Unit         5         380         27.6         4 b9           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         457.69251 Unit         5         380         27.6         4 b4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         452.286411 Unit         5         380         27.6         4 b4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         481.289485 Unit         5         380         27.6         4 b1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         482.398544 Unit         5         380         27.6         4 y6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.295633 Unit         5         380         27.6         4 y6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         552.339175 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.336652 Unit         5         380         27.6         4 y1	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 385.25	578 Uni	t 5 3	80	27.6	4 y3
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         445.770928 Unit         5         380         27.6         4 b9           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         452.7669251 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         452.28641 Unit         5         380         27.6         4 b1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         481.289485 Unit         5         380         27.6         4 b10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         481.289485 Unit         5         380         27.6         4 y4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.295633 Unit         5         380         27.6         4 y4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.295635 Unit         5         380         27.6         4 b1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.83765 Unit         5         380         27.6         4 b5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.356222 Unit         5         380         27.6         4 y5	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 397.244	1546 Uni	t 5 3	80	27.6	4 b8
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         454.769251 Unit         5         380         27.6         4 y8           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         455.286411 Unit         5         380         27.6         4 bd           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         482.308544 Unit         5         380         27.6         4 y0           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.295633 Unit         5         380         27.6         4 y0           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.295633 Unit         5         380         27.6         4 y0           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.295633 Unit         5         380         27.6         4 b1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         552.339175 Unit         5         380         27.6         4 b5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.336652 Unit         5         380         27.6         4 y1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356222 Unit         5         380         27.6         4 y5	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 419.250	694 Uni	t 5 3	80	27.6	4 y7
TGFBR3	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 445.770	928 Uni	t 5 3	80	27.6	4 b9
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         481.289485 Unit         5         380         27.6         4 b10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         452.308544 Unit         5         380         27.6         4 y4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         53.295633 Unit         5         380         27.6         4 y9           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         557.831517 Unit         5         380         27.6         4 b11           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         552.339175 Unit         5         380         27.6         4 b5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.837665 Unit         5         380         27.6         4 y10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356222 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         596.351471 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         601.860806 Unit         5         380         27.6         4 b12	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 454.769	251 Uni	t 5 3	80	27.6	4 y8
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         482.308544 Unit         5         380         27.6         4 y4           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         503.295633 Unit         5         380         27.6         4 y9           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         538.31517 Unit         5         380         27.6         4 b1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.837665 Unit         5         380         27.6         4 y10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.837665 Unit         5         380         27.6         4 y10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356222 Unit         5         380         27.6         4 y1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356222 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         601.860860 Unit         5         380         27.6         4 b12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b12	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 455.286	411 Uni	t 5 3	80	27.6	4 b4
TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         503.295633 Unit         5         380         27.6         4 y9           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         537.831517 Unit         5         380         27.6         4 b11           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         552.339175 Unit         5         380         27.6         4 b15           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         559.837665 Unit         5         380         27.6         4 y10           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         595.35665 Unit         5         380         27.6         4 y11           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         596.351471 Unit         5         380         27.6         4 y5           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         699.350650 Unit         5         380         27.6         4 b12           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b12           TGFBR3         ILLDFGALPALQNPPIR         899.532903 Unit         623.8606954 Unit         5         380         27.6         4 b12<	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 481.289	485 Uni	t 5 3	80	27.6	4 b10
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         537.831517 Unit         5         380         27.6         4 b11           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         552.339175 Unit         5         380         27.6         4 b5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.837665 Unit         5         380         27.6         4 y10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356222 Unit         5         380         27.6         4 y1           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         596.351471 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         601.860806 Unit         5         380         27.6         4 b12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 y12 <td>TGFBR3</td> <td>ILLDPGALPALQNPPIR</td> <td>899.532903</td> <td>Unit 482.308</td> <td>8544 Uni</td> <td></td> <td></td> <td></td> <td>•</td>	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 482.308	8544 Uni				•
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         552.339175 Unit         5         380         27.6         4 b5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.837665 Unit         5         380         27.6         4 y10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356222 Unit         5         380         27.6         4 y11           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356121 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         601.860860 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         623.866954 Unit         5         380         27.6         4 b6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.689938 Unit         5         380         19.9	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 503.295	633 Uni	t 5 3	80	27.6	4 y9
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         559.837665 Unit         5         380         27.6         4 y10           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         595.356222 Unit         5         380         27.6         4 y11           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         596.351471 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         601.860806 Unit         5         380         27.6         4 b12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         623.866954 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPIR         899.532903 Unit         658.88227 Unit         5         380         27.6         4 b13           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.689938 Unit         5         380         19.9	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 537.831	.517 Uni				
TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 595.356222 Unit 5 380 27.6 4 y11 TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 596.351471 Unit 5 380 27.6 4 y5 TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 601.860806 Unit 5 380 27.6 4 b12 TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 609.360639 Unit 5 380 27.6 4 b12 TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 609.360639 Unit 5 380 27.6 4 b6 TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 623.866954 Unit 5 380 27.6 4 y12 TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 658.88227 Unit 5 380 27.6 4 y12 TGFBR3 ILLDPGALPALQNPPIR 899.532903 Unit 658.88227 Unit 5 380 27.6 4 b13 VEGF-A HLFVQDPQTC[IAA alkylation]K 686.837536 Unit 370.689938 Unit 5 380 19.9 4 b6 VEGF-A HLFVQDPQTC[IAA alkylation]K 686.837536 Unit 374.668346 Unit 5 380 19.9 4 b5 VEGF-A HLFVQDPQTC[IAA alkylation]K 686.837536 Unit 398.218666 Unit 5 380 19.9 4 b3 VEGF-A HLFVQDPQTC[IAA alkylation]K 686.837536 Unit 398.218666 Unit 5 380 19.9 4 b3	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 552.339	175 Uni				4 b5
TGFBR3         ILLDPGALPALQNPPIR         899.332903 Unit         596.351471 Unit         5         380         27.6         4 y5           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         601.860806 Unit         5         380         27.6         4 b12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         623.866954 Unit         5         380         27.6         4 y12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         652.866954 Unit         5         380         27.6         4 y12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         652.866954 Unit         5         380         27.6         4 y12           TGFBR3         ILLPGALPALQNPPIR         899.532903 Unit         658.837536 Unit         5         380         27.6         4 b13           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.68938 Unit         5         380         19.9         4 b6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 559.837	'665 Uni		80		4 y10
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         601.860806 Unit         5         380         27.6         4 b12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         623.866954 Unit         5         380         27.6         4 y12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         658.88227 Unit         5         380         27.6         4 b13           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.689938 Unit         5         380         19.9         4 b6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         374.668346 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         408.19131 Unit         5         380         19.9         4 b3	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 595.356	222 Uni		80	27.6	4 y11
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         609.360639 Unit         5         380         27.6         4 b6           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         623.866954 Unit         5         380         27.6         4 y12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         658.88227 Unit         5         380         27.6         4 b13           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.689938 Unit         5         380         19.9         4 b6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         374.668346 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         408.191131 Unit         5         380         19.9         4 y3	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 596.351	.471 Uni		80	27.6	4 y5
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         623.866954 Unit         5         380         27.6         4 y12           TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         658.88227 Unit         5         380         27.6         4 b13           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.689938 Unit         5         380         19.9         4 b6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         374.668346 Unit         5         380         19.9         4 y6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         408.19113 Unit         5         380         19.9         4 b3	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 601.860	)806 Uni	t 5 3	80		4 b12
TGFBR3         ILLDPGALPALQNPPIR         899.532903 Unit         658.88227 Unit         5         380         27.6         4 b13           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.689938 Unit         5         380         19.9         4 b6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         374.668346 Unit         5         380         19.9         4 y6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         408.191131 Unit         5         380         19.9         4 y3	TGFBR3	ILLDPGALPALQNPPIR	899.532903	Unit 609.360	639 Uni	t 5 3	80	27.6	4 b6
VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         370.689938 Unit         5         380         19.9         4 b6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         374.668346 Unit         5         380         19.9         4 y6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         408.191131 Unit         5         380         19.9         4 y3		ILLDPGALPALQNPPIR	899.532903	Unit 623.866	954 Uni	t 5 3	80	27.6	4 y12
VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         374.668346 Unit         5         380         19.9         4 y6           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         408.191131 Unit         5         380         19.9         4 y3									
VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         398.218666 Unit         5         380         19.9         4 b3           VEGF-A         HLFVQDPQTC[IAA alkylation]K         686.837536 Unit         408.191131 Unit         5         380         19.9         4 y3	VEGF-A		686.837536	Unit 370.689	938 Uni				4 b6
VEGF-A HLFVQDPQTC[IAA alkylation]K 686.837536 Unit 408.191131 Unit 5 380 19.9 4 y3									•
VEGF-A HLFVQDPQTC[IAA alkylation]K 686.837536 Unit 419.21632 Unit 5 380 19.9 4 b7		· · · · · · · · · · · · · · · · · · ·	686.837536	Unit 408.191	.131 Uni		80		•
	VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 419.21	.632 Uni	t 5 3	80	19.9	4 b7

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell Fragme	tor Collision Energy	Cell Accelera	tor \ Ion Name
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 438.697634	Unit 5	380	19.9	4 y7
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 483.245609	Unit 5	380	19.9	4 b8
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 488.231841	Unit 5	380	19.9	4 y8
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 497.28708	Unit 5	380	19.9	4 b4
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 533.769448	Unit 5	380	19.9	4 b9
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 536.249708	Unit 5	380	19.9	4 y4
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 561.766048	Unit 5	380	19.9	4 y9
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 613.784772	Unit 5	380	19.9	4 b10
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 618.30808	Unit 5	380	19.9	4 y10
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 625.345657	Unit 5	380	19.9	4 b5
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 633.302472	Unit 5	380	19.9	4 y5
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 740.3726	Unit 5	380	19.9	4 b6
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 748.329415	Unit 5	380	19.9	4 y6
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 837.425364	Unit 5	380	19.9	4 b7
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536	Unit 876.387993	Unit 5	380	19.9	4 y7